

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 16, 2001, 17:52:55 ; Search time 101.07 Seconds
(without alignments)
332.373 Million cell updates/sec

Title: US-09-488-265-31_COPY_27_467
Perfect score: 2342
Sequence: 1 NSHSCDTVDGQYQCFPEISH.....DVEGLSFARSGNWECEFA 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1810	77.3	467	1 JN0889	3-phytase (EC 3.1.1)
2	1806	77.1	467	1 JN0656	3-phytase (EC 3.1.1)
3	1787	76.3	441	1 JN0482	3-phytase (EC 3.1.1)
4	394	16.8	467	1 PABYC	acid phosphatase (
5	391	16.7	467	1 PABYCC	acid phosphatase (
6	388	16.6	467	2 S33476	acid phosphatase (
7	388	16.6	467	2 S48996	acid phosphatase (
8	369	15.8	468	2 S52495	acid phosphatase h
9	360.5	15.4	479	1 JN0715	3-phytase (EC 3.1.1)
10	354.5	15.1	479	1 JN0890	acid phosphatase (
11	345.5	14.8	468	2 J04285	acid phosphatase (
12	328	14.0	453	2 A25326	acid phosphatase (
13	311.5	13.3	463	2 T39929	thiamin-repressibl
14	303.5	13.0	463	2 S14119	acid phosphatase (
15	153	6.5	465	2 J03069	histidine acid pho
16	149.5	6.4	468	2 A86233	hypothetical prote
17	142	6.1	755	2 T19118	acid phosphatase h
18	130	5.6	449	2 T15933	hypothetical prote
19	127.5	5.4	423	2 A33395	acid phosphatase (
20	118.5	5.1	421	2 S14742	acid phosphatase (
21	118	5.0	380	2 T16883	hypothetical prote
22	115.5	4.9	381	2 JH0152	acid phosphatase (
23	114.5	4.9	423	1 S06167	acid phosphatase (
24	109.5	4.7	730	2 T16455	acid phosphatase (
25	107	4.6	354	2 T21241	hypothetical prote
26	103.5	4.4	602	2 A36715	hypothetical prote
27	102.5	4.4	1225	2 T16346	exo-poly-alpha-gal
28	102	4.4	452	2 T20556	hypothetical prote
29	101.5	4.3	413	2 JN0889	glucose-1-phosphat

30	101.5	4.3	413	2	B85636	periplasmic glucos
31	101	4.3	408	2	T20893	hypothetical prote
32	100.5	4.3	630	2	T77346	hypothetical prote
33	99.5	4.2	642	2	E69144	probable formate C
34	99	4.2	385	1	JH0610	acid phosphatase (
35	99	4.2	438	2	S64682	acid phosphatase (
36	98	4.2	844	2	T37690	hypothetical prote
37	97.5	4.2	693	1	S61067	homoacnitase hydr
38	97	4.1	464	2	H82928	ATP synthase beta
39	97	4.1	776	1	H69430	probable formate C
40	96.5	4.1	1433	2	A71444	probable LFR retro
41	96	4.1	721	2	T27570	hypothetical prote
42	95.5	4.1	609	1	KSPSCY	copper resistance
43	95.5	4.1	1052	2	T00067	hypothetical prote
44	95	4.1	537	2	S54770	secreted acid phos
45	95	4.1	886	2	T46726	secreted acid phos

ALIGNMENTS

RESULT 1
JN0889
3-phytase (EC 3.1.3.8) A precursor - Aspergillus awamori
N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein
C:Species: Aspergillus awamori
C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999
C:Accession: JN0889
R:Piddington, C.S.; Houston, C.S.; Palohelmo, M.; Cantrell, M.; Miettinen-Oinonen, A.
Gene 133, 55-62, 1993
A:Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-op
A:Reference number: JN0889; MUID:94040796
A:Accession: JN0889
A:Molecule type: DNA
A:Residues: 1-467 <PID>
A:Cross-references: GB:L02421; NID:gl66518; PIDN:AAA1698.1; PID:gl66519
A:Experimental source: strain ALK0243
A:Note: part of the sequence, including the amino end of the mature protein, was conf
C:Comment: This enzyme catalyzes the conversion of phytate to inositol and inorganic
C:Genetics:
A:Gene: phyA
A:Introns: 15/2
C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-467/Product: 3-phytase A #status experimental <MAT>
F:27,59,105,120,207,230,339,352,376,388/Binding site: carbohydrate (Asn) (covalent) #
F:81,361/Active site: Arg, His #status predicted
F:82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 77.3%; Score 1810; DB 1; Length 467;
Best Local Similarity 76.0%; Pred. No. 6.3e-137;
Matches 335; Conservative 40; Mismatches 66; Indels 0; Gaps 0;

QY	1	NSHSCDTVDGQYQCFPEISHLWGYSPPFSLADESAISPDVPGKCRVTFVQVLSRHGARY 60	
Db	27	NOSTCDTVDGQYQCFSESHLWGQYAPFSLANESAISSPDVPGKCRVTFVQVLSRHGARY 86	
QY	61	PTSSASKAYSALIEIAIOKNAFAKGYAFKLYNTLTGADLTTPFGQQWVNSGINKFYRR 120	
Db	87	PTESGKKYSALIEIQONVTFDGKFAFLKTYNSUGADLTTPFGQELVNSGINKFYQR 146	
QY	121	YKALARKTVPIRSGSDRVIASAEKTFEGFSAKLADPGANPHQASPVINVIPEGAGY 180	
Db	147	YESLTRNIPPIRSGSSRVIASGEKTFEGFSQTKLKDPRAPQSQSPKIDVVISASS 206	
QY	181	NNTLDHGLCTAFESESGDDVEANFTAVFAPPTRARLEAHLPGVNLTDDEVNLMDCSF 240	
Db	207	NNTLDPGTCVFESELEADTVANFTATFAPSIRQLENDLSGVTLTDEVTYLMDCSF 266	
QY	241	DTVARTSDATQLSPFCDLFTHDEWIOYDYQLQSLGKYGYGAGNPLGPAQGVGFVNELIAR 300	

Thu Oct 18 11:34:55 2001

Db 267 DTISTVDTKLSPPCDLFTTHDEWIHYDYLQSLKKYKYGAGNPLGPTQGVYANELLAR 326

Qy 301 LTHSPVQDHTSTNHTLDSNPATPLNATLYADFSHDNTMVSIFFFALGLYNGTKPLSTTSV 360

Db 327 LTHSPVHDDTSSNHTLDSNPATPLNATLYADFSHDNGIISILFALGLYNGTKPLSTTIV 386

Qy 361 ESIEETDGYASNTVPPFAARAYVEMMOCEAEKEPLRVLRVNDVRVPLHGGCGVDKLGCRKR 420

Db 387 ENITQTDGFSASNTVPPASRLYVEMMOCEAEKEPLRVLRVNDVRVPLHGGCPDIALGRCTR 446

Qy 421 DDFVEGLSFARSGGNWEECA 441

Db 447 DSFVRGLSFARSGGDWAECSA 467

RESULT 2

JN0656

3-phytase (EC 3.1.3.8) A precursor - Aspergillus niger

N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein

C:Species: Aspergillus niger

C:Date: 03-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999

C:Accession: JN0656; S28456

R:van Hartingsveldt, W.; van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk, M.A.M.J.

Gene 127, 87-94, 1993

A:Title: Cloning, characterization and overexpression of the phytase-encoding gene (phyA)

A:Reference number: JN0656; MUID:93252284

A:Accession: JN0656

A:Molecule type: DNA

A:Residues: 1-467 <V>

A:Cross-references: GB:216414; NID:q2392; PIDN:CAA78904.1; PID:q2393

A:Experimental source: strain NRRL3135

A:Note: parts of the sequence, including the amino end of the mature protein, were confirmed by sequencing.

C:Comment: This enzyme catalyzes the hydrolysis of phytic acid into myo-inositol and inorganic orthophosphate

C:Genetics:

A:Gene: phyA

A:Introns: 15/2

C:Superfamily: yeast acid phosphatase

C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phospho

F:24-467/Domain: signal sequence #status predicted <SIG>

F:27,59,105,120,207,230,339,352,376,388/Binding site: carboxylate (Asn) (covalent) #sta

F:81,361/Active site: Arg, His #status predicted

F:82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 77.1%; Score 1806; DB 1; Length 467;

Best Local Similarity 76.0%; Pred. No. 1.3e-136;

Matches 335; Conservative 40; Mismatches 66; Indels 0; Gaps 0;

Qy 1 NSHSCDVTGQYQCFPEISHLWGYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARY 60

Db 27 NOSSCDTVDGQYQCFSETSHLWGYAPFFSLANESVISEPVAGCRVTFVQVLSRHGARY 86

Qy 61 PTSSASKAYSALIEAIOKNATFAGKYAFKTYNTYLGADDTLPFGQOMVNSGKIFRR 120

Db 87 PTDSKGGKYSALIEEIQNATTFDGYAFKTYNYSIGADDTLPFGQELVNSGKIFRR 146

Qy 121 YKALARKIVPFIASGSDRVIAAEKFEFGQSAKLADPGANPHOASPVINVIIEGAGY 180

Db 147 YESLTRNIVPFIASGSDRVIAAEKFEFGQSAKLADPGANPHOASPVINVIIEGAGY 206

Qy 241 DTARTSDATQSPFCDLFTTHDEWIHYDYLQSLKKYKYGAGNPLGPTQGVYANELLAR 300

Db 267 DTISTVDTKLSPPCDLFTTHDEWIHYDYLQSLKKYKYGAGNPLGPTQGVYANELLAR 326

Qy 301 LTHSPVQDHTSTNHTLDSNPATPLNATLYADFSHDNTMVSIFFFALGLYNGTKPLSTTSV 360

Db 327 LTHSPVHDDTSSNHTLDSNPATPLNATLYADFSHDNGIISILFALGLYNGTKPLSTTIV 386

Qy 361 ESIEETDGYASNTVPPFAARAYVEMMOCEAEKEPLRVLRVNDVRVPLHGGCGVDKLGCRKR 420

Db 387 ENITQTDGFSASNTVPPASRLYVEMMOCEAEKEPLRVLRVNDVRVPLHGGCPDIALGRCTR 446

Qy 421 DDFVEGLSFARSGGNWEECA 441

Db 447 DSFVRGLSFARSGGDWAECSA 467

RESULT 3

JN0482

3-phytase (EC 3.1.3.8) A - Aspergillus ficuum

N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein

C:Species: Aspergillus ficuum

C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 07-May-1999

C:Accession: JN0482; PN0023

R:Ullah, A.H.J.; Dischinger Jr., H.C.

Biochem. Biophys. Res. Commun. 192, 747-753, 1993

A:Title: Aspergillus ficuum phytase: Complete primary structure elucidation by chemi

A:Reference number: JN0482; MUID:93249451

A:Accession: JN0482

A:Molecule type: protein

A:Residues: 1-441 <U>

A:Note: authors state that the 9 Asn followed by Thr or Ser after an intervening resi

R:Ullah, A.H.J.; Cummins, B.J.; Dischinger Jr., H.C.

Biochem. Biophys. Res. Commun. 178, 45-53, 1991

A:Title: Cyclohexanediol modification of arginine at the active site of Aspergillus

A:Reference number: PN0023; MUID:91298982

A:Accession: PN0023

A:Molecule type: protein

A:Residues: 48-70 <U>

C:Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phyt

C:Superfamily: yeast acid phosphatase

C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph

C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph

F:4,36,82,97,184,207,316,329,353,365/Binding site: carboxylate (Asn) (covalent) #sta

F:58,338/Active site: Arg, His #status predicted

F:59/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 76.3%; Score 1787; DB 1; Length 441;

Best Local Similarity 75.8%; Pred. No. 4e-135;

Matches 332; Conservative 40; Mismatches 66; Indels 0; Gaps 0;

Qy 1 NSHSCDVTGQYQCFPEISHLWGYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARY 60

Db 4 NOSSCDTVDGQYQCFSETSHLWGYAPFFSLANESVISEPVAGCRVTFVQVLSRHGARY 63

Qy 61 PTSSASKAYSALIEAIOKNATFAGKYAFKTYNTYLGADDTLPFGQOMVNSGKIFRR 120

Db 64 PTDSKGGKYSALIEEIQNATTFDGYAFKTYNYSIGADDTLPFGQELVNSGKIFRR 123

Qy 121 YKALARKIVPFIASGSDRVIAAEKFEFGQSAKLADPGANPHOASPVINVIIEGAGY 180

Db 124 YESLTRNIVPFIASGSDRVIAAEKFEFGQSAKLADPGANPHOASPVINVIIEGAGY 183

Qy 181 NPTLDHGLCTAFESSELGDDVEANFTAVFAPPFIRARLEAHLPGVNLTDDEYVNLMDMCP 240

Db 184 NPTLDHGLCTAFESSELGDDVEANFTAVFAPPFIRARLEAHLPGVNLTDDEYVNLMDMCP 243

Qy 241 DTARTSDATQSPFCDLFTTHDEWIHYDYLQSLKKYKYGAGNPLGPTQGVYANELLAR 300

Db 244 DTISTVDTKLSPPCDLFTTHDEWIHYDYLQSLKKYKYGAGNPLGPTQGVYANELLAR 303

Qy 301 LTHSPVQDHTSTNHTLDSNPATPLNATLYADFSHDNTMVSIFFFALGLYNGTKPLSTTSV 360

Db 304 LTHSPVHDDTSSNHTLDSNPATPLNATLYADFSHDNGIISILFALGLYNGTKPLSTTIV 363

Qy 361 ESIEETDGYASNTVPPFAARAYVEMMOCEAEKEPLRVLRVNDVRVPLHGGCGVDKLGCRKR 420

Db 364 ENITQTDGFSASNTVPPASRLYVEMMOCEAEKEPLRVLRVNDVRVPLHGGCPDIALGRCTR 423

Qy 421 DDFVEGLSFARSGGNWEECA 438

Db 423 DYAEKRVAGCTDFLK 436

RESULT 6
S53476
acid phosphatase (EC 3.1.3.2) precursor - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YAR071w
C:Species: Saccharomyces cerevisiae
C>Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Apr-2000
C:Accession: S53476; JCI018
R:Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Ka
submitted to the EMBL Data Library, February 1994
A:Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of th
A:Reference number: S53458
A:Accession: S53476
A:Molecule type: DNA
A:Residues: 1-467 <BAJ1>
A:Cross-references: EMBL:L28920; NID:g1616966; PIDN:AA09508.1; PID:g456155; MIPS:YAR
R:Chen, J.Y.; Gong, Y.; Ao, S.Z.
Acta Biochim. Biophys. Sin. 21, 437-444, 1989
A:Title: The primary structure of acid phosphatase gene PHO1 in S. cerevisiae and co
A:Reference number: JCI018
A:Accession: JCI018
A:Molecule type: DNA
A:Residues: 1-16, 'L', 18-149, 'H', 151-353, 'Q', 355-422, 'G', 424-467 <CHE>
A:Note: this paper is in Chinese, with an English abstract
C:Genetics:
A:Gene: SGD:PHO1
A:Cross-references: SGD:S0000094; MIPS:YAR071w
A:Map position: 1R
C:Superfamily: yeast acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydr
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-467/Product: acid phosphatase #status predicted <MAT>
F:74/Active site: Arg #status predicted
F:75/Active site: His (phosphohistidine intermediate) #status predicted
F:97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 16.6%; Score 388; DB 2; Length 467;
Best Local Similarity 26.1%; Pred. No. 3,3e-23;
Matches 116; Conservative 62; Mismatches 194; Indels 72; Gaps 13;
QY 17 EISHLWGTSPEFLADESAISPDVPGKCRVTFVQVLSRHGARYPTSSASKAYSALIEAI 76
DB 36 EIPFPGSGPIPGDYGISRDLPESCENKQVQVGRHGERPTVSKAKSINTTWYKL 95
QY 77 QKNATAFKGYAFK-----TNYTL-----GADLTFF-GEQMVNSGKFEYR 120
DB 96 SNYTGSGALSFNDYEFFIRDTKLEMETTLANSVNLNPTGEMNAKRHRDFAQ 155
QY 121 YKALARKIVPF-IRASGSDRVITASAEKFTFGQSAKLADPGANPHQASPVINVI----- 174
DB 156 YGVNVENQTSFAVFTSNRCHDTAQYFDG-----LGDK-----FNISLQITSE 200
QY 175 PEGAGVNTLDHGLCTAFEESELGDDVEANFTAVFAPPFIRARLEAHLPGVNLTDVNNL 234
DB 201 AESAGANTLSAHSCPAWDD-DVNDLILKYDTKYLSGLAKRLNKENGLNLTSSDANTE 259
QY 235 MDMCPFTVARTSDATQISPFCDLFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFV 294
DB 260 FAWCAVEINAR-----GYSDICNIFTKDELVRFSYQDLETYYQTGPGDVVRSVGNLF 314
QY 295 NELLIALTHSPVDHTSTNHTLDSNPATFPLNATLYADFSDHNTMTVSIFFFALGLVNGTKP 354
DB 315 NASVKLLKESEVQQ-----KWLSFTHTDILNLTITIGIIDDKN 356
QY 355 LSTTSVESIETDGYASWTVPFAARAYVEMMOCEAKEPELVRLVNDVRVPLHCGVDK 414
DB 357 LTAHVFPMENT--FHRSWVYVPOGARVYTEKFCQ--SNDTYRVYVINDAVVPIETCSTGCP 412
QY 415 LGRCKRDF-----VEGLSEAR 431

A:Residues: 1-467 <MAN>
A:Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g476050
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R:Feldmann, H.; Mannhaupt, G.; Schwarzlöse, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45927
A:Accession: S45960
A:Molecule type: DNA
A:Residues: 1-467 <FE2>
A:Cross-references: EMBL:Z35961; NID:g536362; PIDN:CAA85045.1; PID:g536363; GSPDB:GN0000
R:Balwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A:Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A:Reference number: S05794; MUID:85037940
A:Accession: S05794
A:Molecule type: DNA
A:Residues: 1-218, 'MKT', 222-467 <BAJ1>
A:Cross-references: EMBL:X01080; NID:g41148; PIDN:CAA25557.1; PID:g758281
A:Note: the authors translated the codon AAT for residue 134 as Asp and TAC for residue
R:Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Phill, C
Mol. Cell. Biol. 6, 1855-1865, 1986
A:Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within
A:Reference number: A93074; MUID:87064474
A:Accession: A25241
A:Molecule type: DNA
A:Residues: 1-44 <TAI>
C:Genetics:
A:Gene: SGD:PHO3; MIPS:YBR092C
A:Cross-references: SGD:S0000296; MIPS:YBR092C
A:Map position: 2R
C:Superfamily: yeast acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrol
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-467/Product: acid phosphatase, constitutive #status predicted <MAT>
F:75/Active site: His (phosphohistidine intermediate) #status predicted
F:97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (coval
F:337/Active site: His #status predicted

Query Match 16.7%; Score 391; DB 1; Length 467;
Best Local Similarity 27.0%; Pred. No. 1.9e-23;
Matches 117; Conservative 61; Mismatches 192; Indels 64; Gaps 13;
QY 23 GTSYSPFSLADESAISPDVPGKCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATA 82
DB 42 GGAGPYSPFGDYGISRDLPESCENKQVQVGRHGERPTVSKGATIMKTWYKLSNTRQ 101
QY 83 FKGYAFK-TYNYTLGADD-----LTPF-GEQMVNSGKFEYRYKALAR 126
DB 102 FNGSLFNDYEFFIRDDLEMETTFEANSNDVNLNPTGEMDAKRHRAREFAQGYMFE 161
QY 127 KIVPF-IRASGSDRVITASAEKFTFGQSAKLADPGANPHQASPVINVIPEAGYNNLTD 185
DB 162 NOTSFPIFAASERVHDTAQYFDGL-----GQFNISLQITSEAMSAGA---NTLS 210
QY 186 HG-LCTAFEESELGDDVEANFTAVFAPPFIRARLEAHLPGVNLTDVNNLMDMCPFTVTA 244
DB 211 AGNACPGWDE-DANDDILDKYDTYLDLDAKRLNKENKGLNLTSDANTLFAMCAYELNA 269
QY 245 RTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVFNELIARLTHS 304
DB 270 R-----GYSDVCDITFDELVRYSYQDLSFYQDGPYDMIRSVGANLFNATLKLKQOS 324
QY 305 PVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMTVSIFFFALGLVNGTKPLSTSESTE 364
DB 325 ETQD-----LKVLSFTHTDILNLTITIGIIDDKNLTAEXYVPMG 366
QY 365 ETDGYSASWTVPFAARAYVEMMOCEAKEPELVRLVNDVRVPLHCGVDKLRCKRDF- 423
DB 367 NT--PHKSWYVPOGARVYTEKFCQ--SNDTYRVYVINDAVVPIETCSTGPGFSCINDFY 422
QY 424 -----VEGLSEAR 431

A:Reference number: JN0715; MUID:93371452
A:Accession: JN0715
A:Molecule type: DNA
A:Residues: 1-479 <EHR>
A:Cross-references: GB:L20567
A:Accession: P00594
A:Molecule type: protein
A:Residues: 20-101;133-146;376-399 <EH2>
R:Ullah, A.H.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 192, 754-759, 1993
A:Title: Identification of active-site residues in Aspergillus ficuum extracellular pH 2
A:Reference number: P00460; MUID:93249452
A:Accession: P00460
A:Molecule type: protein
A:Residues: 65-66,68-93 <ULL>
A:Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.3.2), hy
C:Genetics:
A:Gene: phbB
A:Introns: 261/1; 300/2; 335/2
C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-479/Product: 3-phytase #status experimental <MAT>
F:81,337/Active site: Arg, His #status predicted
F:82/Active site: His (phosphohistidine intermediate) #status predicted
F:106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match 15.1%; Score 354.5; DB 1; Length 479;
Best Local Similarity 27.9%; Pred. No. 1.6e-20;
Matches 117; Conservative 53; Mismatches 159; Indels 91; Gaps 15;

QY 23 GTYSPFSLADESAISPDVPGKGRVTFVQVLSRHGARYPTSSASK-AYSALIEAIQKNAT 81
Db 53 GPYSERVSY----GIARDPTSCVDQVIMVKRHRGERSPSAGKDIEEALAKVYSINTT 108
QY 82 AFKGYAFLKTYNTL-----GADDLT-PF-GEQMVNSGKIFRYRYKAL--ARKIVPF 131
Db 109 EYKGDIAFLNDWTYYVFNCEYNAETTSFYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168
QY 132 IRASGSDRVITASAEKFTIEGFSQAKLADPGANPHQASPVINVIPEGAGYNNITLDHGLCTA 191
Db 169 F-SSGGRVETARKEGEGF-----FGYNSYNAALNII 201
QY 192 FESEELG-----DDVEANFTAVFAPPPIR---ARLEAHLPGVNLTDDEVNLM 236
Db 202 SESEVMGADSLTPTCDTNDQTTCDNLTYLPQFKVAAARLNSQNPGLMTASDVYNLMV 261
QY 237 MCPFDTVARTSDATQLSPFCDLTFHDEWIQDYLSGLGKYGYGAGNPLGPAQGVGFVNE 296
Db 262 MASFELNAR-----PFSNWINAFTQDEWVSFGYVEDLNYYICAGPGDKNMAAVGAYANA 316
QY 297 LIARLTHSPVQDHTSTNHTLDSNPATPPLNATLYADFSDNTMVSIFFALGLY--NGTRP 354
Db 317 SLTLNQGPK-----AGSLFFENFAHDTNITPILAAALGVLPINEDLP 358
QY 355 LSTTSVESIETDGYASWTVPFAARAYVEMMOCEA-----EKEPLRVLVNDRVPLHGC 410
Db 359 L-----DRVAFGNPYSIGNIVPMGGHLLTIERLSQATALSDEGTIVRLVNEAVLPFND 413

RESULT 11
JC4285
acid phosphatase (EC 3.1.3.2) precursor - yeast (Pichia pastoris)
N:Alternate names: orthophosphoric-monoester phosphohydrolase (acid optimum); Pho
C:Species: Pichia pastoris
C:Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 29-Oct-1999
C:Accession: JC4285
R:Payne, W.E.; Gannon, P.M.; Kaiser, C.A.
Gene 163, 19-26, 1995
A:Title: An inducible acid phosphatase from the yeast Pichia pastoris: Characterizati
A:Reference number: JC4285; MUID:96001238
A:Accession: JC4285
A:Molecule type: DNA
A:Residues: 1-468 <PAY>
A:Cross-references: GB:U28658; NID:g881955; PIDN:AAA85503.1; PID:g881956
A:Experimental source: GS115
C:Genetics:
A:Gene: pho1
C:Superfamily: yeast acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydr
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-468/Product: acid phosphatase #status predicted <MAT>
F:84/Active site: His (phosphohistidine intermediate) #status predicted
F:163,196,256,321,360,453/Binding site: carbohydrate (Asn) (covalent) #status predict

A:Reference number: JN0715; MUID:93371452
A:Accession: JN0715
A:Molecule type: DNA
A:Residues: 1-479 <EHR>
A:Cross-references: GB:L20567
A:Accession: P00594
A:Molecule type: protein
A:Residues: 20-101;133-146;376-399 <EH2>
R:Ullah, A.H.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 192, 754-759, 1993
A:Title: Identification of active-site residues in Aspergillus ficuum extracellular pH 2
A:Reference number: P00460; MUID:93249452
A:Accession: P00460
A:Molecule type: protein
A:Residues: 65-66,68-93 <ULL>
A:Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.3.2), hy
C:Genetics:
A:Gene: phbB
A:Introns: 261/1; 300/2; 335/2
C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phos
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-479/Product: 3-phytase #status experimental <MAT>
F:81,337/Active site: Arg, His #status predicted
F:82/Active site: His (phosphohistidine intermediate) #status predicted
F:106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match 15.4%; Score 360.5; DB 1; Length 479;
Best Local Similarity 28.3%; Pred. No. 5.4e-21;
Matches 119; Conservative 53; Mismatches 157; Indels 91; Gaps 16;

QY 23 GTYSPFSLADESAISPDVPGKGRVTFVQVLSRHGARYPTSSASKAY-SALLIEAIQKNAT 81
Db 53 GPYSERVSY----GIARDPTSCVDQVIMVKRHRGERSPSAGKSIEEALAKVYSINTT 108
QY 82 AFKGYAFLKTYNTL-----GADDLT-PF-GEQMVNSGKIFRYRYKAL--ARKIVPF 131
Db 109 EYKGDIAFLNDWTYYVFNCEYNAETTSFYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168
QY 132 IRASGSDRVITASAEKFTIEGFSQAKLADPGANPHQASPVINVIPEGAGYNNITLDHGLCTA 191
Db 169 F-SSGGRVETARKEGEGF-----FGYNSYNAALNII 201
QY 192 FESEELG-----DDVEANFTAVFAPPPIR---ARLEAHLPGVNLTDDEVNLM 236
Db 202 SESEVMGADSLTPTCDTNDQTTCDNLTYLPQFKVAAARLNSQNPGLMTASDVYNLMV 261
QY 237 MCPFDTVARTSDATQLSPFCDLTFHDEWIQDYLSGLGKYGYGAGNPLGPAQGVGFVNE 296
Db 262 MASFELNAR-----PFSNWINAFTQDEWVSFGYVEDLNYYICAGPGDKNMAAVGAYANA 316
QY 297 LIARLTHSPVQDHTSTNHTLDSNPATPPLNATLYADFSDNTMVSIFFALGLY--NGTRP 354
Db 317 SLTLNQGPK-----KEAGP-----LFFNLADHTNITPILAAALGVLPINEDLP 358
QY 355 LSTTSVESIETDGYASWTVPFAARAYVEMMOCEA-----EKEPLRVLVNDRVPLHGC 410
Db 359 L-----DRVAFGNPYSIGNIVPMGGHLLTIERLSQATALSDEGTIVRLVNEAVLPFND 413

RESULT 10
JN0890
acid phosphatase (EC 3.1.3.2) precursor - Aspergillus awamori
C:Species: Aspergillus awamori
C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999
C:Accession: JN0890
R:Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; N
Gene 133, 55-62, 1993
A:Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-optim
A:Reference number: JN0889; MUID:94040796
A:Accession: JN0890
A:Molecule type: DNA

Query Match	14.0%;	Score 328;	DB 1;	Length 453;
Best Local Similarity	25.8%;	Pred. No. 2e-18;		

Query Match	13.3%	Score 311.5;	DB 2;	Length 463;
Best Local Similarity	25.3%;	Pred. No. 4.2e-17;		
Matches 113;	Conservative 69;	Mismatches 197;	Indels 67;	Gaps 15;
QY	20	HLWGTY-PPFLADEAISPDVPGKGRVTQVQLSRHGARYPTS--SASKAYSA--	71	
Db	35	HL-GTLPYHEPFDGLDSA-----FETCEIQVHLLQRHSGRNPGDMVTATDVYSQY	88	
QY	72	-----LLEATQKNATAPKGYAFUKTYNYTL---GADDLTPFGGQQVNSGIKPYRR	120	
Db	89	LNNFOEKLNGSPVNFSPYENPLCFKIQKTPVDAENADQLSSRGLRLEFLDGLRQLYQR	148	
QY	121	YKALARKIVPFIKASGSDRVIAEAKFIEGFSQAKIADPCANPHQASPVINVIPEG--A	178	
Db	149	YKLEFDSYVYDINTAEQERVESAKWFTYGLFGDKWVE-----KTFNILLSEKAA	199	
QY	179	GYANTLDHGLCTAFESSEL---GDDVEANFTVAFPPIRARLEAHL-PCVNITDEDVNN	233	
Db	200	GANLSMYNACPVFKONNFHNKATDAAHVWRNIFETPIVNRKAKYFDSYKYKLTINDVRS	259	
QY	234	LMDMCPFDVTARTSDATQISPFCDLFTHDIEWIQYDILQSLGKYGYGAGNPLGPAQGVGF	293	

T39929

thiamin-repressible acid phosphatase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T39929
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z21857
A:Accession: T39929
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-463 <L>N>
A:Cross-references: EMBL:AL023286; PIDN:CAAL8863.1; GSPDB:GN00067; SPDB:SPBC21H7
A:Experimental source: strain 972h; cosmid c21H7
C:Genetics:
A:Gene: SPDB:SPBC21H7.03c
A:Map position: 2
C:Superfamily: yeast acid phosphatase

Query Match
Best Local
Matches 11

[illegible]

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Db 260 LFYCEYEIAIKDH-----SDFCSIFPSEFLNFPEYDSDDLDQAYGGGPVSEWASTLGGAY 314
QY 294 VNELIARLTHSPVDHSTNHTLDSNPATEPLNATLYADFSDHNTMVSIFPFGALGLYNGTK 353
Db 315 INNLADSL-----RNVNPDDEK-----VFLAETHDSNIIIPVEAALGFPPDIT 358
QY 354 PLSTTSVESIEETDGYASASWTVPFAARAYVEMMOCEAEKEPLRVLVNDRVPLHGGVD 413
Db 359 PQLPLTDKNITYTSQKTSPPAGNLTLELFC-SDSKYVVRHLVNOQVYPLIDCGY 417
QY 414 KLGR-----CKRDFVEGLSFARSGN 435
Db 418 PSQSDGLCELOAYLNSPIRANSTSN 443

RESULT 14
S14119
A:Title: acid phosphatase (EC 3.1.3.2) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 10-Dec-1999
C:Accession: S14119; T40455
R:Yang, J.; Schweingruber, M.E.
Curr. Genet. 18, 269-272, 1990.
A:Title: The structural gene coding for thiamin-repressible acid phosphatase in Schizosaccharomyces pombe
A:Reference number: S14119; MUID:91064763
A:Accession: S14119
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-463 <YAN>
A:Cross-references: GB:X56939; NID:X5006; PIDN:CAAA0258.1; PID:G5007
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z21931
A:Accession: T40455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-463 <LYN>
A:Cross-references: EMBL:AL034382; PIDN:CAA22278.1; GSPDB:GN00067; SPDB:SPBC428.03C
A:Experimental source: strain 972h-; cosmid c428
C:Genetics:
A:Gene: SPBC428.03C
A:Map position: 2
A:Superfamily: yeast acid phosphatase
C:Keywords: phosphoric monoester hydrolase

Query Match 13.0%; Score 303.5; DB 2; Length 463;
Best Local Similarity 26.7%; Pred. No. 1.8e-16;
Matches 113; Conservative 63; Mismatches 184; Indels 63; Gaps 16;

QY 20 HLNGTYS-----PFFSLADESAISPDVPGKCRVTFVQVLSRHGARYPT--SSASKAYSA-- 71
Db 35 HL-GTISVHEPYF-----NGPTTSPESCAIKQVHLLQRHGSRNPTGDDTATDVSSAQY 88
QY 72 -----LIEAQKNATAFKYAPLKYNYTL---GADDLTTPFGEQOMVNSGKIFYRR 120
Db 89 IDTFQNKLLNGSIPIVNFSPENPLFYVKKHTPVKAENADQLSSSGRIELFDLGRQVPER 148
QY 121 YKALARKIVPFIIRASGSDRVASAEKFIIGFOSAKUADPGANPHQASPVINVIIEP--CA 178
Db 149 YVELFDYDVIINTAAQERVVDVSAEWSFGM-----FGDDMQNKTNF-----IVLPEDDSA 199
QY 179 GYNTLDHGLCTAFEESELDGDD--VEANFTA---VFAPPTRARLEAHL-PGVNLTDEVDVN 233
Db 200 GANSLAMYISCPYIEDNNIDNTEAHTSWRNFLKPTANRLNKYFDSGYNLTVSDVRS 259
QY 234 LMDMCPEDTIVARTSDATQLSPFCDLTFHDEWIQDYLSLGKYYGYGAGNPLGPAQGVGF 293
Db 260 LYICVVEIALRDN-----SDFCSLFTPSEFLNFPEYDSDDLDQAYGGGPVSEWASTLGGAY 314
QY 294 VNELIARLTHSPVDHSTNHTLDSNPATEPLNATLYADFSDHNTMVSIFPFGALGLYNGTK 353

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Db 315 VNNLANNL-----RKGVNNASDRK-----VFLAETHDSOIIPVEAALGFPPDIT 358
QY 354 PLSTTSVESIEETDGYASASWTVPFAARAYVEMMOCEAEKEPLRVLVNDRVPLHGGVD 413
Db 359 PQLPLTDKNITYTSQKTSPPAGNLTLELFC-SDSKYVVRHLVNOQVYPLIDCGY 417
QY 414 KLGR-----CKRDFVEGLSFARSGN 435
Db 418 PSQSDGLCELOAYLNSPIRANSTSN 443

RESULT 15
JE0369
A:Title: histidine acid phosphatase (EC 3.1.3.-) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C:Accession: JE0369
R:Mullanev, E.J.; Ullah, A.H.J.
Biochem. Biophys. Res. Commun. 251, 252-255, 1998
A:Title: Identification of a histidine acid phosphatase (phyA)-like gene in Arabidopsis
A:Reference number: JE0369; MUID:99009256
A:Accession: JE0369
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-465 <MUL>
C:Superfamily: yeast acid phosphatase
C:Keywords: phosphoric monoester hydrolase

Query Match 6.5%; Score 153; DB 2; Length 465;
Best Local Similarity 22.5%; Pred. No. 0.0002;
Matches 102; Conservative 61; Mismatches 199; Indels 92; Gaps 21;

QY 9 DGYVQCFPEISHLWGT---YSPFSLADESAISPDVPGKCRVTFVQVLSRHGARYPTSSA 65
Db 16 DGGF---DVRHLSIVTRYSTSKDVTQNLIEGNSVPSECTPIHLNLVARHGTSTRPTKKR 71
QY 66 SKAYSAL---IEAQKNATAFK-----GKYAFLKTYNYTLGADDLTPFGEQOMVN 112
Db 72 LREMESLAGRFEKELVRDAEAKLFSDKIPQWLQWK--SPWEGKVGKGLIROGEDLYQ 129
QY 113 SGIKFYPRYKALARK---IVPFIIRASGSDRVASAEKFIIGFOSAK-LADPGANPHQAS 167
Db 130 LGIKVRERFPFLFEEDYHPDVYITRATQIPRASASAVAFGMGLFSEKGNLGPGRNRAFA- 188
QY 168 PVINVIPEGAGYNNTLDHGLCTAFEESELDGDDVEANFTAFAVAPPTRARLEAHLPGVNLT 227
Db 189 -----VTSENRASTDKLRFFEC-----QNY-----KSYRKAKEPAVDKL 223
QY 228 DEVDVNLMDMC---PFDTVARTSDATQLSPFCDLTFHDEWIQDYLSLGKYYGYGAGNP 284
Db 224 KEPLNKITASVAKRYDLKFTKODISSLWFLCKQVALLEW-----TDDLEVFLKKGYS 278
QY 285 LGPAQGVGVFNELIARLTHSPVDHSTNHTLDSNPATEPLNATLYADFSDHNTMVSIFP 344
Db 279 LNYKMGVPLLEDVL---HSMEEAIKAREEKL-PGSYE-KARLA--RFAHAETIVPPFS 329
QY 345 A-LGLYNGTKPLSTTSVESIE-----ETDGYASASWTVPFAARAYVEMMOCEAE 391
Db 330 CLLGLF-----LDGSEFEKIQKEKPLELPPOPPTKTRDFRGSTMAPFGGNLILVYSPAE 384
QY 392 KEP--LYRVLVNDRVPLHGGVDKLGRCRDRDF 423
Db 385 SSPKYFVQVNLNHEPIAVPGC--DCKDFCPLDF 416

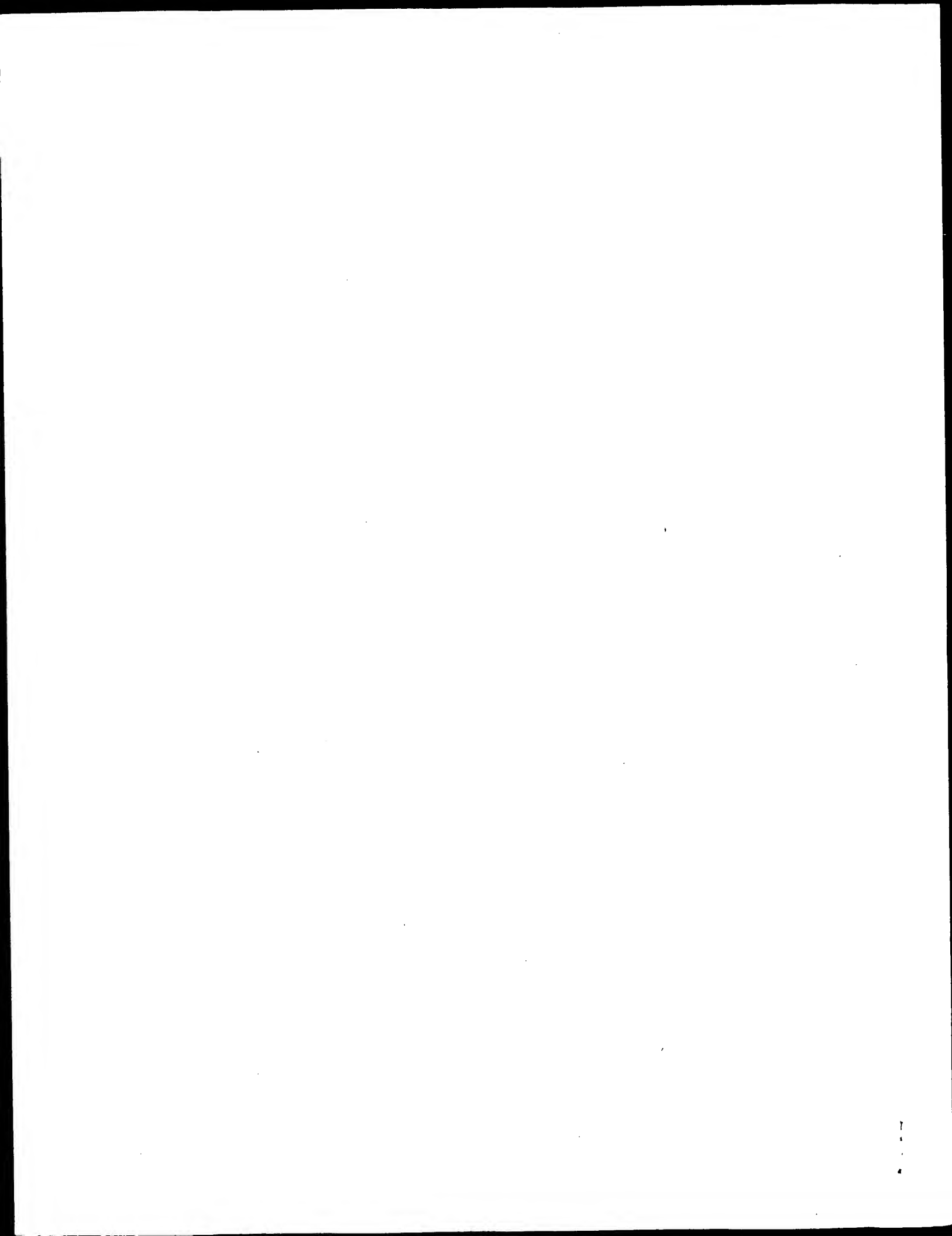
Search completed: October 16, 2001, 17:52:57
Job time: 20216 sec

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Thu Oct 18 11:34:55 2001

us-09-488-265-31_copy_27_467.rpr

Page 9



Result No.	Query No.	Query			DB	ID	Description
		Match	Length	Score			
1	1	1810	77.3	467	1	PHYA_ASAPW	P34753 aspergillus
2	2	1806	77.1	467	1	PHYA_SPNGI	P34752 aspergillus
3	3	1785.5	76.2	463	1	PHFB_EMENI	O00093 emericella
4	4	394	16.8	467	1	PPA5_YEAST	P00635 saccharomyces
5	5	391	16.7	467	1	PPA3_YEAST	P24031 saccharomyces
6	6	388	16.6	467	1	PPAB_YEAST	P35842 saccharomyces
7	7	388	16.6	467	1	PPAC_YEAST	P38693 saccharomyces
8	8	369	15.8	468	1	PPAD_YEAST	P22990 saccharomyces
9	9	362.5	15.5	479	1	PHYB_ASAPW	P34754 aspergillus
10	10	345.5	15.1	479	1	PHYB_SPNGI	P34755 aspergillus
11	11	345.5	14.8	468	1	PPAL_PICPA	P52291 pichia past
12	12	328	14.0	453	1	PPAL_SCHPO	P08091 schizosacch
13	13	328	14.0	469	1	PPA5_KLUJA	P52289 kluyveromyces
14	14	303.5	13.0	463	1	PPA2_SCHPO	O01682 schizosacch
15	15	142	6.1	755	1	PPAX_CAEPL	O09349 caenorhabdi
16	16	127.5	5.4	423	1	PPAL_RAT	P20611 rattus norv
17	17	118.5	5.1	421	1	PPAL_MOUSE	P24638 mus musculus
18	18	115.5	4.9	381	1	PPAP_RAT	P11117 homo sapien
19	19	114.5	4.9	423	1	PPAL_HUMAN	P15922 erwinia chr
20	20	103.5	4.4	602	1	PEFX_ERWCH	P19226 escherichia
21	21	101.5	4.3	413	1	AGP_ECOLI	P15309 homo sapien
22	22	99	4.2	386	1	PPAP_HUMAN	O13712 schizosacch
23	23	98	4.2	844	1	YD25_SCHPO	P49367 saccharomyc
24	24	97.5	4.2	693	1	LYS4_YEAST	O10944 caenorhabdi
25	25	97	4.1	411	1	PPAY_CAEPL	P23316 caenorhabdi
26	26	96	4.1	721	1	NICA_CAEPL	P12374 pseudomonas
27	27	95.5	4.1	609	1	COPA_PBSRM	P09870 clostridium
28	28	94.5	4.0	526	1	CLOS_CLOHI	P25075 bacillus fi
29	29	94	4.0	467	1	ATPX_BACFI	P81132 saccharomyc
30	30	93.5	4.0	845	1	CC47_YEAST	Q12923 homo sapien
31	31	93.5	4.0	2485	1	PTND_HUMAN	O34092 staphylococ
32	32	93	4.0	428	1	GSA_STAAU	Q32611 flavobacter
33	33	93	4.0	777	1	ISOA_FLASP	

```

FT CARBOHYD 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 467 AA; 51075 MW; 118B28A5D7EC661 CRC64;

Query Match 77.3%; Score 1810; DB 1; Length 467;
Best Local Similarity 76.0%; Pred. No. 6.3e-141;
Matches 335; Conservative 40; Mismatches 66; Indels 0; Gaps 0;

QY 1 NNSHSDTVDGGVQCPEISHLWGTYSPPFSLADESAISPDVPGKCRVTFFVLSRHGARY 60
DB 27 NOSTCDTVDGGVQCPEISHLWGTYSPPFSLADESAISPDVPGKCRVTFFVLSRHGARY 86
QY 61 PTSSASKAYSALIEATQKNATAFKGYAFLKTYNTLGGADDLTPFGEQMVNSGKIFVRR 120
DB 87 PTESGKKYSALIEELQNNVTTFDCKYAFKTYNSLGADDLTPFGEQELVNSGKIFVRR 146
QY 121 YKALARKIVPFRASGRVIRASAKFTEGFSQAKLADPGANPHQASPVINVIPEGAGY 180
DB 147 YESLRTNIPTFRSSGSSRVIASGEKFEIGFQSTKLKDPRAQPGSSPKIDVISEASS 206
QY 181 NNTLDHGLCTAFEESELGDDVEANTAVFAPPIRARLBAHLPVNLTDDEVNLMDCMPF 240
DB 207 NNTLDHGLCTAFEESELGDDVEANTAVFAPPIRARLBAHLPVNLTDDEVNLMDCMPF 266
QY 241 DTVARTSDATQSPFCDFTHDEWIOYDYLQSLGYGYGAGNPLGPAQGVFNWELIAR 300
DB 267 DTISTSTVDTKLSPCCDLFTHDEWIDYDYLQSLKYYGAGNPLGPAQGVFNWELIAR 326
QY 301 LTHSPVDHTSTNHTLSDNPATFPLNATLYADFSHDNTMVSIFALGNGKPLSTTV 360
DB 327 LTHSPVHDHTSSNHTLSDNPATFPLNATLYADFSHDNTMVSIFALGNGKPLSTTV 386
QY 361 ESTEETDGSASNTVTPFAARAYVEMMQCAEKEPLRVLVNDRVVRPLHGGCVDKLGRCKR 420
DB 387 ENITQDGFSSANTVTPFAARAYVEMMQCAEKEPLRVLVNDRVVRPLHGGCVDKLGRCKR 446
QY 421 DDFVEGLSFASSGNNWEECPA 441
DB 447 DSFVRGLSFASSGNNWEECPA 467

RESULT 2
ID PHVA_ASPNG STANDARD; PRT: 467 AA.
AC P34752;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
DE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
DE PHOSPHOHYDROLASE A).
GN PHVA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP STRAIN-NRRL 3135 / VAN TIEGHEM / FICUUM;
EX MEDLINE=93252284; PubMed=8387447;
RA van Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M.,
RA Gouka R.J., Suykerbuyk M.E.G., Luiten R.G.M., van Paridon P.A.,
RA Seiten G.C.M., Veenstra A.E., van Gorcom R.F.M.,
RA "van den Hondel C.A.M.J.J.;

"Cloning, characterization and overexpression of the phytase-encoding
gene (PhyA) of Aspergillus niger.";
Gene 127:87-94 (1993).
[2]
RN SEQUENCE FROM N.A.
RA Mullane E.J.;
RA Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE OF 24-464.
RP STRAIN-NRRL 3135 / VAN TIEGHEM / FICUUM;
RP MEDLINE=93249451; PubMed=8387289;
RA Ullah A.H.J., Dischinger H.C. Jr.;
RA "Aspergillus ficuum phytase: complete primary structure elucidation
by chemical sequencing.";
Biochem. Biophys. Res. Commun. 192:747-753(1993).
[4]
RN SEQUENCE OF 71-93.
RP STRAIN-NRRL 3135 / VAN TIEGHEM / FICUUM;
RP MEDLINE=91298982; PubMed=1648914;
RA Ullah A.H.J., Cummins B.J., Dischinger H.C. Jr.;
RA "Cyclohexanediolone modification of arginine at the active site of
Aspergillus ficuum phytase.";
Biochem. Biophys. Res. Commun. 178:45-53(1991).
[5]
RN CHARACTERIZATION, AND PARTIAL SEQUENCE.
RP STRAIN-NRRL 3135 / VAN TIEGHEM / FICUUM;
RP MEDLINE=89160685; PubMed=2852807;
RA Ullah A.H.J.;
RA "Aspergillus ficuum phytase: partial primary structure, substrate
selectivity, and kinetic characterization.";
Prep. Biochem. 18:459-471(1988).
[6]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RP STRAIN-NRRL 3135 / VAN TIEGHEM / FICUUM;
RP MEDLINE=97307250; PubMed=9164457;
RA Kostrewa D., Gruninger-Leitch F., D'Arcy A., Broger C., Mitchell D.,
RA van Loon A.P.;
RA "Crystal structure of phytase from Aspergillus ficuum at 2.5-A
resolution.";
Nat. Struct. Biol. 4:185-190(1997).
CC - FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
FROM PHYTASE.
CC - CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
CC - BIOTECHNOLOGY: IS USED AS A FOOD AND FEED ADDITIVE. IT CAN
FACILITATE THE DEGRADATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS
USED AS FOOD FOR MONOGASTRIC ANIMALS. SOLD BY NOVO NORDISK UNDER
THE NAME PHYTASE NOVO.
CC - SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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EMBL; Z16414; CAA78904.1; -.
EMBL; M94550; AAA32705.1; -.
PIR; JN0482; JN0482.
PIR; P00023; P00023.
PIR; JN0656; JN0656.
PDB; 1IHP; 18-MAR-98.
InterPro; IPR000560; -.
PIR; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; 3D-structure.
SIGNA 1 23
CHAIN 24 467
ACT_SITE 82 82
ACT_SITE 361 361

```

van Loon A.P. ;
"Cloning of the phytases from *Emericella nidulans* and the
thermophilic fungus *Talaromyces thermophilus*,"
Biochim. Biophys. Acta 1353:217-223(1997).
-!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
FROM PHYTATE.
-!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.

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[illegible]

Qy 422 DFVEGLSFARSGGNWECF 440
Db 443 DWVEGLNFARSGGNWTKCF 461

RESULT 4
ID PPA5_YEAST STANDARD; PRT; 467 AA.
AC P00635;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (P60).
GN PHO5 OR YBR093C OR YBR0814.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-26.
RX MEDLINE=83168913; PubMed=6300772;
RA Arima K., Oshima T., Kubota I., Nakamura M., Mizunaga T., Toh-E A.;
RT "The nucleotide sequence of the yeast PHO5 gene: a putative precursor
of repressible acid phosphatase contains a signal peptide."
RL Nucleic Acids Res. 11:1657-1672(1983).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-45.
RX MEDLINE=85037940; PubMed=6093051;
RA Bajwa W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinnen A.;
RT "Structural analysis of the two tandemly repeated acid phosphatase
genes in yeast."
RL Nucleic Acids Res. 12:7721-7739(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C;
RX MEDLINE=95208357; PubMed=7900426;
RA Mannhaupt G., Stucka R., Ehnlé S., Vetter I., Feldmann H.;
RT "Analysis of a 70 kb region on the right arm of yeast chromosome II."
RL Yeast 10:1363-1381(1994).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=87064474; PubMed=3537710;
RA Tait-Kamradt A.G., Turner K.J., Kramer R.A., Elliott Q.D.,
RA Bostian S.J., Thill G.P., Rogers D.T., Bostian K.A.;
RT "Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene
cluster within the acid phosphatase multigene family of Saccharomyces
cerevisiae."
RL Mol. Cell. Biol. 6:1855-1865(1986).
CC -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
ALCOHOL + ORTHOPHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- INDUCTION: REPRESSED BY INORGANIC PHOSPHATE.
CC -!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC
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CC
CC EMBL; V01320; CAA24630.1;
CC EMBL; X01079; CAA25555.1;
CC EMBL; X78993; CAA55598.1;
CC EMBL; Z35962; CAA85046.1;
CC EMBL; X01080; CAA25556.1;
CC PIR; S05795; PABYC.
CC PIR; B25241; B25241.
CC HSP; P34752; 1IHP.
CC -Sgd; S0000297; PHO5.

DR InterPro; IPR000560; -.
DR pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 17
FT CHAIN 18 467
FT ACT_SITE 75 75
FT ACT_SITE 337 337
FT CARBOHYD 97 97
FT CARBOHYD 103 103
FT CARBOHYD 162 162
FT CARBOHYD 192 192
FT CARBOHYD 250 250
FT CARBOHYD 315 315
FT CARBOHYD 356 356
FT CARBOHYD 390 390
FT CARBOHYD 439 439
FT CARBOHYD 445 445
FT CARBOHYD 456 456
FT CARBOHYD 461 461
FT CONFLICT 36 36
FT CONFLICT 130 130
FT CONFLICT 294 294
FT CONFLICT 446 446
FT CONFLICT 462 462
FT CONFLICT 466 466
SQ SEQUENCE 467 AA; 52858 MW; DC3C9504BC2D3D0C CRC64;

REPRESSIBLE ACID PHOSPHATASE.
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
D -> Y (IN REF. 1).
A -> G (IN REF. 1).
H -> Q (IN REF. 1).
S -> V (IN REF. 1).
AS -> DT (IN REF. 1).
R -> K (IN REF. 1).

Query Match 16.8%; Score 394; DB 1; Length 467;
Best Local Similarity 26.3%; Pred. No. 8.4e-25;
Matches 115; Conservative 57; Mismatches 194; Indels 72; Gaps 13;

Qy 23 GTYSPFSLADESAISPDVPGKGRVTFVOVLSRHSRGARYPTSSASALIEAIOKNATA 82
Db 42 GGAGPIYSPGDYGISRDLPCEGEMKQLOMVGHRGERTVSLAKTIKSTWYKLSNYTRQ 101
Qy 83 FGKGYAFLK-TYNYTLGADD-----LTPF-GEOMVNSGKIFRYRRYKALAR 126
Db 102 FNGSLSLNDYDEFFIRDDDDLEMETTFANSDVNLNPTTGEMNAKRHRDFAQYGYMVE 161
Qy 127 KIVPFF-IRASGSDRVASAEKFEIGQSOKLADPGANPHQASPVINVII-----PEGACY 180
Db 162 NQTSFAVFTSNKRCHDTAQYFDG-----LGQD-----FNITQTVSEAESAGA 206
Qy 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPTRARLEAHLPGVNLTDDEYVNLMDMCPF 240
Db 207 NTLACNSCPAW-DYDANDDIVNEYDTYLLDLDIAKLKENKGLNLTSTDASTLFSWCAF 265
Qy 241 DTVARTSDATQLSPFCDLFTFHEWIOYDYLSLQSGKYGYGAGNPLGPAOGVGFVNELIAR 300
Db 266 EV-----NAGYSDVCDIETKDELVHYSYQDLHTYHESGPGYDIKSVGSLFNASVKL 320
Qy 301 LTHSPQDHTSTNHTLDSNPATPLNATLYADFSDHNTWVSIFPFGALGLYNGTKPLSTTSV 360
Db 321 LKQSEIODQ-----KWLSTFHTDILNFLTASIIDDKNNLTAEIV 362
Qy 361 ESIEETDGYSGASWTVPFAARAYVEMQCEAEKPLVRLVNDVRVPLHGCGVKLGRCKR 420
Db 363 PFMGNT--FHRSWVPGQARVYTEKFC--SNDTVRYVINDAVVPIETCSTGPGFSCFI 418
Qy 421 DDF-----VEGLSFAR 431
Db 419 NDFYDYAEAKRVAGTDFLK 436

RESULT 5
ID PPA3_YEAST STANDARD; PRT; 467 AA.
AC P24031;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)

[illegible]

QY 121 YKALARKIVPF-IRASGSDRVIASAEKTEGFSQAKLADPGANPHQASPVINVII----- 174
 Db 156 YGVYVENQTSFAVFTSNRCHDTAQYFDG-----LGDK-----FNISLQITISE 200
 QY 175 PEGAGVNTLDHGLCTAFESGLGDDVEANFTAVFAPPIRARLEAHLPGVNLTDSDVNL 234
 Db 201 AESAGANTLSAHSHPAMD-DVNDILK3YDKYKLSGLAKRLNKGKLNLTSSDANTF 259
 QY 235 MDWCPEDTAVRTSDATQSPFCDLTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVFV 294
 Db 260 FAWCAYEINAR-----GYSDICNIFTKDELVRFSYQDLETYYQTPGCVVRSVGANLF 314
 QY 295 NELIARLTHSPVQDHTSTNHTLSDNPATPLNATLYADFSDHNTMVSFFALGKLYNGTKP 354
 Db 315 NASVRLKKESEYQDQ-----KWLSTHDTDLNLTLLTIGIIDQNN 356
 QY 355 LSTTSVESIEETDGSASWTVPFAARAIVEMMQCEAEKEPLRVLVNDRVVPLHGCYVDK 414
 Db 357 LTAHVHPMENT--FHRSWYVPOGARVYTERFQC--SNDTVRVVINDAVVPIETCSTGP 412
 QY 415 LGRCRDRDF-----VEGLSFAR 431
 Db 413 GFSCIEINDFYAEKRVAGTDFLK 436

RESULT 8

ID PPAD_YEAST STANDARD; PRT; 468 AA.
 AC P52290;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE PROBABLE ACID PHOSPHATASE YDL024C PRECURSOR (EC 3.1.3.2).
 GN YDL024C OR D2815.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Andre B., Vissers S., Urrestarazu L.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
 CC ALCOHOL + ORTHOPHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC
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 CC
 CC EMBL; Z48432; CAA88335.1; --
 CC EMBL; Z74072; CAA98583.1; --
 CC SGD; S0002182; YDL024C.
 CC InterPro; IPR000560; --
 CC Pfam; PF00328; acid_phosphat; 1.
 CC PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 CC PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 CC Hydrolase; Glycoprotein; Signal; Multigene family.
 KW SIGNAL
 FT CHAIN 1 20
 FT ACT_SITE 21 468 PROBABLE ACID PHOSPHATASE YDL024C.
 FT ACT_SITE 76 76 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT CARBOHYD 338 338 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 357 357 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 468 AA; 53076 MW; 1F07FF374DDF162C CRC64;
 Query Match 15.8%; Score 369; DB 1; Length 468;
 Best Local Similarity 25.3%; Pred. NO. 9.5e-23;
 Matches 117; Conservative 60; Mismatches 27; Indels 110; Gaps 14;
 QY 23 GTYSPFSLADESAISPDVPGKGRVTFVQVLSRHGARYPTSSKASKAYSALIEAIQNATA 82
 Db 43 GGSAPYFSPFANYGIPDIDPEGCLTQVQMGIRGERYPTRSEAKDIFEWYKISNYTK 102
 QY 83 FKGYAFLKT-YNYTL-----GADDLTPF-GEQOMVNSGKIFRYRYKALAR 126
 Db 103 YEGSLSFLNGYEFFIPDESLEMETTLQNSIDLNPYTGMNAKRHAREFLAKYKGLME 162
 QY 127 KIVPF-IRASGSDRVIASAEKTEGFSQAKLADPGANPHQASPVINVIPEGAGYNTLD 185
 Db 163 NCTNEPIFTNSKRIYDTAQYFAEL-----GDGFNISLO 197
 QY 186 HGLCTAFEESELG-----DDVEANFTAVFAPPIRARLEAHLPGVNL 227
 Db 198 ----TLSENSSSGANTLAAKSSCPNWNANNDILMSYRDYLENIDRLNDENKGLNLS 253
 QY 228 DEDVNLMDMCPEDTAVRTSDATQSPFCDLTHDEWIOYDYLQSLGKYGYGAGNPLGP 287
 Db 254 RKDAALFSWCAPEL-----NAGYSNICDIFSAELIHYSETDLTSPYQNGPGYKLIK 308
 QY 288 AGGVGVN---ELIARLTHSPVQDHTSTNHTLSDNPATPLNATLYADFSDHNTMVSIF 344
 Db 309 SIGANLFNATVKLIQSAH-----LDQKWLSTHDTDLNLT 347
 QY 345 ALGLYNGTPELSTTSVESIEETDGSASWTVPFAARAIVEMMQCEAEKEPLRVLVNDRV 404
 Db 348 TAGLIDDTRLNTNHNHVPFRDHS--YHRSWIPOGARVYTERFQC--SNDYSYRVVNDVAV 403
 QY 405 VPLHGCYVDKLGRCRDRDFE-----GLSFARSGGNWEEC 439
 Db 404 VPESCSGPGFSGEGTFYFAKDLRGVSP-----YEDC 439

RESULT 9

PHYB_ASPNG
 ID PHYB_ASPNG STANDARD; PRT; 479 AA.
 AC P34754;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE 3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
 DE 3-PHOSPHOHYDROLASE B) (3 PHYTASE B) (MYO-INOSITOL HEXAKISPHOSPHATE
 DE PHOSPHOHYDROLASE B).
 GN Aspergillus niger.
 OS Aspergillus niger.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 20-101; 133-141 AND 376-399.
 RX MEDLINE-93371452; PubMed-7916610;
 RA Erlich K.C., Montalbano B.G., Mullaney E.J., Dischinger H.C. Jr.,
 RA Ullah A.H.J.;
 RT "Identification and cloning of a second phytase gene (phyB) from
 RT Aspergillus niger (fium).";
 RL Biochem. Biophys. Res. Commun. 195;53-57(1993).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTASE.
 CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
 CC D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.

CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC
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CC
CC EMBL; L20567; AAA02934.1; -
CC InterPro; IP000560; -
CC Pfam; PF00328; acid_phosphat; 1.
CC PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
CC PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
CC Hydrolase; Glycoprotein; Signal.
CC
CC SIGNAL 1 19
CC CHAIN 20 479
CC ACT_SITE 81 81
CC
CC ACT_SITE 82 82
CC ACT_SITE 337 337
CC CARBOHYD 106 106
CC CARBOHYD 191 191
CC CARBOHYD 227 227
CC CARBOHYD 250 250
CC CARBOHYD 315 315
CC CARBOHYD 425 425
CC CARBOHYD 442 442
CC CARBOHYD 458 458
CC SEQUENCE 479 AA; 52611 MW; 395DADA2B50DFDC4 CRC64;
CC
CC Query Match 15.5%; Score 362.5; DB 1; Length 479;
CC Best Local Similarity 28.3%; Pred. No. 3.3e-22;
CC Matches 119; Conservative 54; Mismatches 156; Indels 91; Gaps 16;
CC
CC QY 23 GTYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARYPTSSASKAY-SALIEAIQKNAT 81
CC DB 53 GPYSERVSY-----GIARDPPTSCVDQVIMVKGHERYPSAGKASIEALAKVYSINT 108
CC
CC QY 82 AFKGYAFLKTYNYTL-----GADLI-T-PF-GEQMVNSGKIFRYRYKAL--ARKIVPF 131
CC DB 109 EYKGLDLFLNDWTYYVNPNCYNAETTSQPYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168
CC
CC QY 132 IRASGSDRVIAAEKPIEQFQSAKLADPCANPHQASPVNIIIPGAGYNTLDHGLCTA 191
CC DB 169 F-SSGYGRVETARKFGEF-----FGYNSTNAALNII 201
CC
CC QY 192 FEESELG-----DDVEANFTAVFAPPRI--ARLEAHLPGVNLTDDEYVNLMD 236
CC DB 202 SESEVNGADSLPTCTDNDQTTCDNLTYQLPQFKVAARLNSQNGMNLTAASDVNLI 261
CC
CC QY 237 MCPFDIVARTSDATQLSPFCDLTFDEWTDYDYLQSLGKYGYGAGNPLGPAQGVGFVNE 296
CC DB 262 MAGSFELN-----PESNNINAFQDEWVSFGYVEDLNYTCAGPDGKNMAAVGAVYANA 316
CC
CC QY 297 LIARLTHSPQDHTSNHTLDSNPATFPLNATLYADFSHDNTMVSIFFFALGLY--NGTKP 354
CC DB 317 SLTLNNOGP-----KEAGP-----LFFNFAHDNTITPILAAGLVLIPIEDLP 358
CC
CC QY 355 LSTTSVESIEETDGYASWTVPFAARAYVEMMOCEA-----EKEPLVRVLNDRVPLHGC 410
CC DB 359 L-----DRVAFNPYSIGNIVPVGHLHTIERLSCQATLSDKTYVRLVNLNEAVLPFND 413
CC
CC RESULT 10
CC PHYB ASPAW
CC ID PHYB ASPAW
CC AC P34755; STANDARD; PRT; 479 AA.
CC DT 01-FEB-1994 (Rel. 28, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT ~30-MAY-2000 (Rel. 39, Last annotation update)

DE 3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
DE 3-PHOSPHOHYDROLASE B) (PH 2.5 OPTIMUM ACID PHOSPHATASE).
DE PHYB OR APH.
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ALK0243;
RX MEDLINE=94040796; PubMed=8224894;
RA Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A.,
RA Miettinen-Oinonen A., Nevalainen H., Rambosek J.A.;
RT "The cloning and sequencing of the genes encoding phytase (phy) and
RT PH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
RT awamori.";
RL Gene 133:55-62(1993).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=99264417; PubMed=10329192;
RA Kostrewa D., Wyss M., D'Arcy A., van Loon A.P.;
RT "Crystal structure of Aspergillus niger pH 2.5 acid phosphatase at
RT 2.4-A resolution.";
RL J. Mol. Biol. 288:965-974(1999).
CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC FROM PHYTATE.
CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
CC D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC
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CC
CC EMBL; L02420; AAA16897.1; -
CC PIR; JN0890; JN0890.
CC PDB; LOEX; 19-APR-00.
CC InterPro; IP000560; -
CC Pfam; PF00328; acid_phosphat; 1.
CC PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
CC PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
CC Hydrolase; Glycoprotein; Signal; 3D-structure.
CC SIGNAL 1 19
CC CHAIN 20 479
CC ACT_SITE 82 82
CC ACT_SITE 337 337
CC DISULFID 71 387
CC DISULFID 128 472
CC DISULFID 216 441
CC DISULFID 225 298
CC DISULFID 413 421
CC CARBOHYD 191 191
CC CARBOHYD 315 315
CC CARBOHYD 458 458
CC SEQUENCE 479 AA; 52678 MW; 4F8E0F3778CC3B08 CRC64;
CC
CC Query Match 15.1%; Score 354.5; DB 1; Length 479;
CC Best Local Similarity 27.9%; Pred. No. 1.5e-21;
CC Matches 117; Conservative 53; Mismatches 159; Indels 91; Gaps 15;
CC
CC QY 23 GTYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARYPTSSASKAY-SALIEAIQKNAT 81
CC DB 53 GPYSERVSY-----GIARDPPTSCVDQVIMVKGHERYPSAGKASIEALAKVYSINT 108
CC
CC QY 82 AFKGYAFLKTYNYTL-----GADLI-T-PF-GEQMVNSGKIFRYRYKAL--ARKIVPF 131
CC DB 109 EYKGLDLFLNDWTYYVNPNCYNAETTSQPYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168

Query Match 14.8%; Score 345.5; DB 1; Length 468;
Best Local Similarity 25.3%; Pred. No. 8e-21;
Matches 115; Conservative 74; Mismatches 177; Indels 89; Gaps 19;

```

QY 18 ISHLMGTYSPE-----FSLADESAISPDVPGRCRVTFVOVLRSRGARYPTSSASKAYSAL 72
   ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 47 LRHL-GGLGPIGYNGWIAESEI-----PSCITDQHLLMRGERVPSTNVGKQLEAL 100
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 73 IE-AIQNATAPKGKYAFKLYNYTLG-----ADLTTPFEQQMNSGIKF---VRRYKA 123
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 101 YOKLLDADVEVPTGPLSFQDYDFVSDAANVEQETTKGFYSGLNTAFDCTLRERYDH 160
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 124 L-----ARKVIPFRASSDRVTASAEKFTIEGFSQAKLADPGANPHQASPVINVIPE- 176
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 161 LINTSEEKKL-SVWAGSQERVDVTAYKFAQGGMKSNYTD-----MVETVALEE 208
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 177 -GAGYNNTLDHGLCT-----AFBESELGDVV--EANFTAVFAPPFARLEAHLPGVNL 226
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 209 EKSQGLNSLTRISCNPVNSHIYKDGFDPNDIAEREAD-----RLNTLSFGENI 257
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 227 TDEDVNLMDCPEDTIVARTSDATQLSPFCDLFTHDEWIQDYLOSIGKYGYGAGNPLG 286
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 258 TADDIPTILCYGCELNVNRGE-----SSFCDVLSREALLYTAYURDLGWYYVNGNGNPLG 312
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 287 PAQGVGFVNELIARLTHSPVQDHTSTNHLDNSNPATPLNATLVYADFSHONTWYSIFFAL 346
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 313 KTICGVVAN-----ATQLENTPAD-PRDYPFLSFSHTDLLQOVFTSL 356
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 347 GLYNGTK-PLSTTSVESITEFDGYSASWTVPFAARAYVENMQC--EAEKEPFLVRVLVNDR 403
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 357 GLFNWTDLP-----DOIQTQTSFKSTEIVPMGARLLTERLICTVEEGEKKYVRTILNDA 411
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 404 VVPLHGCGVDKLGRCKRDDFEGLGSFARSNGWEE 438
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 412 VFPLSDCSSGFGFSCPUNDYVSRLEALNEDSDFAE 446
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

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RESULT 12
PPAL_SCHPO STANDARD; PRT; 453 AA.

ID PPAL_SCHPO STANDARD; PRT; 453 AA.
AC P08091;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
GN PHO1 OR SPBP4G3.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
ON NCBI_TaxId=4896;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86140050; PubMed=3005272;
RA Elliott S., Chang C., Schweingruber M.E., Schaller J., Rickli E.E.,
RA Carbon J.;
RA "Isolation and characterization of the structural gene for secreted
RT acid phosphatase from Schizosaccharomyces pombe.";
RL J. Biol. Chem. 261:2936-2941(1986).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC Rieger M., McDougall R.C., Rajandream M.A., Barrell B.G.;
RA Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC -! CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
CC ALCOHOL + ORTHOPHOSPHATE.
CC -! SUBCELLULAR LOCATION: CELL WALL.
CC -! INDUCTION: REpressed BY PHOSPHATE AND WEAKLY BY THIAMINE.
CC -! SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL; M11857; AAA35321.1; -
CC EMBL; AL137099; CAB68657.1; -
CC PTR; A25326; A25326.
CC HSP; P34752; 11HP.
CC InterPro; IPR000560; -
CC Pfam; PF00328; acid_phosphat; 1.
CC PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
CC PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
CC Hydrolase; Glycoprotein; Cell wall; Signal.
CC -----
CC SIGNAL 1 18
CC CHAIN 19 453 ACID PHOSPHATASE.
CC FT ACT_SITE 69 69 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
CC FT ACT_SITE 330 330 PROTON DONOR (BY SIMILARITY).
CC FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 193 193 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 243 243 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 410 410 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 429 429 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 443 443 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 453 AA; 50557 MW; 7CF891256EB154D1 CRC64;

Query Match 14.0%; Score 328; DB 1; Length 453;
Best Local Similarity 25.8%; Pred. No. 2.1e-19;
Matches 103; Conservative 60; Mismatches 187; Indels 50; Gaps 9;

QY 25 YSPFSLADESAISPDVPGKGRVTFVQVLSRHGARYPTSSASKAYSA-----LIE 74
DB 43 HKPYF-----YGPSIDFTTCKIKQVHTLQRHGSNPT-GGNAAFDAVGIANFOQLLNG 96
QY 75 AIOKNATAPKGYAFKTYNTL---GADLTTPGEOQMVNSGKIFRYRYKALARKIVPF 131
DB 97 SVPIQSVSGNPLSEVPWTPTVIEAANADALSSGRVLFDMGRQFYERYHELFPNASTYN 156
QY 132 IRASGSDRVIAAEAFIEGFQSAKLADPGANPHQASPVINVIIPBAGYNNNTLDHGLCTA 191
DB 157 IYTAQAQRVVDALWYGYGMF-----GEDVHNFTNVLSENATAGSNLSYNACPA 209
QY 192 FFESELGDDVEANFTAVFAPPIRAREALHPLGVNLTDEDVNMDCMCPDFTVARTSDATQ 251
DB 210 SDADDTTTPALEARNVYMPPIRQRLNPFYSNYLTNDLILNYGICSYETALQ-----D 264
QY 252 LSPFCDLFTHDWIOYDYLQSLGKYGYGAGNPLGPAQGVGVFNELIARLTHSPVQDHTS 311
DB 265 YSEFCKLFNSVDLFNFEYEGDLSFSYGMNSVKWGSIFGGAYANSLANS-LSRVENNTQ 322
QY 312 TNHTLDSNPATPELNATLADFSHNTMWSIPFALGLXNGTKPLSTTSVESIEETFDGYS 371
DB 323 -----QVFATTHANIIPVETALGFFTDNTPENPLTYSYQVHSHSKA 366
QY 372 SWTPFPAARAYVEMMQEAEKPLRVLVNDRVPLHGCG 411
DB 367 SEVPFPAGNLITELFCEDSKY-YVRHLVNEEVFPLSDCG 405

RESULT 13
ID PPAS_KLUFA STANDARD; PRT; 469 AA.
AC P52289;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE *REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).

GN PHO5.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 2359/152;
RA Ferninan E.;
RL Thesis (1995), University of Salamanca, Spain.
CC -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O - AN
CC ALCOHOL + ORTHOPHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- INDUCTION: REPRESSED BY INORGANIC PHOSPHATE (BY SIMILARITY).
CC -!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL; Z33995; CAAB3964.1; -
CC InterPro; IPR000560; -
CC Pfam; PF00328; acid_phosphat; 1.
CC PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
CC PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
CC Hydrolase; Glycoprotein; Signal; Multigene family.
CC -----
CC SIGNAL 1 16
CC CHAIN 17 469 REPRESSIBLE ACID PHOSPHATASE.
CC FT ACT_SITE 77 77 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
CC FT ACT_SITE 339 339 PROTON DONOR (BY SIMILARITY).
CC FT CARBOHYD 23 23 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 31 31 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 32 32 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 201 201 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 229 229 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 250 250 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 317 317 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 447 447 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 469 AA; 52532 MW; 863B528D0740AA7E CRC64;

Query Match 14.0%; Score 328; DB 1; Length 469;
Best Local Similarity 24.4%; Pred. No. 2.2e-19;
Matches 113; Conservative 69; Mismatches 196; Indels 86; Gaps 15;

QY 9 DGGYQCF-----PEISHLWGTYSPPFFSLADESAISPDVPGKGRVTFVQVLSRHGARY 60
DB 22 DNGTVCYALNNSITDESIFSLNGQGPHYDYPQSGIPVEVPDQCTVEHVQMLARHGERY 81
QY 61 PTSASKAYGALIEAIOKNATAPKGYAFKTYNTLGTADDLTPFGEOQMVNSGIFRYR 120
DB 82 PTASKGKLMIALMDKLKE---FQGYQ-----NDPLEVFNDEYFVNTKTFDQ 126
QY 121 Y-----KALARKIVPFIR-----ASGSDRVIAAEAFIEGFQSAKLADPG 160
DB 127 LTNSTDVDPSPYAGAKTAHGLKYIAYNGDLFSNPNVFTSSSGRVH--QTAKYVSS 184
QY 161 ANPHQASPVINVIPEG--AGYNNLTLDHGLCTAFEESELGDDVEANFTAVFAPPIARLE 218
DB 185 LEEELDIQLDQLIQENETSGANSLTPADSCWY-NGDLGDEYFENATLPYLDIKNRW 243
QY 219 AHLFGVNLIT--DEDVNMDCMCPDFTVARTSDATQLSPFCDLFTHDWIOYDYLQSLGKY 276
DB 244 KKNLNLTLEHDDIELLDVDMCAFETNVKSSAV-----CDLFRNDLVAYSYYANVNF 298
QY 277 YGYGAGNPLGPAQGVGVFNELIARLTHSPVQDHTSTNHTLDSNPATPELNATLYADEFSHD 336


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Db      299 YRGAGNPNMPTIGSVLVNASYNLLTQADELND-::: |||::: |||::: |||::: |||:::
QY      337 NTMVSTIFFAGLY-NGTKPLSTTSVESIBETDGYASWTVPTFAARAYVEMMOCEAKEPL 395
Db      341 TDIQFISALGLDNG---VTEYSLDQVDFQNIQLSWTPMGGRIFTEKLKC--GNASY 395
QY      396 VRYLVNDRVPLHGGVDVKLGRCKRDDF-----VEGLSFARS 432
Db      396 VRYIIINDVIIPVGCTSGPGFSCPIEDFDYITNRLNGIDYVSS 439

RESULT 14
PPA2_SCHPO
ID      PPA2_SCHPO      STANDARD;      PRT;      463 AA.
AC      001682;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      01-OCT-2000 (Rel. 40, Last annotation update)
DE      THIAMINE-REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
GN      PHO4 OR SPBC428.03C.
OS      Schizosaccharomyces pombe (Fission yeast).
OC      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC      Schizosaccharomycetales; Schizosaccharomycetaceae;
OC      Schizosaccharomycetes.
OX      NCBI_TaxID=4896;
RN      [1]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 19-30.
RX      MEDLINE=91064763; PubMed=2249257;
RA      Yang J., Schweingruber M.E.;
RT      "The structural gene coding for thiamin-repressible acid phosphatase
RT      in Schizosaccharomyces pombe.";
RL      Curr. Genet. 18:269-272(1990).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=972;
RA      Lyne M., Rajandream M.A., Barrell B.G., Baker S., Mungall K.;
RL      Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: MAY DEPHOSPHORYLATE THIAMINE PHOSPHATES.
CC      -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
CC      ALCOHOL + ORTHOPHOSPHATE.
CC      -1- SUBCELLULAR LOCATION: CELL WALL.
CC      -1- INDUCTION: REPRESSED BY THIAMINE.
CC      -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      -----
DR      EMBL; X56939; CA040258.1; -.
DR      EMBL; AL034382; CA22278.1; -.
DR      PIR; S14119; S14119.
DR      InterPro; IPR000560; -.
DR      Pfam; PF00328; acid_phosphat; 1.
DR      PROSITE; PS006116; HIS_ACID_PHOSPHAT_1; 1.
DR      PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW      Hydrolase; Glycoprotein; Cell wall; Signal.
FT      SIGNAL          1      18
FT      CHAIN           19      463
FT      ACT_SITE        69      69
FT      ACT_SITE        340     340
FT      CARBOHYD        98      98
FT      CARBOHYD       104     104
FT      CARBOHYD       186     186
FT      CARBOHYD       221     221
FT      CARBOHYD       251     251
FT      CARBOHYD       328     328
FT      CARBOHYD       433     433
FT      CARBOHYD       439     439
FT      FT              19      463
FT      FT              69      69
FT      FT              340     340
FT      FT              98      98
FT      FT              104     104
FT      FT              186     186
FT      FT              221     221
FT      FT              251     251
FT      FT              328     328
FT      FT              433     433
FT      FT              439     439
FT      FT              19      463
FT      FT              69      69
FT      FT              340     340
FT      FT              98      98
FT      FT              104     104
FT      FT              186     186
FT      FT              221     221
FT      FT              251     251
FT      FT              328     328
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FT      FT              340     340
FT      FT              98      98
FT      FT              104     104
FT      FT              186     186
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FT      FT              433     433
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FT      FT              340     340
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FT      FT              251     251
FT      FT              328     328
FT      FT              433     433
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FT      FT              19      463
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FT      FT              340     340
FT      FT              98      98
FT      FT              104     104
FT      FT              186     186
FT      FT              221     221
FT      FT              251     251
FT      FT              328     328
FT      FT              433     433
FT      FT              439     439
FT      FT              19      463
FT      FT              69      69
FT      FT              340     340
FT      FT              98      98
FT      FT              104     104
FT      FT              186     186
FT      FT              221     221
FT      FT             
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Search completed: October 16, 2001, 17:57:31
Job time: 569 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 16, 2001, 17:56:25 ; Search time 197.94 Seconds
 (without alignments)
 294.769 Million cell updates/sec

Title: US-09-488-265-31_COPY_27_467
 Perfect score: 2342
 Sequence: 1 NSHSCDTVDGGYQCFPEISH.....DFVEGLSFARSGNWECPA 441

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1878.5	80.2	465	3 000092	000092 aspergillus
2	1805	77.1	467	3 Q9U0Z7	Q9U0Z7 aspergillus
3	1799	76.8	467	3 Q93838	Q93838 aspergillus
4	1786	76.3	467	3 Q9HEQ0	Q9HEQ0 aspergillus
5	1702.5	72.7	466	3 000096	000096 talaromyces
6	1696	72.4	466	3 000100	000100 aspergillus
7	1668.5	71.2	466	3 000085	000085 aspergillus
8	1320.5	56.4	487	3 000107	000107 thielavia h
9	334.5	14.3	442	3 074677	074677 pichia anqu
10	327	14.0	489	3 Q9X846	Q9X846 kluyveromyc
11	311.5	13.3	463	3 060172	060172 schizosach
12	204.5	8.7	460	5 Q9VW72	Q9VW72 drosophila
13	196	8.4	451	11 Q35217	Q35217 rattus norv
14	196	8.4	467	5 Q96421	Q96421 drosophila
15	188	8.0	487	4 Q95172	Q95172 homo sapien
16	187	8.0	481	11 Q922L6	Q922L6 mus musculu
17	187	8.0	487	4 Q9UNW1	Q9UNW1 homo sapien
18	185	7.9	487	4 Q9UCA3	Q9UCA3 homo sapien
19	178.5	7.6	453	5 Q96420	Q96420 drosophila

20	177.5	7.6	449	13	Q92170	Q92170 gallus gall
21	177.5	7.6	453	5	Q9W438	Q9W438 drosophila
22	168.5	7.2	198	3	Q9UTX1	Q9UTX1 schizosacch
23	149.5	6.4	468	10	O04509	O04509 arabidopsis
24	144	6.1	274	11	Q9JJD5	Q9JJD5 mus musculu
25	130	5.6	449	5	Q19076	Q19076 caenorhabdi
26	128.5	5.5	374	11	Q9JMG5	Q9JMG5 mus musculu
27	127.5	5.4	381	11	Q9QXG5	Q9QXG5 mus musculu
28	121	5.2	513	2	Q46334	Q46334 comamonas t
29	118	5.0	380	5	Q22525	Q22525 caenorhabdi
30	113.5	4.8	381	11	Q9QXH7	Q9QXH7 mus musculu
31	110	4.7	683	5	O00838	O00838 leishmania
32	110	4.7	707	5	O00839	O00839 leishmania
33	109.5	4.7	730	5	Q20826	Q20826 caenorhabdi
34	108.5	4.6	758	4	Q9P2C1	Q9P2C1 homo sapien
35	108.5	4.6	827	2	Q47871	Q47871 eubacterium
36	107	4.6	354	5	Q19709	Q19709 caenorhabdi
37	107	4.6	513	2	O24719	O24719 comamonas t
38	106	4.5	763	2	Q9R6Y7	Q9R6Y7 anabaena sp
39	103	4.4	421	4	Q9UIG6	Q9UIG6 homo sapien
40	103	4.4	428	4	Q9NPH0	Q9NPH0 homo sapien
41	102.5	4.4	1225	5	O20330	O20330 caenorhabdi
42	102	4.4	452	5	O19175	O19175 caenorhabdi
43	101	4.3	408	5	O19461	O19461 caenorhabdi
44	100.5	4.3	630	2	P73409	P73409 synechocyst
45	99.5	4.2	642	1	O26446	O26446 methanobact

ALIGNMENTS

RESULT 1
 000092
 ID 000092 PRELIMINARY; PRT; 465 AA.
 AC 000092;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-
 DE PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
 DE PHOSPHOHYDROLASE A).
 GN PHVA.
 OS Aspergillus fumigatus (Sartorya fumigata).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_taxid=5085;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-37.
 RC STRAIN=ATCC 34625;
 RX MEDLINE=97288063; PubMed=9143104;
 RA Pasamontes L., Haiker M., Wyss M., Tessier M., van Loon A.P.G.M.;
 RT "Gene cloning, purification, and characterization of a heat-stable
 RT phytase from the fungus Aspergillus fumigatus.";
 RL Appl. Environ. Microbiol. 63:1696-1700(1997).
 RL -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 FROM PHYTATE.
 CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
 CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- MISCELLANEOUS: SHOWS HIGH ACTIVITY WITH 4-NITROPHENYL PHOSPHATE AT
 CC A PH RANGE OF 3 TO 5 AND WITH PHYTIC ACID AT A PH RANGE OF 2.5 TO
 CC 7.5. IT IS ABLE TO WITHSTAND TEMPERATURES UP TO 100 DEGREES
 CC CELSIUS OVER A PERIOD OF 20 MIN, WITH A LOSS OF ONLY 10% OF THE
 CC INITIAL ENZYMIC ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC EMBL; U59804; AAB96872.1; -;
 DR HSSP; P34752; 1IHP.
 DR InterPro; IPR000560; -;
 DR Pfam; PF00328; acid.phosphat.1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1;
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 DR Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 26

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FT CHAIN 27 465 3-PHYTASE A. 81 81 REQUIRED FOR BINDING SUBSTRATE (BY  
FT ACT_SITE 81 81 SIMILARITY).  
FT ACT_SITE 82 82 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).  
FT ACT_SITE 359 359 PROTON DONOR (BY SIMILARITY).  
FT DISULFID 30 39 BY SIMILARITY.  
FT DISULFID 70 412 BY SIMILARITY.  
FT DISULFID 213 463 BY SIMILARITY.  
FT DISULFID 262 280 BY SIMILARITY.  
FT DISULFID 434 442 BY SIMILARITY.  
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 465 AA; 50836 MW; 86FCID9058C9B2C9 CRC64;  
  
Query Match 80.2%; Score 1878.5; DB 3; Length 465;  
Best Local Similarity 79.8%; Pred. No. 1.6e-144;  
Matches 351; Conservative 35; Mismatches 53; Indels 1; Gaps 1;  
  
QY 2 SHSCDVTGGYQCPEISHLMGTYSPPFSLADESAISPDVPGKGRVTFVQVLSRHGARYP 61  
DB 27 SKSCDVTDLGYQCSPATSHLMGQYSPFSLADELSVSKLPKDCRITLVQVLSRHGARYP 86  
  
QY 62 TSSASKYSALEIAEQKNAFAKGYAFKTYNTLTGADDLTPFGEQOMVNSGKIFYRRY 121  
DB 87 TSSKSKYKLVTAIQANATDFKGFALFKTYNTLTGADDLTPFGEQOMVNSGKIFYRRY 146  
  
QY 122 KALARKIVPFRASGSDRVIAAEKFIQFQSAKLADPGANPHQASPVINVIIEGAGY 181  
DB 147 KALARSVVPFRASGSDRVIAAEKFIQFQSAKLADPGAT-NRAAPALSVIIESETFN 205  
  
QY 182 NTLDHGLCTAFRESELGDDVEANFTAVAPPRIARLEAHLPGVNLTDDEVDVNLDMCPSF 241  
DB 206 NTLDHGVCTKFAESQLGDEVAANFTALPADIRARAEKHLPGVTLTDDEVDVNLDMCPSF 265  
  
QY 242 TVARTSDATQLSPFCDLTFHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIARL 301  
DB 266 TVARTSDASQLSPFCDLTFHDEWIKYNYLQSLGKYGYGAGNPLGPAQGVGFVNELIARL 325  
  
QY 302 THSPVQDHTSTNHTLDSNPATPLNATLYADSHONTWVSIFFFALGLNGTKPLSTTSVE 361  
DB 326 TRSPVQDHTSTNHTLDSNPATPLNATLYADSHONTWVSIFFFALGLNGTKPLSTTSVE 385  
  
QY 362 STIETDGYASWTVPFAARAYVEMMOCAEKEPLVRLVNDRVPLHGCVDKLGRCRKR 421  
DB 386 SAKELDGYASWVVPFARAYFETMCKSEKEPLVRLVNDRVPLHGCVDKLGRCRKLN 445  
  
QY 422 DFVEGLSFARSGNWECEFA 441  
DB 446 DFVKGLSWARSGNWECEFS 465  
  
RESULT 2  
Q90U27 PRELIMINARY; PRT; 467 AA.  
ID AC Q90U27  
AC Q90U27  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
DE MTO-INOSITOL HEXAPHOSPHATE PHOSPHOHYDROLASE PRECURSOR (EC 3.1.3.8).  
OS Aspergillus niger.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OX NCBI_TaxID=5061;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hongning W., Qi W., Jing X.;  
RT "PCR, cloning and characterization of the phytase (phyA) gene of
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RT Aspergillus niger (China Strain).";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF218813; AAF25481.1; -.  
DR HSSP; P34752; 1IHP.  
DR InterPro; IPR000560; -.  
DR Pfam; PF00328; acid_phosphat; 1.  
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.  
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.  
KW Signal; Lyase; Hydrolase.  
FT SIGNAL 1 19 POTENTIAL.  
SQ SEQUENCE 467 AA; 51029 MW; F4300A8F165EBF92 CRC64;  
  
Query Match 77.1%; Score 1805; DB 3; Length 467;  
Best Local Similarity 75.7%; Pred. No. 1.6e-138;  
Matches 334; Conservative 43; Mismatches 64; Indels 0; Gaps 0;  
  
QY 1 NGSCHDVTGGYQCPEISHLMGTYSPPFSLADESAISPDVPGKGRVTFVQVLSRHGARY 60  
DB 27 NQSTCDTVQGYQCFSETSHLMGQYAPFPFSLANESAISPDVPGKGRVTFVQVLSRHGARY 86  
  
QY 61 PTSSASKYSALEIAEQKNAFAKGYAFKTYNTLTGADDLTPFGEQOMVNSGKIFYRR 120  
DB 87 PTDSKGGKYSALEIEEQNATTFDGYAFKTYNTLTGADDLTPFGEQOMVNSGKIFYRR 146  
  
QY 121 YKALARKIVPFRASGSDRVIAAEKFIQFQSAKLADPGANPHQASPVINVIIEGAGY 180  
DB 147 YESLTRNLPFRIRSSGSDRVIAAEKFIQFQSAKLADPGAT-NRAAPALSVIIESETFN 206  
  
QY 181 NNTLDHGLCTAFRESELGDDVEANFTAVAPPRIARLEAHLPGVNLTDDEVDVNLDMCPSF 240  
DB 207 NNTLDHGLCTAFRESELGDDVEANFTAVAPPRIARLEAHLPGVNLTDDEVDVNLDMCPSF 266  
  
QY 241 DTVARTSDATQLSPFCDLTFHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIAR 300  
DB 267 DTISTSTVDTKLSFCDLTFHDEWIKYNYLQSLGKYGYGAGNPLGPTQGVGYVANELIAR 326  
  
QY 301 LTHSPVQDHTSTNHTLDSNPATPLNATLYADSHONTWVSIFFFALGLNGTKPLSTTSV 360  
DB 327 LTHSPVQDHTSTNHTLDSNPATPLNATLYADSHONTWVSIFFFALGLNGTKPLSTTSV 386  
  
QY 361 ESTIETDGYASWTVPFAARAYVEMMOCAEKEPLVRLVNDRVPLHGCVDKLGRCRKR 420  
DB 387 ONITQDGTGSSAWTVPFAARAYVEMMOCAEKEPLVRLVNDRVPLHGCVDKLGRCRKR 446  
  
QY 421 DFVEGLSFARSGNWECEFA 441  
DB 447 DSFVKGLSFARSGNWECEFA 467  
  
RESULT 3  
O93838 PRELIMINARY; PRT; 467 AA.  
ID O93838  
AC O93838  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
DE PHYTASE.  
GN PHYA.  
OS Aspergillus niger.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OX NCBI_TaxID=5061;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SK-57;  
RA Nagashima T., Kondo H., Anazawa H., Terasaki Y.;  
RT "Phytase having high-affinity for phytic acid."  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB022700; CAB19824.1; -.  
DR HSSP; P34752; 1IHP.  
DR InterPro; IPR000560; -.  
DR Pfam; PF00328; acid_phosphat; 1.
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DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ SEQUENCE 467 AA; 51028 MW; 7A38AD543F

Query Match

Query Match 76.8%; Score 1799; DB 3; Length 467;
Best Local Similarity 74.8%; Pred. No. 4.8e-138;
Matches 330; Conservative 47; Mismatches 64; Indels

QY	1	NHSHCDTVDGGYQCQFPBESHLMGTYSPPFSLADESAISPDVPKGRVTFVOVLSRHGARY	60
Db	27	NOSTDCTVDQGYQCQFSETSHLQGYAPFTSLANKSAISPDVPACHVTFAGVLSRHGARY	86
QY	61	PTSSASKAYSALIEAIOKNATAKGYAYFLKYNNTLGADDLTPFGEOQMVNSGKIFPYRR	120
Db	87	PTDSKGKYSALIEIQONNATTEGKYAYFLKYNNTSLAGADDLTPFGELVNSGVAFYQR	146
QY	121	YKALARKIVPFIIRASGSDRVIASEAERFIEGFSQAKLADPGANPHQASPVNLVITIPGAGY	180
Db	147	YESLTRNLVPIIRSSGSSRVIASSGNKFIEGFOSTKLQAPQACQSPFKIDVVISASSTS	206
QY	181	NNTLDHGLCTAFESSELGDDVEANFTAVTAPPIRARLEAHLPGVNLTDDEVNLMDCPF	240
Db	207	NNTLDPGTCTVFDESELAADIEANFTATVPISIRQRENDSLGSVSLDTEVTVLMDCSF	266
QY	241	DTVARTSDATQSPFCDLFTHDWICYDYQLQSLGKYYGYGAGNPLGPAQGVGVFNELIAR	300
Db	267	DTISTSTVDTKLSPCDLFTHEWINDYQLQSLNKYYGHGAGNELPGTQGVGVANELIAR	326
QY	301	LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMWSIFFALGLYNGTKPLSTTSV	360
Db	327	LTHSPVHDYDTSNHTLDSNPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLSSTTA	386
QY	361	ESIETDGYSGASWTVPFAARAYVENMOCEAEKPEPLRVLVNDRVPLHGGCVDKLGRCKR	420
Db	387	ENITQDTGFSASWTVPFASRMVVENMOQCEQEPLRVLVNDRVPLHGGCPVDALGRCTR	446
QY	421	DDFVEGLSFSARSGGNWEECEFA	441
Db	447	DSFVKGLSFSARSGDWDGECFA	467

RESULT 4

Q9HEQO		PRELIMINARY;	PRT; 467 AA.
ID	Q9HEQO		
AC	Q9HEQO		
DT	01-MAR-2001	(TREMBLrel. 16, Created)	
DD	01-MAR-2001	(TREMBLrel. 16; Last sequence update)	
DE	01-MAR-2001	(TREMBLrel. 16, Last annotation update)	
DE	PHYTASE.		
OS	Aspergillus ficuum.		
OC	Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;		
CC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.		
XX	[NCBI_TaxID=5058;		
NR	[1]		
RP	SEQUENCE FROM N.A.		
RR	Zhang L., An L., Wang Y., Yuan X.;		
RRL	Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.		
RS	EMBL; AY013315; AAG4085.; -		
SQ	SEQUENCE 467 AA; 51012 MW; 3F69AD543C0B565B CRC64;		

Query Match

[illegible]

Qy	121	YKALARKIVPFI	RASGSDRVIA	SAEKFIEGFQ	SAKLADPGAN	PHQASPVIN	VIPEGAGY	180		
Db	147	YESLTRNIVPFI	RSSGSSRVIA	SGNKFIEGFQ	STKLDPRAQ	PCQSSPKIDV	IVISEASTS	206		
Qy	181	NNTLDHGLCTAF	RESELGDVEA	NFTAVFAPP	TRARLEAHL	PGVNLTDE	VNLMDCPF	240		
Db	207	NNTLDPCITVF	EDELADDEI	EAFTATFVP	SIRQLEND	LSGVSLTDE	VTYLMDCSF	266		
Qy	241	DTVARTSDATQ	LSFPFCDL	FTHDEWI	QYDYLO	SLGKYYGY	GAGNPLGPA	QGVGFVNELIAR	300	
Db	267	DTISTSTVDT	KLSPFCDL	FTHDEWI	QYDYLO	SLGKYYGY	GAGNPLGPT	QGVGVANELIAR	326	
Qy	301	LTHSPVODHT	STNHTLDSN	PATPLNAT	LYADFSH	DNTWVS	IFFALGLYNG	TKPLSTSV	360	
Db	327	LTHSPVHDDT	SNHTLDSN	PATPLN	STLYADF	SHDNGIIS	ILFALGLYNG	TKPLSSTA	386	
Qy	361	ESTIETDGS	ASNTVPFAA	RAYVEM	QCAKEPL	RVRLVND	RVPLHCG	VDKLGRCR	420	
Db	387	ENTQTDG	SSARTVPF	ASRMVYEM	QCOSE	QEP	PLRVRLVND	RVPLHCG	CPVDALGRCR	446
Qy	421	DDFVEGLS	FARS	SGNWE	ECFA	441				
Db	447	DSFVKGLS	FARS	SGDWA	ECFA	467				
RESULT	5									
ID	000096									
AC	000096									
DT	01-JUL-1997	(TREM)Rel. 04, Created)								
DT	01-JUL-1997	(TREM)Rel. 04, Last sequence update)								
DT	01-JUL-2021									

RESULT 5

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000096
ID 000096 PRELIMINARY; PRT; 466 AA.
AC 000096;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-
DE PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
DE PHOSPHOHYDROLASE A).
GN PHYA.
OS Talaromyces thermophilus
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Talaromyces.
OX NCBI_Taxid=28565;
RN [1]
RS SEQUENCE FROM N.A.
RP STRAIN=ATCC 20186;
RX MEDLINE=98007872; PubMed=9349716;
RA Pasmantounis L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
RA van Loon A.P.G.M.;
RT "Cloning of the phytases from Emericella nidulans and the thermophilic
RT fungus Talaromyces thermophilus."
RL Biochim. Biophys. Acta 1353:217-223(1997).
CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC FROM PHITATE.
CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
CC -1- MISCELLANEOUS: HAS POTENTIAL AS FOOD AND FEED ADDITIVE. IT CAN
CC FACILITATE THE DEGRADATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS
CC USED AS FOOD FOR MONOGASTRIC ANIMALS.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
DR EMBL; U59802; AAB96873.1; -.
DR HSSP; P34752; 1IHP.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 15 466
FT ACT_SITE 79 79
FT ACT_SITE 357 357
FT DISULFID 28 37
FT DISULFID 68 410
FT DISULFID 212 461
FT DISULFID 261 278

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FT DISULFID 432 440 BY SIMILARITY.
 FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 466 AA; 51450 MW; FC4575B52A5C929 CRC64;
 SQ SEQUENCE 466 AA; 51450 MW; FC4575B52A5C929 CRC64;
 Query Match 72.7%; Score 1702.5; DB 3; Length 466;
 Best Local Similarity 71.9%; Pred. No. 3.4e-130;
 Matches 317; Conservative 38; Mismatches 85; Indels 1; Gaps 1;
 QY 1 NSHSCTVDGGYQCFPEISHLWMTYSPFFSLADESAISPDVPGKRVTFVQVLSRHGARY 60
 DB 24 DSHSNTVEGGYQCFPEISHLWMTYSPFFSLADESAISPDVPGKRVTFVQVLSRHGARY 83
 QY 61 PTSSAKAYSALIEAIOKNAFAKGYAFLKTYNTLGADLTTPFGQOMVNSGKIFYRR 120
 DB 84 PTSSAKAYSALIEAIOKNAFAKGYAFLKTYNTLGADLTTPFGQOMVNSGKIFYRR 143
 QY 121 YKALARKIVPFIRASGDRVIAAEKIEGFSQAKLADPGANPHQASPVINVIPEGAGY 180
 DB 144 YKSLARNVAVPVRCSGDRVIAAEKIEGFSQAKLADPGANPHQASPVINVIPEGAGY 203
 QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRLEAHLPGVNLTDDEVNLMDCPF 240
 DB 204 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRLEAHLPGVNLTDDEVNLMDCPF 263
 QY 241 DTVARTSDATQSPDCDLTFHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVFNELIAR 300
 DB 264 ETLARNHDT-LSPCALSTOEQWQAYDYQSLGKYGYGAGNPLGPAQGVFNELIAR 322
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMWSIFFALGLYNGTKPLSTTSV 360
 DB 323 MTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMWSIFFALGLYNGTKPLSTTSV 382
 QY 361 ESIEETDGYASMTVPFAARAYVEMMOCEAEKPLVRLVNDVRVPLHGCVDKLGCRKR 420
 DB 383 KSIEETDGYASMTVPFAARAYVEMMOCEAEKPLVRLVNDVRVPLHGCVDKLGCRKR 442
 QY 421 DDFVEGLSFARSGGNWEECF 441
 DB 443 DDFVEGLSFARSGGNWEECF 463
 RESULT 6
 ID 000100 PRELIMINARY; PRT: 466 AA.
 AC 000100;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 13, Last sequence update)
 DE 3-PHYTASE PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAKISPHOSPHATE 3-
 DE PHOSPHOHYDROLASE) (3 PHYTASE) (MYO-INOSITOL HEXAKISPHOSPHATE
 DE PHOSPHOHYDROLASE).
 OS Aspergillus terreus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_Taxid=33178;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS 116.46;
 RA Pasamontes L., Halter M., Henriquez Huecas M., Hug D., Mitchell D.B.,
 RA Broger C., van Loon A.P.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
 CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL; U60412; AAB58465.1; .

DR HSSP: P34752; 1IHP.
 DR InterPro: IPR000560;
 DR Pfam: PF00328; acid_phosphat: 1.
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1. UNKNOWN_1.
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 466 3-PHYTASE.
 FT ACT_SITE 82 82 REQUIRED FOR BINDING SUBSTRATE (BY
 SIMILARITY).
 FT ACT_SITE 83 83 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 31 40 BY SIMILARITY.
 FT DISULFID 71 414 BY SIMILARITY.
 FT DISULFID 215 465 BY SIMILARITY.
 FT DISULFID 264 282 BY SIMILARITY.
 FT DISULFID 436 444 BY SIMILARITY.
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 466 AA; 51055 MW; F2AECBCIAF7C22C4 CRC64;
 Query Match 72.4%; Score 1696; DB 3; Length 466;
 Best Local Similarity 70.7%; Pred. No. 1.1e-129;
 Matches 311; Conservative 46; Mismatches 83; Indels 0; Gaps 0;
 QY 1 NSHSCTVDGGYQCFPEISHLWMTYSPFFSLADESAISPDVPGKRVTFVQVLSRHGARY 60
 DB 27 NSHSCTVDGGYQCFPEISHLWMTYSPFFSLADESAISPDVPGKRVTFVQVLSRHGARY 86
 QY 61 PTSSAKAYSALIEAIOKNAFAKGYAFLKTYNTLGADLTTPFGQOMVNSGKIFYRR 120
 DB 87 PTSSAKAYSALIEAIOKNAFAKGYAFLKTYNTLGADLTTPFGQOMVNSGKIFYRR 146
 QY 121 YKALARKIVPFIRASGDRVIAAEKIEGFSQAKLADPGANPHQASPVINVIPEGAGY 180
 DB 147 YDLTRHINEFVRADSSRVHESAEKIEGFSQAKLADPGANPHQASPVINVIPEGAGY 206
 QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRLEAHLPGVNLTDDEVNLMDCPF 240
 DB 207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRLEAHLPGVNLTDDEVNLMDCPF 266
 QY 241 DTVARTSDATQSPDCDLTFHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVFNELIAR 300
 DB 267 ETVSLTDDAHTLSPDCDLTFHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVFNELIAR 326
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMWSIFFALGLYNGTKPLSTTSV 360
 DB 327 LTRSPVHDHTCVNNTLDANPATFPLNATLYADFSDHNTMWSIFFALGLYNGTKPLSTTSV 386
 QY 361 ESIEETDGYASMTVPFAARAYVEMMOCEAEKPLVRLVNDVRVPLHGCVDKLGCRKR 420
 DB 387 EDITRTDGYAAAWTPFAARAYVEMMOCEAEKPLVRLVNDVRVPLHGCVDKLGCRKR 446
 QY 421 DDFVEGLSFARSGGNWEECF 440
 DB 447 DDFVEGLSFARSGGNWEECF 466
 RESULT 7
 ID 000085 PRELIMINARY; PRT: 466 AA.
 AC 000085
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAKISPHOSPHATE 3-

DE PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
 GN PHA.
 OS Aspergillus terreus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=33178;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9A1;
 RX MEDLINE=97177792; PubMed=9025298;
 RA Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L., Loon A.P.;
 RT "The phytase subfamily of histidine acid phosphatases: isolation of
 RT genes for two novel phytases from the fungi *Aspergillus terreus* and
 RT *Myceliophthora thermophila*.";
 RL Microbiology 143:245-252(1997).
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
 CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
 CC -!- MISCELLANEOUS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF
 CC 2.5 TO 7.5, WITH MAXIMAL ACTIVITY AT PH 5.5. ALSO ACCEPT 4-
 CC NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA SHIFTED TO
 CC MORE ACIDIC PH VALUES.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL; U59805; AA052507.1; --
 DR HSSP; P34752; 1IHP.
 DR InterPro; IPR000560; --
 DR Pfam; PF00328; acid.phosphat. 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 466 3-PHYTASE A.
 FT ACT_SITE 82 82 REQUIRED FOR BINDING SUBSTRATE (BY
 FT SIMILARITY).
 FT ACT_SITE 83 83 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 31 40 BY SIMILARITY.
 FT DISULFID 71 414 BY SIMILARITY.
 FT DISULFID 215 465 BY SIMILARITY.
 FT DISULFID 264 282 BY SIMILARITY.
 FT DISULFID 436 444 BY SIMILARITY.
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 466 AA; 51093 MW; 21CDB559C96AE66 CRC64;

Query Match 71.2%; Score 1668.5; DB 3; Length 466;
 Best Local Similarity 70.2%; Pred. No. 28-127;
 Matches 308; Conservative 53; Mismatches 77; Indels 1; Gaps 1;
 QY 3 HS-CDTVGGYQCPELISHWGYSPFFSLADESAISPDPKRCRTVFQVLSRHGARYP 61
 DB 28 HSDCNVDHGYQCPELISHWGYSPFFSLADESAISPDPKRCRTVFQVLSRHGARYP 61
 QY 62 TSSAKAYSALIEAIQKNAFAKGYAEKTYTLGADDLTPFGQOQWNSGKIFRYR 121
 DB 88 THSKTAYATTAIAQKSTAFPGKTAFAQSYNSLDSSELTTPFGRNQLDLGAQFYRY 147
 QY 122 KALARKIVPFRASGSDRYIASAEKPIEGFSQAKLADPCANPHQASPVNTNIPSGAGN 181
 DB 148 NALTRHINPFRVATDSRVHSAEKVEFGQTARQDDHANPHQSPRDVAIPGGSAYN 207
 QY 182 NTLDHGLCTAFSESELGDDVEANFTAVAPPTRAEALHPCGNLTDEVDNLMDCPFD 241
 DB 208 NTLHSLCTAFSSSTVGDDAVANFTAVFAPATAQRLEADLPGVQLSTDVDVNLAMCPFE 267

QY 242 TVARTSDATQLSPFCDLFDHDEWIQYDYLQSLGKYGYGAGNPLGPAQGYGVFNELIARL 301
 DB 268 TVSLTDDAHTLSPFCDLFTATEWTQYNYLLSLDKYGYGAGNPLGPAQGYGVFNELIARL 327
 QY 302 THSPVQDHTSTNNHTLDSNPATFPLNATLYADFSDHNTWVSIFPALGLYNGTKPLSTTSVE 361
 DB 328 TRAPVHDHTCVNNTLDASPFATFPLNATLYADFSDHNSLVSFIFWALGLYNGTAPLSQTSVE 387
 QY 362 SIEETDGSASVTPFAARAYVEMQCEAKEPLRVRLVNDVRVPLHGGCVGDKLGRCKRD 421
 DB 388 SVSOTDGYAAATVPFAARAYVEMQCEAKEPLRVRLVNDVRVPLHGGCVGDKLGRCKRD 447
 QY 422 DFVEGLSFARSGGNWEECF 440
 DB 448 AFAVAGLSFAQAAGGNWADCF 466

RESULT 8
 ID 000107 PRELIMINARY; PRT; 487 AA.
 AC 000107;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAKISPHOSPHATE 3-
 DE PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
 DE PHOSPHOHYDROLASE A).
 GN PHA.
 OS Thielavia heterothallica.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Chaetomiaceae; Thielavia.
 OX NCBI_TaxID=78579;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97177792; PubMed=9025298;
 RA Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L.,
 RA van Loon A.P.G.M.;
 RT "The phytase subfamily of histidine acid phosphatases: isolation of
 RT genes for two novel phytases from the fungi *Aspergillus terreus* and
 RT *Myceliophthora thermophila*.";
 RL Microbiology 143:245-252(1997).
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
 CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
 CC -!- MISCELLANEOUS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF
 CC 3.5 TO 8.5, WITH MAXIMAL ACTIVITY BETWEEN PH 5.5 AND 6.0. ALSO
 CC ACCEPT 4-NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA
 CC SHIFTED TO MORE ACIDIC PH VALUES.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL; U59806; AA052508.1; --
 DR HSSP; P34752; 1IHP.
 DR InterPro; IPR000560; --
 DR Pfam; PF00328; acid.phosphat. 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 487 3-PHYTASE A.
 FT DOMAIN 267 270 POLY-SER.
 FT DOMAIN 423 433 POLY-GLY.
 FT ACT_SITE 75 75 REQUIRED FOR BINDING SUBSTRATE (BY
 FT SIMILARITY).
 FT ACT_SITE 76 76 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 368 368 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 26 35 BY SIMILARITY.
 FT DISULFID 64 421 BY SIMILARITY.
 FT DISULFID 208 485 BY SIMILARITY.
 FT DISULFID 260 289 BY SIMILARITY.
 FT DISULFID 456 464 BY SIMILARITY.
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	247	247	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	346	346	N-LINKED (GLCNAC. . .) (POTENTIAL).
TSQ	SEQUENCE	487 AA;	52537 MW;	97D10EDC83D051DB CRC64;

Query Match	56.4%;	Score 1320.5;	DB 3;	Length 487;
Best Local Similarity	55.0%;	Pred. No. 4.1e-99;		
Matches	257;	Conservative	55;	Mismatches 156;
				Indels 29;
				Gaps

QY	2	SHSCVDVGGYOCFPEI	SHLNGTSTPPFSLADESAISPDVPKGCRTVTFVQVLSRHGARYP	61	
DB	23	SRPCOTPDGLGFCGTAISHFWGQSYSPYFSVSE--	LDASIPDDCEVTFQAQVLSRHGARAP	80	
QY	62	TSSASKAYSALTEAQKNATKPAFGYAF	LKTVNYVTLGADLLTPFGEQQMVNSGKFFYRY	121	
DB	81	TLKRAASYVDLDIRLHGAISVPGCYEFLRYDYL	TLGADELTRTGOQQMVNSGKFFYRY	140	
QY	122	KALARKIVPFIIRASGSDRVIASAEKFI	EGFOSAKIADPGANPHQASPVNIIPEGAGYN	181	
DB	141	RALKARISIFVITAGDGRVHVHSAENFTG	FGHALLADRGSTVRPLTPYDMVVIPTAGAN	200	
QY	182	NLTDHGLCTAFEE--	SELGDDVEANFTAVFAAPP	IRARLEAHLPGVNLTDEDVNLMDC	238
DB	201	NLTHDLCCTAFEEGYSTIGDAAQDTYLS	TFCAPITARVNANLPGANLTDATVALMDLC	260	
QY	239	PFTDVARTS-----	DATQLSPFCDLTFHDEWIQYVLQSLGKYYGYGAGNPLGP	287	
DB	261	PFTVASSSSDPATADAGGNGRPLSPFC	RLFSSESWRAYDYLQSVGKWIYGYGPNPLGP	320	
QY	288	AQGVGFVNELIARLTHSPVQDHTSTN	HTLDSNPATFPPLNATLYADFSDHNTMVSIFFALG	347	
DB	321	TOGVGFVNELLARLAVPVRDGTSRT	LDGDPRTFPLGRPIYADFSDHNDMMGVLGALG	380	
QY	348	LYNGTKPLSTTSVESIEETDGY	SASVTVPFAARAYVEMMQ-----	BAEKEP	394
DB	381	AYDGVPELDTARRDPEELGGYAA	SWAVFAARIYVEKMKRCGGGGGGGGEGROEKDEE	440	
QY	395	LVRVLVNDRVPLHGGVDVKLGRCK	RDDFVEGLSFAIRSGNWECEFA	441	
DB	441	MVRVLVNDRVYTLKGGCADERG	CMCTLERFIESNAFARGNKWDLCEFA	487	

RESULT	9
074677	PRELIMINARY; PRT; 442 AA.
ID	074677;
AC	01-NOV-1998 (TrEMBLrel. 08, Created)
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE	REPRESSIBLE ACID PHOSPHATASE (EC 3.1.3.2).
GN	PHO1.
OS	Pichia angusta (Yeast) (Hansenula polymorpha).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC	Saccharomycetales; Saccharomycetaceae; Pichia.
OC	NCBI_TaxID=4905;
EN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ATCC34438;
RC	MEDLINE=98386672; Pubmed=9720203;
RA	Phongdara A., Merckelbach A., Keup P., Gellissen G., Hollenberg C.P.;
RA	"Cloning and characterization of the gene encoding a repressible acid
FT	phosphatase (PHO1) from the methylotrophic yeast Hansenula
FT	polymorpha.";
FT	Appl. Microbiol. Biotechnol. 50:77-84(1998).
RL	EMBL; AF051161; AAC62537.1; -.
DR	HSSP; P34755; 10FX.
DR	InterPro; IPR000560;
DR	Pfam; PF00328; acid_phosphat; 1.
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW	Hydrolase.
SQ	SEQUENCE. 442 AA; 49370 MW; 7087D91A85B05C31 CRC64;

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Db 82 PTASKGLKLTALWDKLEKFGQGYNGMEVFNDEYFVSNTKYFDQLTNSTVDPSNPYAG 141
QY 107 EQQVNSGKFKYRRYKALARKIVPIRAGSDRVIAIAAEKFIQFQSAKLADPGANPHQA 166
Db 142 AKTAQHLGKYIAYNGDLFSNPN-VFTSSGRVHQTKARYVSSLEEE----- 188
QY 167 SPVINY-----IPEG--AGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPARLEA 219
Db 189 ---LDQLDLQIIOENETSGANSLPADSCWY-NGDUGDEYFENATLPYLTIDKNRMK 244
QY 220 HLPQVNLT--DEVVNMDMCPDFTVARTSDATQSPFCDLTFHDEWIQYDYLQSLGKY 277
Db 245 KNSNLNLTLEHDDIELLDVWCAFEVTKGSSAV-----CDLFEKNDLVAYSYANVNFY 299
QY 278 GYGAGNPLGAGGVGVNELARLTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSH 337
Db 300 RGAGNPMNSPIGSLVNASVNLTOADELDN-----KWLFSFSHDT 341
QY 338 TMVSIFFAIGLY-NGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMOCBAKEP 396
Db 342 DIQQFISALGLDNG---VTEYSLDQVDFQNIQQLSWTPMGGGRIFTEKLC--GNASYV 396
QY 397 RVLVNDRVVPLHGGCVKGLKCRKDDF-----VEGLSFARS 432
Db 397 RYIINDVPIPVPGCTSGRFGFSCPTIEDFDYITNRLNGIDYVSS 439

RESULT 11
O60172 PRELIMINARY; PRT; 463 AA.
AC O60172;
DT 01-AUG-1998 (TremBLrel. 07, Created)
DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)
DE PROBABLE ACID PHOSPHATASE (EC 3.1.3.2).
GN SPC21H7.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX Schizosaccharomycetes.
NCBI_TaxID=4896;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M., Rajadream M.A., Barrell B.G., Xiang Z., Aves S.;
RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -i- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
CC ALCOHOL + ORTHOPHOSPHATE.
CC -i- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
DR EMBL; AL023286; CAAL18863.1; -.
DR HSSP; P34755; IQFX.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Glycoprotein.
FT ACT_SITE 69 69 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 340 340 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 439 439 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 463 AA; 52758 MW; 6C41AF422C6D24A CRC64;

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Query Match 13.3%; Score 311.5; DB 3; Length 463;
 Best Local Similarity 25.3%; Pred. No. 4e-17;
 Matches 113; Conservative 69; Mismatches 197; Indels 67; Gaps 15;
 QY 20 HLMGTYS-----PFFSLADEAISPDVPGKRVTFVQVLSRHGARYPTS--SASKAYSAA-- 71

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Db 35 HL-GTLSPYHEPYFDGLDSA-----FPETCEIQVHLLQRHSGNPTGDTATDVSSQY 88
QY 72 -----LIEAQKNATAFKGYAFKTNLYL---GADDLTPFGQQMVNSGIKFYRR 120
Db 89 LNNFQEKLLNGSIPVNFSPENPLCFIKQWTPVIDAENADQLSSRLRFLDLGRQLYQR 148
QY 121 YKALARIVPIFIRASGSDRVIAIAAEKFIQFQSAKLADPGANPHQASPVINVIPEG--A 178
Db 149 YKLFDSYVVDINTAEQEVVESAKWFTYGLFGDKWE-----KTNFLLISEKAA 199
QY 179 GYNTLDHGLCTAFESL-----GDDVEANFTAVFAPPARLEAHL-PCGNLTDEEDVN 233
Db 200 GANSLSYNACPVKDNFKNFKNATDAHAHVNRNFIETPIVNRKAYFDSYKLTINDVRS 259
QY 234 LMDMCPDFTVARTSDATQSPFCDLTFHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGF 293
Db 260 LFICEYEIAIKOH-----SDFCSIFTPSEFLNFYDSDLDQAYGGPVSEWASTLGGAY 314
QY 294 VNELIARLTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSHNTWVSIFFALGLYNGTK 353
Db 315 INNLADSL-----RNVNPDGFRK-----VLAFTHDSNIIPVEAALGFFPDIT 358
QY 354 PLSTTSVESIEETDGYASWTVPFAARAYVEMMOCBAKEPVLVNDRVVPLHGGCVGD 413
Db 359 PQNPLPTDKNIYTSQKTSFVFPFAGNLITELFFC--SDSKYVVRHLVNOQVYPLDLCGYG 417
QY 414 KLGR----CKRDDFVEGLSFARSNGN 435
Db 418 PSCTSGLCELQAYLNSPIRANSTSN 443

RESULT 12
Q9VV72 PRELIMINARY; PRT; 460 AA.
AC Q9VV72;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DE MIPPI PROTEIN.
GN MIPPI OR CG4123.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbavani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fessler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ihegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

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RA Merkulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003527; AAF49450.1;
DR FlyBase: FBgn0026061; Mippl.
DR InterPro: IPR000560;
DR Pfam: PF00328; acid_phosphat; 1
SQ SEQUENCE 460 AA; 52685 MW; F00B25718E40807D CRC64;

Query Match 8.7%; Score 204.5; DB 5; Length 460;
Best Local Similarity 23.9%; Pred. No. 2e-08;
Matches 106; Conservative 64; Mismatches 171; Indels 103; Gaps 22;

QY 40 DVPK-----GCRVTFVQVLSRHGARYPTSS-----ASKAYSALIEAIQKNATAFKCK-----86
Db 46 DIDKQYLVPGCOPQKWMFHRHGRTRLPKSKMINKASRV-AELRLIINNNYQVARTKPTD 104
QY 87 -----YAFKTYNTLGADDTTPGEQMVNSGFKYRYKALKARKIVP-FIRASGSD- 138
Db 105 ALCQTDLIAIKLWKN-----SSITPDMEELTAQGVEDLRGTAKLYQRYPPVILANYNDT 161
QY 139 ---RVIASAEKIEG-FOSAKLADPGANPHQ-----ASPVINV-IIPEGAGYNNTL 184
Db 162 YQRTTESFAEAGLFGSQNAHPVEIPKQDLLRPDYCCSFKNVYKDEGSEYK-- 219
QY 185 DHGLCTAFESLGGDDVFANFTAVTAPIRARLEAHLPG--VNLTDEDVNLMDMCPDPT 242
Db 220 -----FHQSKLYNDTLAD-----ISTRLL-----GFLYTBEEADIKLMDMCRVE- 258
QY 243 VARTSDATQSPFCDLFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGVFNELIARLT 302
Db 259 --QANVDRNSVWCAGFLPEQITVEYLEDLKYYSGVGPFENAHLCRLVQDLLTHLS 316
QY 303 HSPVDQSTNHTLDSNPATFPLNATLYADFSHDNTMWSIFFALGLYNGTRPLSTTSVES 362
Db 317 -NPVSPH-----VVAHFGHSTGLLTLLTALGIGKDDIKLRADNYDS 356
QY 363 IETDGYASNTVPPFAARYVEMQCEA--EKEPLRVLVNDRVVPPLHGCYVDKLGCRKR 420
Db 357 L-TSRWKSLSLIDPFAANVAVKYDCPADLDREKVY-PFLNQAVQLDWCSV---GLCKW 411
QY 421 DDFVE-----GLSFARSGG 434
Db 412 SDVLEKYKTIADACGEYICRTGG 435

RESULT 13
ID 035217 PRELIMINARY; PRT; 451 AA.
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DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-AUG-1999 (TEMBLrel. 11, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE HEPATIC MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE (EC 3.1.3.-)
DE (MIPPL).
GN MIPPL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

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[1] SEQUENCE OF 11-451 FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RP TISSUE=LIVER;
RX MEDLINE-98028656; PubMed-9359836;
RA Craxton A., Caffrey J.J., Burkhardt W., Safrany S.T., Shears S.B.;
RT "Molecular cloning and expression of a rat hepatic multiple inositol
RT polyphosphate phosphatase."
RL Biochem. J. 328:75-81(1997).
[2]
RN CATALYTIC ACTIVITY.
RP MEDLINE-91358435; PubMed-1653239;
RX Nogimori K., Hughes P.J., Glennon M.C., Hodgson M.E., Putney J.W. Jr.;
RA Shears S.B.;
RT "Purification of an inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase
RT activity from rat liver and the evaluation of its substrate
RT specificity."
RL J. Biol. Chem. 266:16499-16506(1991).
CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INOSITOL 1,3,4,5-
CC TETRAKISPHOSPHATE TO INOSITOL 1,4,5-TRIPHOSPHATE AND INOSITOL
CC 1,3,4,5,6-PENTAKISPHOSPHATE TO INOSITOL 1,4,5,6-TETRAKISPHOSPHATE
CC AND THEN TO INOSITOL 1,4,5-TRIPHOSPHATE. DEPHOSPHORYLATES
CC INOSITOL HEXAKISPHOSPHATE WITHOUT SPECIFICITY TOWARDS A PARTICULAR
CC PHOSPHATE GROUP.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY AND LIVER.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
DR EMBL: AF012714; AAC53453.1;
DR InterPro: IPR000560;
DR InterPro: IPR000896;
DR Pfam: PF00328; acid_phosphat; 2;
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; FALSE_NEG.
KW Hydrolase; Glycoprotein; Phosphorylation; Multifunctional enzyme.
FT ACT_SITE 59 59
FT MOD_RES 146 65
FT MOD_RES 176 176
FT MOD_RES 201 201
FT MOD_RES 218 218
FT MOD_RES 391 391
FT MOD_RES 412 412
FT MOD_RES 435 435
FT MOD_RES 447 447
FT MOD_RES 206 206
FT CARBOHYD 445 445
FT VARIANT 3 3
FT CONFLICT 327 327 S->P (IN AAC53453).
FT SITE 448 451 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 451 AA; 51592 MW; EB1C05512A03020B CRC64;

Query Match 8.4%; Score 196; DB 11; Length 451;
Best Local Similarity 21.3%; Pred. No. 9.5e-08;
Matches 91; Conservative 72; Mismatches 187; Indels 78; Gaps 17;

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QY 71 ALIEAIQKNATAFKGYAFLKTYNTLTGADDLTPFGQQMVNSGIKFYRYKALKARKIVP 130
Db 74 QLGLLQITRESVDGSRVAAALDQWPLWYDD---WMDGQLVEKGRQDMRQLALALAFP 130
QY 131 --FIR-----ASGSDRVIAAEKFIIEGFSQAKLADPGANPHQASPVNIIPEGAG 179
Db 131 DLFRCRENYGRLLITSSKHKRCVDSAAFLQGLW--QHYHGLP-----PDVSDMECDPPR 184
QY 180 YNNTL---DHGLCTAFESLGGDDVFANFTAVF-----APPFIRALE-----AHLPG 223
Db 185 VNDKLMREFDH--CEKFL-----TEVERNATALYHVEAFKGTGPEMOTVLKRVAAATLQVPV 237
QY 224 VNLTDEDVNNLMDMCPDPTVARTSDATQSPFCDLFTHDEWIOYDYLQSLGKYGYGAGN 283
Db 224 VNLTDEDVNNLMDMCPDPTVARTSDATQSPFCDLFTHDEWIOYDYLQSLGKYGYGAGN 283

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Db 238 NNLNADLIOVAFETCSFDLAIQGVH-----SPWCDVDFDADKAVLEYLNDLKQYWKRSYGY 293
QY 284 PLGPAQGVGFVNEILARLTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSDHNTMVSIF 343
Db 294 AINSRSCNLFQDIFLHLDKAVEQKORSO-----PVSSSVILQFGHAETLLPLL 342
QY 344 FALGYNGTKPLSTTSVESIEETDGSASWTVPFAARAYVEMMOCEAEKEP-----LVRVL 399
Db 343 SLMGYFKDKLEPLTAYNFEROVHRE-FRSHIVPYASNLIPLVLYHCEDAQTOERFQIQML 401
QY 400 VNDRVVPL 407
Db 402 LNEKVLPL 409

RESULT 14
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AC O96421;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE 1.
GN MIP1 OR CG4123.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Karyogota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN NCBI_TaxID=7227;
RP SEQUENCE FROM N.A.
RA Chi H., Wang J., Romano P.R., O'keefe R.J., Puzas J.E., Rosier R.N.,
RA Reynolds P.R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF046913; AAD02436.1;
DR FlyBase; FBgn0026061; Mip1.
DR InterPro; IPR000560;
DR Pfam; PF00328; acid_phosphat; 1.
SQ SEQUENCE 467 AA; 53602 MW; 1A0571B9958B2632 CRC64;

Query Match 8.4%; Score 196; DB 5; Length 467;
Best Local Similarity 22.8%; Pred. No. 1e-07;
Matches 103; Conservative 66; Mismatches 172; Indels 110; Gaps 21;

QY 40 DVPK-----GCRVTFQVLSRHGARYPTSS-----ASKAYSALIEATQKNATAFKGK---- 86
Db 46 DIDKQVLPVCGCQKQKMWIFRHGTRLPKSKWINKASRV-AELRDLINNQQVARTKETD 104
QY 87 -----YAFLLTYNYTLGADDLTPFGQQMVNSGIKFRYKALARKIVPFI----- 132
Db 105 ALQOTDLIAIKLKWNN---SSITPDMEYLTAGQYEDLRGTAKLYQRYPTVLTANYNDT 161
QY 133 ----RAGSDRVIASAEKFTFG-FQSALADPGANPHQ-----ASPVINV-IIPGG 177
Db 162 YQFRHTDQRTTESKFAEGFLGSONAHVPEIPQDILLRPDYCSFKNVNTKDEG 221
QY 178 AGYNNTLDHGLCTAFESLGGDVEANFTAVFAPPFARLEAHLPG--VNLTDEDVNNLM 235
Db 222 SEYK-----FHQSILYNDLAD-----ISTRL-----GFLYLEADIKLMY 259
QY 236 DMCPTDVTARTSATQISPCDLFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFVN 295
Db 260 DMCRYE---QAMVDRNSWCMGAFLEQITVFYLEDLKYIYGGYGGFPENAHNCRVQ 316
QY 296 ELIARLTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSDHNTMVSIFALGLYNGTKPL 355
Db 317 DLTLHLS-NPVSPH-----VVXHGHSGLTLLTLLGIXKDDIKL 356
QY 356 STTSVESIEETDGSASWTVPFAAR--AYVEMMOCEAEKEPLRVLVNDRVVPLHGCGVD 413
Db 357 RADNYDSL-TSRNWKSLIDPFAANFVAVKYDLPADLDREKVV--FFLNQQAQVQLDWCSV- 413

QY 414 KLGRCKRDFDVE-----GLSFARSG 434
Db 414 --GLCKWSVLEKVKYKTIADADCGEYCYRTG 442

RESULT 15
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AC O95172;
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DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
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GN MIPP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Chi H., Wang J., Romano P.R., O'keefe R.J., Puzas J.E., Rosier R.N.,
RA Reynolds P.R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF046914; AAD02437.1;
DR InterPro; IPR000560;
DR InterPro; IPR000886;
DR Pfam; PF00328; acid_phosphat; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
SQ SEQUENCE 487 AA; 55157 MW; FCDD827933C39D05 CRC64;

Query Match 8.0%; Score 188; DB 4; Length 487;
Best Local Similarity 21.4%; Pred. No. 4.8e-07;
Matches 89; Conservative 68; Mismatches 172; Indels 86; Gaps 17;

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Db 71 PELLETCTPVLVALIRHGTPTVKQIRKLRLHGLLQPRGSRDGGASS---TGSRD 127
QY 98 GA-----DDLTPFGEQQMVNSGIKFRYKAL-ARKIVPFI--ASGSDRV 140
Db 128 GAALRDWPLWYADWMDGQLVEKGRQDMRHVALRLASLPALFSSRENYGLRLITSSKHC 187
QY 141 IASAEKFTFGFOSAKLADPGANPHQAS-----PVINIIPEGAGYNTLDHGLCTAFEE 194
Db 188 MDSSAAFLQGLW--QHYHPLGLPPDPVADMEFGPTVNDKL-----MRFFDH--CEKFL- 236
QY 195 SELGDDVEANFTAVFAPPFARLEAHLPG-----VNLTDEDVNNLM-MD 236
Db 237 ----TEVEKNATALY-----HVEAFKTPGEMQNLKVAATLQVPVNDLADLIQVAF 286
QY 237 MCPPTVARTSATQISPCDLFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFVN 296
Db 287 TCSFLAIKGVK----SPWCDVDFDIDDAKAVLEYLNDLKQYWKRGYGYTINSRSCCTLFQD 342
QY 297 LIARLTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSDHNTMVSIFALGLYNGTKPLS 356
Db 343 IFQHLDKAVEQKORSO-----PISSPVILQFGHAETLLPLSLMGYFKDKLEPT 391
QY 357 TTSVESIEETDGSASWTVPFAARAYVEMMOCEAEKEP-----LVRVLVNDRVVPL 407
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us-09-488-265-31_copy_27_467.rspt

Thu Oct 18 11:34:57 2001

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2182	93.2	441	4	US-09-121-425-1
2	2044	87.3	467	4	US-09-121-425-2
3	1810	77.3	467	1	US-07-923-724-8
4	1810	77.3	467	2	US-08-609-426A-8
5	1810	77.3	467	2	US-08-374-652C-2
6	1806	77.1	467	1	US-08-151-574-32
7	1806	77.1	467	1	US-08-146-424-20
8	1806	77.1	467	1	US-08-693-709-2
9	1806	77.1	467	2	US-08-419-448-32
10	1806	77.1	467	2	US-08-819-825-3
11	1806	77.1	467	4	US-09-163-642-3
12	1799	76.8	443	4	US-09-155-855-1
13	1799	76.8	467	4	US-09-155-855-3
14	1794	76.6	443	4	US-09-155-855-2
15	1379	58.9	475	4	US-08-819-825-2
16	845.5	36.1	443	3	US-08-993-359-30
17	845.5	35.6	453	3	US-08-993-359-22
18	830.5	35.5	439	3	US-08-993-359-24
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21	825	35.2	442	3	US-08-993-359-28
22	814	34.8	442	3	US-08-993-359-26
23	354.5	15.1	446	1	US-07-627-539G-7
24	354.5	15.1	468	1	US-07-627-539G-2
25	354.5	15.1	479	1	US-07-923-724-2
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28	354.5	15.1	479	2	US-08-374-652C-4	Sequence 4, Appli
29	185.5	7.9	92	3	US-08-993-359-32	Sequence 32, Appli
30	177.5	7.6	449	3	US-08-680-506-7	Sequence 7, Appli
31	122	5.2	113	1	US-08-241-853-8	Sequence 8, Appli
32	122	5.2	113	2	US-08-850-917-8	Sequence 8, Appli
33	120	5.1	318	3	US-08-680-506-3	Sequence 3, Appli
34	115	4.9	24	2	US-08-374-652C-32	Sequence 32, Appli
35	111	4.7	113	1	US-08-241-853-10	Sequence 10, Appli
36	111	4.7	113	2	US-08-917-17-10	Sequence 10, Appli
37	99	4.2	386	1	US-08-758-213-1	Sequence 1, Appli
38	99	4.2	386	2	US-08-692-787-48	Sequence 48, Appli
39	99	4.2	386	4	US-09-097-199-48	Sequence 48, Appli
40	99	4.2	515	2	US-09-146-283-2	Sequence 2, Appli
41	99	4.2	515	3	US-08-579-823A-2	Sequence 2, Appli
42	99	4.2	515	4	US-09-344-195-2	Sequence 2, Appli
43	93.5	4.0	2465	2	US-08-596-291-3	Sequence 2, Appli
44	93.5	4.0	2465	3	US-09-100-804-3	Sequence 3, Appli
45	93.5	4.0	2466	3	US-09-080-855-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-1

Query Match	93.2%	Score 2182;	DB 4;	Length 441;
Best Local Similarity	93.0%	Pred No. 6.5e-222;	Mismatches 20;	Indels 0;
Matches 410;	Conservative 11;			Gaps 0;
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Db	1	NNSHCDTVGGYQCFFPEISHLWGTYSPPFSLADESAISPDVPGKCRVTFVQVLSRHGARY	60	
QY	61	PTSSASKAYSALIEATKKNATKAFKGYAFLKTYNTLGGADLTPFGQQQNSGKPYRR	120	
Db	61	PTSSASKAYSALIEATKKNATKAFKGYAFLKTYNTLGGADLTPFGQQQNSGKPYRR	120	
QY	121	YKALARKIVPFFIRASGSDRVIASAEKFTGFSQAKLADPGANPHQASPVINVIPEGAGY	180	
Db	121	YKALARKIVPFFIRASGSDRVIASAEKFTGFSQAKLADPGANPHQASPVINVIPEGAGY	180	
QY	181	NNTLDHGLCTAFEESELGGDVEANFTAVFAPPIRARLEAHLPGVNLTDDEVDVNLMDMCPF	240	
Db	181	NNTLDHGLCTAFEESELGGDVEANFTAVFAPPIRARLEAHLPGVNLTDDEVDVNLMDMCPF	240	
QY	241	DTVARTSDATQLSPFCDLFTHDEMTQDYDYLQSLGKYGYGAGNPLGPAQGVGFNLIAR	300	
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Db 361 ESIEETDGYASWTVPFARAYVEMMOCEAEKEPLRVLVNDRVVPVPLHGGCAVDKLGCRKR 420
Qy 421 DDFVEGLSFARSGGNWEECEFA 441
Db 421 DDFVEGLSFARSGGNWEECEFA 441

RESULT 2
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus Phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-09-121-425-2

Query Match 87.3%; Score 2044; DB 4; Length 467;
Best Local Similarity 84.6%; Pred. No. 2.7e-207;
Matches 390; Conservative 11; Mismatches 20; Indels 40; Gaps 2;
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Db 27 NNSHCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPGCRVTFVQVLSRHGARY 86
Qy 61 PTSSASKAYSALEIAQKNATAFKGYAFKTYNTLGADDLTPFGEQOMVNSGKIFYRR 120
Db 87 PTSSASKAYSALEIAQKNATAFKGYAFKTYNTLGADDLTPFGEQOMVNSGKIFYRR 126
Qy 121 YKALARKIVPFIIRASGSDRVIAAEKFIIEGFSQAKLADPGANPHQASPVIN 171
Db 127 YKALARKIVPFIIRASGSDRVIAAEKFIIEGFSQAKLADPGANPHQASPVIN 186
Qy 172 -----VITPEGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAH 220
Db 187 TAFGKGYAFKLVIIPEGGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAH 246
Qy 221 LPGAQVGLVNDMDMCPFTVARTSDATQSPFCDLFTHDWIDYDYLQSLGKYGYG 280
Db 247 LPGAQVGLVNDMDMCPFTVARTSDATQSPFCDLFTHDWIDYDYLQSLGKYGYG 306
Qy 291 AGNPLGPAQGVGFYNELIARLTSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMV 340
Db 307 AGNPLGPAQGVGFYNELIARLTSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMV 366
Qy 341 SIFFALGLYNGTAPLSTTSVIESIETDGYASWTVPFAARAYVEMMOCEAEKEPLRVLV 400
Db 367 SIFFALGLYNGTAPLSTTSVIESIETDGYASWTVPFAARAYVEMMOCEAEKEPLRVLV 426
Qy 401 NDRVVPVPLHGGCVDKLGRCKRDDDFEGLSFARSGGNWEECEFA 441
Db 427 NDRVVPVPLHGGCAVDKLGCRCKRDDDFEGLSFARSGGNWEECEFA 467

RESULT 3

US-07-923-724-8
; Sequence 8, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerström, Richard B.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923.724
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0240004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-923-724-8

Query Match 77.3%; Score 1810; DB 1; Length 467;
Best Local Similarity 76.0%; Pred. No. 1.4e-182;
Matches 335; Conservative 40; Mismatches 66; Indels 0; Gaps 0;
Qy 1 NNSHCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPGCRVTFVQVLSRHGARY 60
Db 27 NNSHCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPGCRVTFVQVLSRHGARY 86
Qy 61 PTSSASKAYSALEIAQKNATAFKGYAFKTYNTLGADDLTPFGEQOMVNSGKIFYRR 120
Db 87 PTSSASKAYSALEIAQKNATAFKGYAFKTYNTLGADDLTPFGEQOMVNSGKIFYRR 146
Qy 121 YKALARKIVPFIIRASGSDRVIAAEKFIIEGFSQAKLADPGANPHQASPVINIIPEGAGY 180
Db 147 YESLTRLNIIFFIRSSGSSRVIASGEKFIIEGFSQAKLADPGANPHQASPVINIIPEGAGY 206

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QY 181 NNTLDHGLCTARESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDVVVNLMDMCPF 240
Db 207 NNTLDPGTCTVFESELDATVEANFTATFAPSIRQRLNDLSGVTLTDEVTYLMDCSF 266
QY 241 DTVARTSDATQSPFCDLFTDHEWIDYQYDLSGLKYYGYGAGNPLGPAQGVGVNELIAR 300
Db 267 DTISTSTVDTKLSPFCDLFTDHEWIDYQYDLSGLKYYGYGAGNPLGPAQGVGVNELIAR 326
QY 301 LTHSPVQDHTSNHLDSPATFPLNATLYADFSDHNTMVSIFFFALGLYNGTKPLSTTSV 360
Db 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTMVSIFFFALGLYNGTKPLSTTSV 386
QY 361 ESIEETDGYASWTVPFAARAYVENMQCEAEKEPLRVLVNDRVVPLHGCCGVDKLGRCKR 420
Db 387 ENITQDGFSSAWTVPFASRLYVENMQCEAEKEPLRVLVNDRVVPLHGCCGVDKLGRCKR 446
QY 421 DDFVEGLSFARSGGNWEECFA 441
Db 447 DSFVRGLSFARSGGDWAECSA 467

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RESULT 4

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US-08-609-426A-8
; Sequence 8, Application US/08609426A
; Patent No. 5830733
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.
; APPLICANT: Houston, Christine S.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,426A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,724
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Grant E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 1050.0080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600

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; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-609-426A-8

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Query Match 77.3%; Score 1810; DB 2; Length 467;
Best Local Similarity 76.0%; Pred. No. 1.4e-182;
Matches 335; Conservative 40; Mismatches 66; Indels 0; Gaps 0;
QY 1 NSHSCDVPDGGYOCFPEISHLWGTYSPPFFSLADESAISPDVPGKCRVTFVOVLSRHGARY 60
Db 27 NQSTCDIVDGYOCFSETSHLWGYAPFFSLANESAISSPDVPGACRVTFQAQVLSRHGARY 86
QY 61 PTTSSAKAYSALIEAIQKNATAFKGYAFLKTYNYTLGADDLTPFGEOQMVSNGIKFYRR 120
Db 87 PTEKGGKYSALIEEIQQNVTTFDGYAFLKTYNSLGADDLTPFGQEQLVNSGIKFIYOR 146
QY 121 YKALARKIVPFIRASGSDRVIASAEKPIEGFQSAKLADPGANPHQASPVINVIPEGAGY 180
Db 147 YESLTRNIIPIFIRSSGSSRVIASGEKPIEGFQSTKLDPRAQPGQSSPKIDVVISEASS 206
QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDVVVNLMDMCPF 240
Db 207 NNTLDPGTCTVFESELDATVEANFTATFAPSIRQRLNDLSGVTLTDEVTYLMDCSF 266
QY 241 DTVARTSDATQSPFCDLFTDHEWIDYQYDLSGLKYYGYGAGNPLGPAQGVGVNELIAR 300
Db 267 DTISTSTVDTKLSPFCDLFTDHEWIDYQYDLSGLKYYGYGAGNPLGPTQGVGVNELIAR 326
QY 301 LTHSPVQDHTSNHLDSPATFPLNATLYADFSDHNTMVSIFFFALGLYNGTKPLSTTSV 360
Db 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTMVSIFFFALGLYNGTKPLSTTSV 386
QY 361 ESIEETDGYASWTVPFAARAYVENMQCEAEKEPLRVLVNDRVVPLHGCCGVDKLGRCKR 420
Db 387 ENITQDGFSSAWTVPFASRLYVENMQCEAEKEPLRVLVNDRVVPLHGCCGVDKLGRCKR 446
QY 421 DDFVEGLSFARSGGNWEECFA 441
Db 447 DSFVRGLSFARSGGDWAECSA 467

```

RESULT 5

```

US-08-374-652C-2
; Sequence 2, Application US/08374652C
; Patent No. 5834286
; GENERAL INFORMATION:
; APPLICANT: NEVALAINEN, HELENA K.M.
; APPLICANT: PALOHEIMO, MARJA T.
; APPLICANT: FAGERSTROM, RICHARD B.
; APPLICANT: MIETTINEN-OINONEN, ARJA S.
; APPLICANT: TURUNEN, MARJA K.
; APPLICANT: RAMBOSEK, JOHN A.
; APPLICANT: PIDDINGTON, CHRISTOPHER S.
; APPLICANT: HOUSTON, CHRISTINE S.
; APPLICANT: CANTRELL, MICHAEL A.
; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
; VECTORS AND METHODS FOR EXPRESSING PHYTASE DEGRADING
; ENZYMES IN DESIRED RATIOS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 1050.071001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-374-652C-2

Query Match 77.1%; Score 1810; DB 2; Length 467;
Best Local Similarity 76.0%; Pred. No. 1.4e-182;
Matches 335; Conservative 40; Mismatches 66; Indels 0; Gaps 0;

QY 1 NSHSCDVTDDGGYOCFPEISHLWGTYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARY 60
DB 27 NSTCDTVDGQYOCFSETSHLWGAYAPFFSLANESVISPVPAGCRVTFVQVLSRHGARY 86
QY 61 PTSSASKAYSALIEAIQKNAFAKGYAFLKTYNTLGADDLTPFGEQOMVNSGKIFYYR 120
DB 87 PTESKGGKYSALIEIEIQNVTFDCKYAFKTYNSLGADDLTPFGEQELVNSGKIFYYR 146
QY 121 YKALARKIVPFRASGSDRVASAEKFEQFSQAKLADPGANPHQASPVINVIPEGAGY 180
DB 147 YESLTRNIIPFRSSGSSRVASGKFEQFSQAKLADPGANPHQASPVINVIPEGAGY 206
QY 181 NNTLDHGLCTAFESSELGDVDEANFTAVFAPPFIRARLEAHLPGVNLTDDEVDVNLMDMCP 240
DB 207 NNTLDPGCTCTVFEDELADTVANFTATFAPSIRQRLNDLSGVTLTDTEVTYLMDCSF 266
QY 241 DTVAARTSDATQSPFCDLFTHDEWIQDYQLQSLGKYYGYGAGNPLGPAQGVFNELIAR 300
DB 267 DTISTVDTKLSPPCDLFTHEWIHYDYLQSLKYYGYGAGNPLGPAQGVFNELIAR 326
QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTWVSIFPALGLYNGTKPLSTTSV 360
DB 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTWVSIFPALGLYNGTKPLSTTSV 386
QY 361 ESTEETDGYASWTPFAARAYEMQCEBAKEPLVRVLVNDVRVPLHGGCGVDKIGCRKR 420
DB 387 ENITQDGFSSAWTPFASRLYEMQCEBAKEPLVRVLVNDVRVPLHGGCGVDKIGCRKR 446
QY 421 DDFVEGLSFARSGGNWEECPA 441
DB 447 DSFVRLSFGSGDWAECSA 467

RESULT 6
US-08-151-574-32
; Sequence 32, Application US/08151574

Patent No. 5436156
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,574
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-151-574-32

Query Match 77.1%; Score 1806; DB 1; Length 467;
Best Local Similarity 76.0%; Pred. No. 3.7e-182;
Matches 335; Conservative 40; Mismatches 66; Indels 0; Gaps 0;

QY 1 NSHSCDVTDDGGYOCFPEISHLWGTYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARY 60
DB 27 NSTCDTVDGQYOCFSETSHLWGAYAPFFSLANESVISPVPAGCRVTFVQVLSRHGARY 86
QY 61 PTSSASKAYSALIEAIQKNAFAKGYAFLKTYNTLGADDLTPFGEQOMVNSGKIFYYR 120
DB 87 PTDSKGGKYSALIEIEIQNVTFDCKYAFKTYNSLGADDLTPFGEQELVNSGKIFYYR 146
QY 121 YKALARKIVPFRASGSDRVASAEKFEQFSQAKLADPGANPHQASPVINVIPEGAGY 180
DB 147 YESLTRNIIPFRSSGSSRVASGKFEQFSQAKLADPGANPHQASPVINVIPEGAGY 206
QY 181 NNTLDHGLCTAFESSELGDVDEANFTAVFAPPFIRARLEAHLPGVNLTDDEVDVNLMDMCP 240
DB 207 NNTLDPGCTCTVFEDELADTVANFTATFAPSIRQRLNDLSGVTLTDTEVTYLMDCSF 266
QY 241 DTVAARTSDATQSPFCDLFTHDEWIQDYQLQSLGKYYGYGAGNPLGPAQGVFNELIAR 300
DB 267 DTISTVDTKLSPPCDLFTHEWIHYDYLQSLKYYGYGAGNPLGPAQGVFNELIAR 326
QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTWVSIFPALGLYNGTKPLSTTSV 360
DB 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTWVSIFPALGLYNGTKPLSTTSV 386

US-08-693-709-2

Query Match 77.1%; Score 1806; DB 1; Length 467;
Best Local Similarity 76.0%; Pred. No. 3.7e-182;
Matches 335; Conservative 40; Mismatches 66; Indels 0; Gaps 0;

Qy 1 NSHSCDVTGGYQCFPSHLMGTYSPFFSLADESAISPDVPGKGRVTFVQVLSRHGARY 60
Db 27 NOSSCDVTGGYQCFPSHLMGTYSPFFSLADESAISPDVPGKGRVTFVQVLSRHGARY 86
Qy 61 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLTGADDLTPFGEOQMVNSGKIFYRR 120
Db 87 PTDSKGGKYSALIEEIQONATTFDGKYAFLKTYNYSLGADDLTPFGEOQMVNSGKIFYR 146
Qy 121 YKALARKIVPPIRAGSDRVIAAEKIEGFSQAKLADPGANPHQASPVNVIPEGAGY 180
Db 147 YESLTRNIVPPIRSGSSRVIAAGKIEGFSQAKLADPGANPHQASPVNVIPEGAGY 206
Qy 181 NNTLDHGLCTAFEESELGDVVEANFTAFVAPPFIRARLEAHLPGVNLTDVVDVNLMDMCP 240
Db 207 NNTLDHGLCTAFEESELGDVVEANFTAFVAPPFIRARLEAHLPGVNLTDVVDVNLMDMCP 266
Qy 241 DTVARTSDATQSPFCDLFTHDEWIQDYQLQSLGKYYGYGAGNPLGPAQGVGVFNELIAR 300
Db 267 DTISTSTVDTKLSFPFCDLTHDEWIQDYQLQSLGKYYGYGAGNPLGPAQGVGVFNELIAR 326
Qy 301 LTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSDHNTMVSIFFALGLYNGTKPLSTTSV 360
Db 327 LTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSDHNTMVSIFFALGLYNGTKPLSTTSV 386
Qy 361 ESIEETDGYASWTVPFAARAYVEMMOCEAEKPEPLRVNLVNDRVVPLHGCVPDGLGRCTR 420
Db 387 ENITQDGFSSAWTVPFAARAYVEMMOCEAEKPEPLRVNLVNDRVVPLHGCVPDGLGRCTR 446
Qy 421 DDFVEGLSFARSGGNWEECEFA 441
Db 447 DSFVRLSFAARSGGNWEECEFA 467

RESULT 9

US-08-419-448-32
Sequence 32, Application US/08419448
Patent No. 5863533
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorpom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Seltin
TITLE OF INVENTION: Cloning and Expression of Microbial
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,448
FILING DATE: 10-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.10
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-419-448-32

Query Match 77.1%; Score 1806; DB 2; Length 467;
Best Local Similarity 76.0%; Pred. No. 3.7e-182;
Matches 335; Conservative 40; Mismatches 66; Indels 0; Gaps 0;

Qy 1 NSHSCDVTGGYQCFPSHLMGTYSPFFSLADESAISPDVPGKGRVTFVQVLSRHGARY 60
Db 27 NOSSCDVTGGYQCFPSHLMGTYSPFFSLADESAISPDVPGKGRVTFVQVLSRHGARY 86
Qy 61 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLTGADDLTPFGEOQMVNSGKIFYRR 120
Db 87 PTDSKGGKYSALIEEIQONATTFDGKYAFLKTYNYSLGADDLTPFGEOQMVNSGKIFYR 146
Qy 121 YKALARKIVPPIRAGSDRVIAAEKIEGFSQAKLADPGANPHQASPVNVIPEGAGY 180
Db 147 YESLTRNIVPPIRSGSSRVIAAGKIEGFSQAKLADPGANPHQASPVNVIPEGAGY 206
Qy 181 NNTLDHGLCTAFEESELGDVVEANFTAFVAPPFIRARLEAHLPGVNLTDVVDVNLMDMCP 240
Db 207 NNTLDHGLCTAFEESELGDVVEANFTAFVAPPFIRARLEAHLPGVNLTDVVDVNLMDMCP 266
Qy 241 DTVARTSDATQSPFCDLFTHDEWIQDYQLQSLGKYYGYGAGNPLGPAQGVGVFNELIAR 300
Db 267 DTISTSTVDTKLSFPFCDLTHDEWIQDYQLQSLGKYYGYGAGNPLGPAQGVGVFNELIAR 326
Qy 301 LTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSDHNTMVSIFFALGLYNGTKPLSTTSV 360
Db 327 LTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSDHNTMVSIFFALGLYNGTKPLSTTSV 386
Qy 361 ESIEETDGYASWTVPFAARAYVEMMOCEAEKPEPLRVNLVNDRVVPLHGCVPDGLGRCTR 420
Db 387 ENITQDGFSSAWTVPFAARAYVEMMOCEAEKPEPLRVNLVNDRVVPLHGCVPDGLGRCTR 446
Qy 421 DDFVEGLSFARSGGNWEECEFA 441
Db 447 DSFVRLSFAARSGGNWEECEFA 467

RESULT 10

US-08-819-825-3
Sequence 3, Application US/08819825
Patent No. 5866118
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
AND Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

; APPLICANT: ANAZAWA, Hideharu
 ; APPLICANT: KANEKO, Syunichi
 ; APPLICANT: NAGASHIMA, Tadashi
 ; APPLICANT: TANGE, Tatsuya
 ; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
 ; FILE REFERENCE: 81356/124
 ; CURRENT APPLICATION NUMBER: US/09/155,855
 ; CURRENT FILING DATE: 1998-10-05
 ; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
 ; EARLIER FILING DATE: 1997-04-04
 ; EARLIER APPLICATION NUMBER: JP 084314
 ; EARLIER FILING DATE: 1996-04-05
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 443
 ; TYPE: PRT
 ; ORGANISM: Aspergillus niger
 US-09-155-855-1

Query Match 76.8%; Score 1799; DB 4; Length 443;
 Best Local Similarity 74.8%; Pred. No. 1.9e-181;
 Matches 330; Conservative 47; Mismatches 64; Indels 0; Gaps 0;
 QY 1 NNSCDDTVDDGYQCFPEISHLWGTYSPPFFSLADESAISPDVPGKCRVTFVQVLSRHGARY 60
 Db 3 NQSTCDTVDDGYQCFSETSHLWQYAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGARY 62
 QY 61 PTSSAKAYSALIEAIOKNATAFGKYAFKTYNTYTLGADDLTPFGEQOMVNSGKIFYRR 120
 Db 63 PTDSKGGKYSALIEIOQNATTEGKYAFKTYNTYTLGADDLTPFGEQELVNSGVKFYQR 122
 QY 121 YKALARKIVPFIRASGSDRVIAAEKFIQFQSAKLADPGANPHQASPVINVIPEGAGY 180
 Db 123 YESLTRNIVPFISSGSRVIAASGNKFIQFQSTKLKDPRAQPGQSSPKIDVWISEASTS 182
 QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPTRARLEAHLPGVNLTDDEVNLMDCPF 240
 Db 183 NNTLDPGCTVFESELDADIEANFTATVPISIRQLENDLSGVSLTDTEVTYLMDCSF 242
 QY 241 DTAVTSDATQSLPFCDLTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIAR 300
 Db 243 DTISTSTVDTKLSPPCDLTHDEWINDYLSLKNKYGHGAGNPLGPTQCGVGYANELIAR 302
 QY 301 LTHSPVQDHTSTNHTLDSNPATPLNATLYADFSDHNTMVSIFTFALGLYNGTKPLSTTSV 360
 Db 303 LTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSDHNGIISILFALGLYNGTKPLSSTA 362
 QY 361 ESIEETDGYASWTVPFAARAYVEMMOCEAEKEPLRVLVNDRVPLHGGVCKLGRCKR 420
 Db 363 ENITQDTGFSASWTVPFASRMVEMMQCQSEQEPPLRVLVNDRVPLHGGCPVDALGRCTR 422
 QY 421 DDFVEGLSFARSGGNWCECA 441
 Db 423 DSFKGLSFARSGGDWCECA 443

RESULT 13
 US-09-155-855-3
 ; Sequence 3, Application US/09155855
 ; Patent No. 6139902
 ; GENERAL INFORMATION:
 ; APPLICANT: KONDO, Hidemasa
 ; APPLICANT: ANAZAWA, Hideharu
 ; APPLICANT: KANEKO, Syunichi
 ; APPLICANT: NAGASHIMA, Tadashi
 ; APPLICANT: TANGE, Tatsuya
 ; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
 ; FILE REFERENCE: 81356/124
 ; CURRENT APPLICATION NUMBER: US/09/155,855
 ; CURRENT FILING DATE: 1998-10-05
 ; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175

; EARLIER FILING DATE: 1997-04-04
 ; EARLIER APPLICATION NUMBER: JP 084314
 ; EARLIER FILING DATE: 1996-04-05
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 467
 ; TYPE: PRT
 ; ORGANISM: Aspergillus niger
 US-09-155-855-3
 Query Match 76.8%; Score 1799; DB 4; Length 467;
 Best Local Similarity 74.8%; Pred. No. 2e-181;
 Matches 330; Conservative 47; Mismatches 64; Indels 0; Gaps 0;
 QY 1 NNSCDDTVDDGYQCFPEISHLWGTYSPPFFSLADESAISPDVPGKCRVTFVQVLSRHGARY 60
 Db 27 NQSTCDTVDDGYQCFSETSHLWQYAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGARY 86
 QY 61 PTSSAKAYSALIEAIOKNATAFGKYAFKTYNTYTLGADDLTPFGEQOMVNSGKIFYRR 120
 Db 87 PTDSKGGKYSALIEIOQNATTEGKYAFKTYNTYTLGADDLTPFGEQELVNSGVKFYQR 146
 QY 121 YKALARKIVPFIRASGSDRVIAAEKFIQFQSAKLADPGANPHQASPVINVIPEGAGY 180
 Db 147 YESLTRNIVPFISSGSRVIAASGNKFIQFQSTKLKDPRAQPGQSSPKIDWISEASTS 206
 QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPTRARLEAHLPGVNLTDDEVNLMDCPF 240
 Db 207 NNTLDPGCTVFESELDADIEANFTATVPISIRQLENDLSGVSLTDTEVTYLMDCSF 266
 QY 241 DTAVTSDATQSLPFCDLTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIAR 300
 Db 267 DTISTSTVDTKLSPPCDLTHDEWINDYLSLKNKYGHGAGNPLGPTQCGVGYANELIAR 326
 QY 301 LTHSPVQDHTSTNHTLDSNPATPLNATLYADFSDHNTMVSIFTFALGLYNGTKPLSTTSV 360
 Db 327 LTHSPVHDDTSSNHTLDSNPATPLNSTLYADFSDHNGIISILFALGLYNGTKPLSSTA 386
 QY 361 ESIEETDGYASWTVPFAARAYVEMMOCEAEKEPLRVLVNDRVPLHGGVCKLGRCKR 420
 Db 387 ENITQDTGFSASWTVPFASRMVEMMQCQSEQEPPLRVLVNDRVPLHGGCPVDALGRCTR 446
 QY 421 DDFVEGLSFARSGGNWCECA 441
 Db 447 DSFKGLSFARSGGDWCECA 467

RESULT 14
 US-09-155-855-2
 ; Sequence 2, Application US/09155855
 ; Patent No. 6139902
 ; GENERAL INFORMATION:
 ; APPLICANT: KONDO, Hidemasa
 ; APPLICANT: ANAZAWA, Hideharu
 ; APPLICANT: KANEKO, Syunichi
 ; APPLICANT: NAGASHIMA, Tadashi
 ; APPLICANT: TANGE, Tatsuya
 ; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
 ; FILE REFERENCE: 81356/124
 ; CURRENT APPLICATION NUMBER: US/09/155,855
 ; CURRENT FILING DATE: 1998-10-05
 ; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
 ; EARLIER FILING DATE: 1997-04-04
 ; EARLIER APPLICATION NUMBER: JP 084314
 ; EARLIER FILING DATE: 1996-04-05
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 443
 ; TYPE: PRT
 ; ORGANISM: Aspergillus niger

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 16, 2001, 17:49:21 ; Search time 124.2 Seconds
(without alignments)
215.259 Million cell updates/sec

Title: US-09-488-265-31_COPY_27_467

Perfect score: 2342

Sequence: 1 NSHSCDVTGGYQCFEISH.....DFVEGLSPARSGGNWEECF 441

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601:*

- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT:*
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- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT:*
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- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2342	100.0	467	20 AAY43170	Consensus phytase-
2	2342	100.0	467	21 AAB20527	Consensus phytase
3	2342	100.0	467	21 AAY69569	Mutant phytase-10,
4	2330	99.5	467	21 AAB20534	Consensus phytase
5	2325	99.3	467	21 AAB20533	Consensus phytase
6	2322	99.1	441	21 AAB20523	Consensus phytase
7	2322	99.1	467	21 AAB20524	Consensus phytase
8	2322	99.1	467	21 AAY69566	Phytase-10, a cons
9	2241	95.7	467	21 AAB20532	Consensus phytase-
10	2236	95.5	467	20 AAY43169	Consensus phytase-
11	2236	95.5	467	21 AAB20526	Consensus phytase

12	2236	95.5	467	21 AAB20531	Consensus phytase
13	2236	95.5	467	21 AAY69568	Mutant phytase-1,
14	2188	93.4	467	20 AAW93382	Fungal consensus p
15	2182	93.2	441	21 AAB20514	Consensus phytase
16	2182	93.2	467	20 AAY39906	Ascomycete consens
17	2182	93.2	467	20 AAW93380	Fungal phytase pro
18	2182	93.2	467	20 AAW93381	Consensus phytase
19	2182	93.2	467	21 AAB20515	Consensus phytase
20	2182	93.2	467	21 AAY69558	Phytase-1, a conse
21	2181	93.1	467	20 AAW93383	Fungal consensus p
22	2179	93.0	467	20 AAW93384	Fungal consensus p
23	2173	92.8	467	20 AAW93385	Fungal consensus p
24	2171	92.7	467	21 AAB20530	Consensus phytase
25	2171	92.7	467	21 AAY69572	Consensus phytase
26	2093	89.4	437	21 AAB20525	Consensus phytase
27	2093	89.4	437	21 AAY69567	Consensus phytase
28	2064	88.1	467	20 AAY43172	Phytase-11, a cons
29	2064	88.1	467	21 AAY69571	Phytase-7, a deriv
30	2061	88.0	467	21 AAB20529	Consensus phytase
31	2056	87.8	431	21 AAB20535	Consensus phytase
32	2056	87.8	431	21 AAY69557	Consensus phytase
33	2028.5	86.6	424	21 AAB20536	Initial consensus
34	2028.5	86.6	424	21 AAY69574	Mutant Aspergillus
35	1925.5	82.2	467	21 AAY69574	A. fumigatus phyta
36	1905.5	81.4	467	20 AAY43171	Aspergillus fumiga
37	1905.5	81.4	467	21 AAB20528	Mutant Aspergillus
38	1905.5	81.4	467	21 AAY69570	Aspergillus fumiga
39	1878.5	80.2	440	21 AAY69549	Aspergillus fumiga
40	1878.5	80.2	465	19 AAW84356	Aspergillus fumiga
41	1878.5	80.2	465	20 AAY39905	A. fumigatus phyta
42	1875.5	80.1	440	21 AAB20507	Aspergillus fumiga
43	1875.5	80.1	440	21 AAY69550	Aspergillus fumiga
44	1870.5	79.9	440	21 AAB20508	Aspergillus fumiga
45	1870.5	79.9	440	21 AAY69551	Aspergillus fumiga

ALIGNMENTS

RESULT 1

AAV43170
ID AAY43170 standard; Protein; 467 AA.

AC AAY43170;

XX 06 JAN-2000 (first entry)

DT Consensus phytase-10-thermo(3)-Q50T-K91A protein sequence.
DE Phytase; animal feed preparation; thermostable phytase; transgenic plant;
XX consensus sequence.

KW Synthetic.

XX WO9948380-A1.

PN 30-SEP-1999.

XX 22-MAR-1999; 99WO-DK00154.

XX 23-MAR-1998; 98DK-0000407.

PR 19-JUN-1998; 98DK-0000806.

PR 18-SEP-1998; 98DK-0001176.

PR 22-JAN-1999; 99DK-0000091.

XX 22-JAN-1999; 99DK-0000093.

PA (NOVO) NOVO-NORDISK AS.

XX Petersen S; *different inventor*.

PI WPT; 1999-591030/50.

XX DR N-PSDB; AAZ31521.

PT Preparing animal feed using a thermostable phytase -

PS Example 3; Fig 10; 71pp; English.

XX This sequence represents the consensus phytase-10-thermo(3)-O50T-K91A.

CC The invention relates to a process for preparing animal feed by

CC agglomerating feed ingredients with a thermostable phytase, which is

CC added before or during agglomeration. The thermostable phytase is useful

CC for expression in transgenic plants. These plants are useful in the

CC preparation of animal feed itself. The thermostable phytase allows animal

CC feed to be produced more efficiently, in addition to improved

CC phytase-expressing transgenic plants. These plants provide a feed

CC ingredient and a feed additive (phytase) simultaneously.

XX Sequence 467 AA;

SQ

Query Match 100.0%; Score 2342; DB 20; Length 467;

Best Local Similarity 100.0%; Pred. No. 1.2e-228; Indels 0; Gaps 0;

Matches 441; Conservative 0; Mismatches 0;

QY 1 NSHSCDTVDGGYQCPEISHLWGTYSPPFSLADESAISPDVPGKCRVTFVOVLSRHGARY 60

DB 27 nshscdtvdggyqcpeishlwgtysppfsladesaispdvpgkcrvtfvqlsrhgary 86

QY 61 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNTLGADDLTPFGQOMVNSGKIFYRR 120

DB 87 ptssaskaysalieaioknatafkgyafktyntlgaddltpfgeqgmvnsgikfyrr 146

QY 121 YKALARKIVPFIIRASGSDRVVIASAEKFTGFSQAKLADPGANPHQASPVINVIIEGAGY 180

DB 147 ykalarkivpfiirassgdrvviaseekftgfsqakladpganphqaspvinviipegagy 206

QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPPIRAREAHLPVGNLTDEDVNLMDMCPF 240

DB 207 nntldhglctafeeselgddveanftavfappirarleahlpvgvnltdedvnlmdmcpf 266

QY 241 DIVARTSDATOLSPCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVFVNELIAR 300

DB 267 dtvartsdatslpcdlfthdewiqdydylqslgkyygygagnplgpaqgvfveliar 326

QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFTFALGLYNGTKPLSTTSV 360

DB 327 lthspvqdhtstnhtldsnpatfplnatlyadfsdntmvsiffalglyngtkplsttsv 386

QY 361 ESTEETDGYASWTVPFAARAYVEMMOCEAKEPLVRVLVNDRVVPLHGCYVDKLGCRKR 420

DB 387 esieetdgyaswtvpfaarayvemmqceakeplvrvlvndrvvplhgcgvdklgrckr 446

QY 421 DDFVEGLSFARSGGNWEECFA 441

DB 447 ddfveglsfarsggnweecfa 467

RESULT 2

AAB20527

ID AAB20527 standard; Protein; 467 AA.

XX AAB20527;

AC AAB20527;

XX 05-DEC-2000 (first entry)

DT Consensus phytase 10 thermo 3 q50t, k91a protein SEQ ID NO:31.

DE Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;

XX temperature stability; pH profile; temperature profile; reaction rate;

KW specific activity; substrate specificity; substrate cleavage pattern;

KW substrate binding; position specificity; phytate degradation rate;

KW food; feed; phytate; manure.

XX Synthetic.

OS WO200043503-A1.

FN

XX 27-JUL-2000.

PD

XX 21-JAN-2000; 2000WO-DK00025.

PF

XX 22-JAN-1999; 99DK-0000092.

PR

XX 21-SEP-1999; 99DK-0001340.

PR

XX (NOVO) NOVO NORDISK AS.

PA

XX Lehmann M;

PI

XX WPI; 2000-491161/43.

DR

XX N-PSDB; AAA73234.

DR

XX Novel phytases with improved properties such as temperature stability,

PT pH stability and substrate specificity, for use in pharmaceuticals and

PT compound foods and feeds -

PT

XX Claim 4; Fig 8a-c; 240pp; English.

PS

XX The present invention describes improved phytases, preferably with

CC increased thermostability, and methods for producing them. The methods

CC can be used for producing phytases with improved properties e.g.

CC temperature stability, pH stability, pH profile, temperature profile,

CC specific activity, substrate specificity, the velocity and level of

CC substrate binding, position specificity, substrate cleavage pattern,

CC release of phosphate from corn, reaction rate, phytate degradation rate,

CC and end level of released phosphate. The phytases can be used to produce

CC pharmaceutical compositions or compound food or feeds. The feed can be

CC used to reduce levels of phytate in animal manure, by converting it

CC into lower inositol phosphates and/or inositol and inorganic phosphate.

CC The present sequence represents a phytase sequence from the present

CC invention.

XX Sequence 467 AA;

SQ

Query Match 100.0%; Score 2342; DB 21; Length 467;

Best Local Similarity 100.0%; Pred. No. 1.2e-228; Indels 0; Gaps 0;

Matches 441; Conservative 0; Mismatches 0;

QY 1 NSHSCDTVDGGYQCPEISHLWGTYSPPFSLADESAISPDVPGKCRVTFVOVLSRHGARY 60

DB 27 nshscdtvdggyqcpeishlwgtysppfsladesaispdvpgkcrvtfvqlsrhgary 86

QY 61 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNTLGADDLTPFGQOMVNSGKIFYRR 120

DB 87 ptssaskaysalieaioknatafkgyafktyntlgaddltpfgeqgmvnsgikfyrr 146

QY 121 YKALARKIVPFIIRASGSDRVVIASAEKFTGFSQAKLADPGANPHQASPVINVIIEGAGY 180

DB 147 ykalarkivpfiirassgdrvviaseekftgfsqakladpganphqaspvinviipegagy 206

QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPPIRAREAHLPVGNLTDEDVNLMDMCPF 240

DB 207 nntldhglctafeeselgddveanftavfappirarleahlpvgvnltdedvnlmdmcpf 266

QY 241 DIVARTSDATOLSPCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVFVNELIAR 300

DB 267 dtvartsdatslpcdlfthdewiqdydylqslgkyygygagnplgpaqgvfveliar 326

QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFTFALGLYNGTKPLSTTSV 360

DB 327 lthspvqdhtstnhtldsnpatfplnatlyadfsdntmvsiffalglyngtkplsttsv 386

QY 361 ESTEETDGYASWTVPFAARAYVEMMOCEAKEPLVRVLVNDRVVPLHGCYVDKLGCRKR 420

DB 387 esieetdgyaswtvpfaarayvemmqceakeplvrvlvndrvvplhgcgvdklgrckr 446

QY 421 DDFVEGLSFARSGGNWEECFA 441

DB 447 ddfveglsfarsggnweecfa 467

XX PD 27-JUL-2000.
XX PD 21-JAN-2000; 2000WO-DK00025.
XX PF 22-JAN-1999; 99DK-0000092.
XX PR 21-SEP-1999; 99DK-0001340.
XX PA (NOVO) NOVO NORDISK AS.
XX PI Lehmann M;
XX KW WPI; 2000-491161/43.
XX DR N-PSDB; AAA73293.
XX KW Novel phytases with improved properties such as temperature stability,
XX PT pH stability and substrate specificity, for use in pharmaceuticals and
XX PT compound foods and feeds -
XX PS Disclosure; Fig 25a-c; 240pp; English.
XX CC The present invention describes improved phytases, preferably with
XX CC increased thermostability, and methods for producing them. The methods
XX CC can be used for producing phytases with improved properties e.g.
XX CC temperature stability, pH stability, pH profile, temperature profile,
XX CC specific activity, substrate specificity, substrate cleavage pattern,
XX CC substrate binding, position specificity, the velocity and level of
XX CC release of phosphate from corn, reaction rate, phytate degradation rate,
XX CC and end level of released phosphate. The phytases can be used to produce
XX CC pharmaceutical compositions or compound food or feeds. The feed can be
XX CC used to reduce levels of phytate in animal manure, by converting it
XX CC into lower inositol phosphates and/or inositol and inorganic phosphate.
XX CC The present sequence represents a phytase sequence from the present
XX CC invention.
XX SQ Sequence 467 AA;
Query Match 99.5%; Score 2330; DB 21; Length 467;
Best Local Similarity 99.5%; Pred. No. 1.9e-227; Indels 0; Gaps 0;
Matches 439; Conservative 0; Mismatches 2;
QY 1 NNSHCDTVDGGYQCPEISHLWGTYSPPFFSLADESAISPDPKGRVTFVQVLSRHGARY 60
DB 27 nshscdtvoggycpeshlwgtyspffsladesaispdpvkgrvtfvqvlshrghary 86
QY 61 PTSSASKAYSALIEAIOKNATAPKGYAFKTYNTLGGADDLTPFGEOQMVNSGKIFYYR 120
DB 87 ptssaskaysalialqknatafkgyafktyntlgaddltpfgedqmvnsgikfyrr 146
QY 121 YKALARKIYVPIFRASGSDRVIASAEKFLGGFOSAKLADPGANPHOASPVINVIPEGAGY 180
DB 147 ykalarikiyvfiragsdrviasaekflggfqsakladpganphoaspvinvipegagy 206
QY 181 NNTLDHGLCTAFESLGDVDEANFTAVFAPPPIRARLEAHLFGVNLTDDEVVNLMDCMCP 240
DB 207 nntldhglctafeestlgdveanftavfappirarleahlgpvnltgedvvnldmcmcp 266
QY 241 DTVARTSDATQSLSPFCDLTHDEWTOYDLSGLGKYGYGAGNPLGPAQGVGVNELLAR 300
DB 267 dtvartsdatspfdlthdewtoydylsglgkygygagntp.lgpaqgvgvfnellar 326
QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFFAILGYNKPKLSTTSV 360
DB 327 lthspvqdhctstnhtldsnpatfplnatlyadfshdntmvsiffalglyngtkp.lsttsv 386
QY 361 ESIEETDGYASVTPFAARAYVEMMQCEAEKPLVRVLVNDVRVPLHCGGVKDLGRCKR 420
DB 387 esieetdgyasvtpfaarayvemmqceaekep1vrvlvndvrvp1hgcavdcklgrckr 446
QY 421 DDFVEGLSFARSGGNWEECEFA 441
DB 447 ddfveglstargsggnweecfa 467

RESULT 5
AAB20533
ID AAB20533 standard; Protein; 467 AA.
XX AC AAB20533;
XX DT 05-DEC-2000 (first entry)
XX DE Consensus phytase 10 thermo 5 Q50T protein SEQ ID NO:95.
XX KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
XX KW temperature stability; pH profile; temperature profile; reaction rate;
XX KW specific activity; substrate specificity; substrate cleavage pattern;
XX KW substrate binding; position specificity; phytate degradation rate;
XX KW food; feed; phytate; manure.
XX OS Synthetic.
XX PN WO200043503-A1.
XX PD 27-JUL-2000.
XX PF 21-JAN-2000; 2000WO-DK00025.
XX PR 22-JAN-1999; 99DK-0000092.
XX PR 21-SEP-1999; 99DK-0001340.
XX PA (NOVO) NOVO NORDISK AS.
XX PI Lehmann M;
XX DR WPI; 2000-491161/43.
XX DR N-PSDB; AAA73292.
XX PT Novel phytases with improved properties such as temperature stability,
XX PT pH stability and substrate specificity, for use in pharmaceuticals and
XX PT compound foods and feeds -
XX PS Disclosure; Fig 24a-c; 240pp; English.
XX CC The present invention describes improved phytases, preferably with
XX CC increased thermostability, and methods for producing them. The methods
XX CC can be used for producing phytases with improved properties e.g.
XX CC temperature stability, pH stability, pH profile, temperature profile,
XX CC specific activity, substrate specificity, substrate cleavage pattern,
XX CC substrate binding, position specificity, the velocity and level of
XX CC release of phosphate from corn, reaction rate, phytate degradation rate,
XX CC and end level of released phosphate. The phytases can be used to produce
XX CC pharmaceutical compositions or compound food or feeds. The feed can be
XX CC used to reduce levels of phytate in animal manure, by converting it
XX CC into lower inositol phosphates and/or inositol and inorganic phosphate.
XX CC The present sequence represents a phytase sequence from the present
XX CC invention.
XX SQ Sequence 467 AA;
Query Match 99.3%; Score 2325; DB 21; Length 467;
Best Local Similarity 99.3%; Pred. No. 6.1e-227;
Matches 438; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 NNSHCDTVDGGYQCPEISHLWGTYSPPFFSLADESAISPDPKGRVTFVQVLSRHGARY 60
DB 27 nshscdtvoggycpeshlwgtyspffsladesaispdpvkgrvtfvqvlshrghary 86
QY 61 PTSSASKAYSALIEAIOKNATAPKGYAFKTYNTLGGADDLTPFGEOQMVNSGKIFYYR 120
DB 87 ptssaskaysalialqknatafkgyafktyntlgaddltpfgedqmvnsgikfyrr 146
QY 121 YKALARKIYVPIFRASGSDRVIASAEKFLGGFOSAKLADPGANPHOASPVINVIPEGAGY 180
DB 447 ddfveglstargsggnweecfa 467

Db 147 ykalkarivpfiragsdrviasaekfiegfsakladpganphqaspvlnviipegagy 206
 QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPARARLEAHLPGVNLTDDEVNLMDCPF 240
 Db 207 nntldhglctafeesclgddveanftavfappirarleahlpvnltdedvnlmdmcpf 266
 QY 241 DTVARTSDATQLSPFCDFLTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIAR 300
 Db 267 dtvartsdatqlspfcdfthdewiqdyqlgkygygagnp.lgpaqgvfvnelliar 326
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFFFALGLYNGTKPLSTTSV 360
 Db 327 lthspvqdhstnthtlidsnpatfplnatlyadfshdntmvsiffalglngtkplsttsv 386
 QY 361 ESIEETDGYASWTVPFAARAYVENMOCFAEKEPLVRVLVNDRVVPLHGGVGDKLGCRKR 420
 Db 387 esieetdgyaswtvpfaarayvenmqceakeplvrvlvndrvvplhgcavdklgrckr 446
 QY 421 DDFVEGLSFARSGGNWEECFA 441
 Db 447 ddfveglsfarsggnweecfa 467

RESULT 6

AAB20523
 ID AAB20523 standard; Protein; 441 AA.

AC AAB20523;

DT 05-DEC-2000 (first entry)

DE Consensus phytase 10 (Fcp10) SEQ ID NO:24.

XX KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.

OS Synthetic.

XX WO2000043503-A1.

XX 27-JUL-2000.

XX 21-JAN-2000; 2000WO-DK00025.

XX 22-JAN-1999; 99DK-0000092.

XX 21-SEP-1999; 99DK-0001340.

XX (NOVO) NOVO NORDISK AS.

XX Lehmann M;

XX WPI; 2000-491161/43.

XX Novel phytases with improved properties such as temperature stability,
 PT pH stability and substrate specificity, for use in pharmaceuticals and
 PT compound foods and feeds -

XX Example 2; Fig 4a-d; 240pp; English.

XX The present invention describes improved phytases, preferably with
 CC increased thermostability, and methods for producing them. The methods
 CC can be used for producing phytases with improved properties e.g
 CC temperature stability, pH stability, pH profile, temperature profile,
 CC specific activity, substrate specificity, substrate cleavage pattern,
 CC substrate binding, position specificity, the velocity and level of
 CC release of phosphate from corn, reaction rate, phytate degradation rate,
 CC and end level of released phosphate. The phytases can be used to produce
 CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.

CC The present sequence represents a phytase sequence from the present
 CC invention.

XX Sequence 441 AA;

Query Match 99.1%; Score 2322; DB 21; Length 441;
 Best Local Similarity 98.9%; Pred. No. 1.1e-226;
 Matches 436; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NSHSCDVTDDGGYQCFFPEISHLWGTYSFFSLADESALSPDVPKRCRTFVQVLSRHGARY 60
 Db 1 nshscdvtddggycfpeishlwgtysffsladesalspdvpkrcrtfvqvlsrhgary 60

QY 61 PTSSAKAYSALIEAIOKNATAFKGYAFLKTYNTLTGADDLTPFGEOOMVNSGKIFYRR 120
 Db 61 ptssakskysalleaigkntafkgyafiktyntltgaddltpfgeeqmvsngikfyrr 120

QY 121 YKALARKIVPPIRASGDRVIASAEKPIEGFSQAKLADPGANPHQASPVINVIPEGAGY 180
 Db 121 ykalkarkivpfvrasgsdrviasaekfiegfsakladpganphqaspvlnviipegagy 180

QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPARARLEAHLPGVNLTDDEVNLMDCPF 240
 Db 181 nntldhglctafeesclgddveanftavfappirarleahlpvnltdedvnlmdmcpf 240

QY 241 DTVARTSDATQLSPFCDFLTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIAR 300
 Db 241 dtvartsdatqlspfcdfthdewiqdyqlgkygygagnp.lgpaqgvfvnelliar 300

QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFFFALGLYNGTKPLSTTSV 360
 Db 301 lthspvqdhstnthtlidsnpatfplnatlyadfshdntmvsiffalglngtkplsttsv 360

QY 361 ESIEETDGYASWTVPFAARAYVENMOCFAEKEPLVRVLVNDRVVPLHGGVGDKLGCRKR 420
 Db 361 esieetdgyaswtvpfaarayvenmqceakeplvrvlvndrvvplhgcavdklgrckr 420

QY 421 DDFVEGLSFARSGGNWEECFA 441
 Db 421 ddfveglsfarsggnweecfa 441

RESULT 7

AAB20524
 ID AAB20524 standard; Protein; 467 AA.

AC AAB20524;

DT 05-DEC-2000 (first entry)

DE Consensus phytase 10 SEQ ID NO:26.

XX KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.

OS Synthetic.

XX WO2000043503-A1.

XX 27-JUL-2000.

XX 21-JAN-2000; 2000WO-DK00025.

XX 22-JAN-1999; 99DK-0000092.

XX 21-SEP-1999; 99DK-0001340.

XX (NOVO) NOVO NORDISK AS.

XX Lehmann M;

CC sequences from a variety of fungi: (AAV69544-Y69546, AAV69548-Y69556,
 CC AAV69564) and the Basidiomycetes phytase consensus AAV69563 and
 CC additionally contains the *Aspergillus terreus* cbs116.46 signal peptide at
 CC the N-terminus.

SQ Sequence 467 AA;

Query Match 99.1%; Score 2322; DB 21; Length 467;
 Best Local Similarity 98.9%; Pred. No. 1.2e-226;
 Matches 436; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NSHSCDTVDGGYQCFPEISHLMGTYSPFFSLADESAISPDVPKGRVTFVQVLSRHGARY 60
 DB 27 nshscdtvdggyqcfpeishlwgyqspffsladesaispdvpkgrvtfvqvlshrngary 86
 QY 61 PTSSASKAYSALIEAIQKNATAFKGYAFKTYNTLTGADDLTPRGEQMVNSGKIFYRR 120
 DB 87 ptssaskaysalieaiqknatafkgyafktyntltgaddltprgeqmvnsgikfyrr 146
 QY 121 YKALARKIVPFTIRASGSDRVIASAEKFTIEGFSQAKLADPGANPHQASPVINVIIEGAGY 180
 DB 147 ykalarikipfirasgsdrviasaekftiegfsqakladpganphqaspvinviiepegagy 206
 QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPPIRARLEAHLPGVNLTDDEVNLMDCMPF 240
 DB 207 nntldhglctafeeselgdvdeanftavfapppirarleahlpgvnltddevnldmncpf 266
 QY 241 DTVARTSDATOLSPFCDLFTHDEWTDYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIAR 300
 DB 267 dtvartsdatlspfcldlthdewtdydyqlqslgkygygagnplgpaqgvgfvnelliar 326
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTWVSIFPFGALGLYNGTKPLSTTSV 360
 DB 327 lthspvqghtstnhtldsnpatfplnatlyadfshdntwvsifalglgntgkplstsv 386
 QY 361 ESIEETDGYASWTVPFAARAYVEMMOCEAKEPLVRVLRVNDRVVPLHGGGVDKLGRCKR 420
 DB 387 esieetdgyaswtvpfaarayvemmqceakeplvrvlrvndrvvplhggvdklgrckr 446
 QY - 421 DDFVEGLSFARSGGNWEECEFA 441
 DB 447 ddfveglsfarsggnweecfa 467

RESULT 9

AAB20532
 ID AAB20532 standard; Protein; 467 AA.

XX AC AAB20532;

XX DT 05-DEC-2000 (first entry)

XX DE Consensus phytase 3 thermo 11 Q50T K91A protein SEQ ID NO:93.

XX KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.

XX OS Synthetic.

XX PN WQ200043503-A1.

XX PD 27-JUL-2000.

XX PF 21-JAN-2000; 2000WO-DK00025.

XX PR 22-JAN-1999; 99DK-0000092.

XX PR 21-SEP-1999; 99DK-0001340.

XX PA (NOVO) NOVO NORDISK AS.

XX Lehmann M;

XX WPI: 2000-491161/43.
 XX N-PSDB: AAA73291.

XX Novel phytases with improved properties such as temperature stability,
 PT pH stability and substrate specificity, for use in pharmaceuticals and
 PT compound foods and feeds -

XX Disclosure; Fig 23a-c; 240pp; English.

XX The present invention describes improved phytases, preferably with
 CC increased thermostability, and methods for producing them. The methods
 CC can be used for producing phytases with improved properties e.g.
 CC temperature stability, pH stability, pH profile, temperature profile,
 CC specific activity, substrate specificity, substrate cleavage pattern,
 CC substrate binding, position specificity, the velocity and level of
 CC release of phosphate from corn, reaction rate, phytate degradation rate,
 CC and end level of released phosphate. The phytases can be used to produce
 CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.
 CC The present sequence represents a phytase sequence from the present
 CC invention.

SQ Sequence 467 AA;

Query Match 95.7%; Score 2241; DB 21; Length 467;
 Best Local Similarity 95.5%; Pred. No. 2e-218;
 Matches 421; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 NSHSCDTVDGGYQCFPEISHLMGTYSPFFSLADESAISPDVPKGRVTFVQVLSRHGARY 60
 DB 27 nshscdtvdggyqcfpeishlwgyqspffsladesaispdvpkgrvtfvqvlshrngary 86
 QY 61 PTSSASKAYSALIEAIQKNATAFKGYAFKTYNTLTGADDLTPRGEQMVNSGKIFYRR 120
 DB 87 ptssaskaysalieaiqknatafkgyafktyntltgaddltprgeqmvnsgikfyrr 146
 QY 121 YKALARKIVPFTIRASGSDRVIASAEKFTIEGFSQAKLADPGANPHQASPVINVIIEGAGY 180
 DB 147 ykalarikipfirasgsdrviasaekftiegfsqakladpganphqaspvinviiepegagy 206
 QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPPIRARLEAHLPGVNLTDDEVNLMDCMPF 240
 DB 207 nntldhglctafeeselgdvdeanftavfapppirarleahlpgvnltddevnldmncpf 266
 QY 241 DTVARTSDATOLSPFCDLFTHDEWTDYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIAR 300
 DB 267 dtvartsdatlspfcldlthdewtdydyqlqslgkygygagnplgpaqgvgfvnelliar 326
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTWVSIFPFGALGLYNGTKPLSTTSV 360
 DB 327 lthspvqghtstnhtldsnpatfplnatlyadfshdntwvsifalglgntgkplstsv 386
 QY 361 ESIEETDGYASWTVPFAARAYVEMMOCEAKEPLVRVLRVNDRVVPLHGGGVDKLGRCKR 420
 DB 387 esieetdgyaswtvpfaarayvemmqceakeplvrvlrvndrvvplhggvdklgrckr 446
 QY 421 DDFVEGLSFARSGGNWEECEFA 441
 DB 447 ddfveglsfarsggnweecfa 467

RESULT 10

AAV43169

ID AAV43169 standard; Protein; 467 AA.

XX AC AAV43169;

XX DT 06-JAN-2000 (first entry)

XX DE Consensus phytase-1-thermo(8)-Q50T-K91A protein sequence.

XX KW Phytase; animal feed preparation; thermostable phytase; transgenic plant;

XX KW consensus sequence.

XX OS Synthetic.

XX PN WO9948380-A1.

XX PD 30-SEP-1999.

XX PF 22-MAR-1999; 99WO-DK00154.

XX PR 23-MAR-1998; 98DK-0000407.

XX PR 19-JUN-1998; 98DK-0000806.

XX PR 18-SEP-1998; 98DK-0001176.

XX PR 22-JAN-1999; 99DK-0000091.

XX PR 22-JAN-1999; 99DK-0000093.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Petersen S;

XX WPI; 1999-591030/50.

XX DR N-PSDB; AAZ31520.

XX PT Preparing animal feed using a thermostable phytase

XX PS Example 3; Fig 9; 7lpp; English.

XX This sequence represents the consensus phytase-1-thermo(8)-Q50T-K91A.

CC The invention relates to a process for preparing animal feed by

CC agglomerating feed ingredients with a thermostable phytase, which is

CC added before or during agglomeration. The thermostable phytase is useful

CC for expression in transgenic plants. These plants are useful in the

CC preparation of animal feed itself. The thermostable phytase allows animal

CC feed to be produced more efficiently, in addition to improved

CC phytase-expressing transgenic plants. These plants provide a feed

CC ingredient and a feed additive (phytase) simultaneously.

XX SQ Sequence 467 AA;

Query Match 95.5%; Score 2236; DB 20; Length 467;

Best Local Similarity 95.2%; Pred. No. 6.5e-218;

Matches 420; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 NNSCSDTVGGYQCPEISHLWGTYSPPFSLADESAISPDVPGKGRVTFVQVLSRHGARY 60

DB 27 nshscdtdvggycfpeishlwtgyspyfsladesaispddcrvtfvqvlshrghary 86

QY 61 PTSSASKAYSALIEATOKNATAFKGYAFKTYNTLGGADLTPEGQQMVNSGKIFYRR 120

DB 87 pssasakaysalialqknatafkgyafktyntlgadltfgenqmvnsqkifyrr 146

QY 121 YKALARKIVPFIRASGSDRVIASAEKFTGFSQAKLADPGANPHQASPVINVIPEGAGY 180

DB 147 ykalar-kivpfirasgsdrviasaeakftiegfsqakladpgsqspqspvinvilpegsgy 206

QY 181 NNTLHGLCTAFESSELGDDVEANFTAVFAPIRARLEAHLPGVNLTDDEVVNLMDMCPF 240

DB 207 nntldhgtctafeselsgdveanftalfapalarleadlpgvtltdedvvylmdmcpf 266

QY 241 DTVARTSDATQSPFCDLTFHDEWIGYDYLSGLKGYGAGNPLGPAQGVGFVNELIAR 300

DB 267 dtvartsdatselpfcalfthdewigdydylsglkygygagnpbgpaggvgfaneliar 326

QY 301 LTHSPVQDHTSTNHTLDSNPATFPFLNATLYADFSDHNTMWSIFFALGLYNGTKPLSTTSV 360

DB 327 lthspvgdhtstnhtldsnpatfpnlaiyadfsdntmwsiffalglngtkplsttsv 386

QY 361 ESTEETDGYTSASVTVPFAARAYVEMMQCEAKEPLVRVLVNDVRVPLHGGCGVDKLGRCRKR 420

DB 387 esieetdgytsasvtvpfaarayvemmqcqaekpivrivlndrvrplhgcavdklgrckr 446

QY 421 DDFVEGLSFARSGNWECEFA 441

DB 447 ddfveglsfarsggnwaecfa 467

RESULT 11

AAB20526

ID AAB20526 standard; Protein; 467 AA.

XX AC AAB20526;

XX DT 05-DEC-2000 (first entry)

XX Consensus phytase 1 thermo 8 q50t, k91a protein SEQ ID NO:29.

KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;

KW temperature stability; pH profile; temperature profile; reaction rate;

KW specific activity; substrate specificity; substrate cleavage pattern;

KW substrate binding; position specificity; phytate degradation rate;

KW food; feed; phytate; manure.

XX OS Synthetic.

XX WO200043503-A1.

XX PD 27-JUL-2000.

XX PF 21-JAN-2000; 2000WO-DK00025.

XX PR 22-JAN-1999; 99DK-0000092.

XX PR 21-SEP-1999; 99DK-0001340.

XX PA (NOVO) NOVO NORDISK AS.

XX Lehmann M;

XX WPI; 2000-491161/43.

XX DR N-PSDB; AAA73233.

XX Novel phytases with improved properties such as temperature stability,

XX pH stability and substrate specificity, for use in pharmaceuticals and

XX compound foods and feeds

XX Claim 5; Fig 7a-c; 240pp; English.

XX The present invention describes improved phytases, preferably with

XX increased thermostability, and methods for producing them. The methods

XX can be used for producing phytases with improved properties e.g.

XX temperature stability, pH stability, pH profile, temperature profile,

XX specific activity, substrate specificity, the velocity and level of

XX substrate binding, position specificity, the phytate degradation rate,

XX release of phosphate from corn, reaction rate, phytase can be used to produce

XX and end level of released phosphate. The phytases can be used to produce

XX pharmaceutical compositions or compound food or feeds. The feed can be

XX used to reduce levels of phytate in animal manure, by converting it

XX into lower inositol phosphates and/or inositol and inorganic phosphate.

XX The present sequence represents a phytase sequence from the present

XX invention.

XX SQ Sequence 467 AA;

Query Match 95.5%; Score 2236; DB 21; Length 467;

Best Local Similarity 95.2%; Pred. No. 6.5e-218;

Matches 420; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 NNSCSDTVGGYQCPEISHLWGTYSPPFSLADESAISPDVPGKGRVTFVQVLSRHGARY 60

DB 27 nshscdtdvggycfpeishlwtgyspyfsladesaispddcrvtfvqvlshrghary 86

61 PTSSASKAYSALIEAIQKNAFAKGYAFKTYNTLGGADLTTPFGEGQOMVNSGKIFYR 120
 87 ptssaskaysalieleaigknaafkgyafktyntlgadlttptfgengmvsugikfyrr 146
 121 YKALARKIVPFIRASGSDRVIAAEKFIQFQSAKLADFGANPHQASPVINVIIEGAGY 180
 147 ykalararkivpfirassgdrviaseakfiqfqsakladpgsqphqaspvinvilpegsy 206
 181 NNTLDHGLCTAFESSELGGDDVEANFTAVFAPPFIRARLEAHLPGVNLTDDEVVNLMDMCPF 240
 207 nntldhgtctafeselselgddveanftalfapairleadlpgvntltdevvylmdmcpf 266
 241 DTVARTSDATQSPFCDLTFHDEWIOYDYLQSLGKYYGYGAGNPLGPAQGVGVNELIAR 300
 267 dtvartsdatselpfcalfthdewiqdyqlslgkygygagnpplgpaqgvgfaneliar 326
 301 LTHSPVQDHTSNHTLDSNPATFPLNATLYADFSHDNTMVSIFPFGALGYNKFKPLSTTSV 360
 327 lthspvqdhstsnhtldsnpatfplnatlyadfsdntmvsiffalgyngtkplsttsv 386
 361 ESIEETDGYASWTVPFAARAYVEMMQCEAEKEPLRVRLVNDRVVPLHGGCGVDKLGRCR 420
 387 esieetdgyaswtvpfaarayvemmqcqaekplrvrlvndrvvplhgcavdklgrckr 446
 421 DDFVEGLSFARSGGNWECFA 441
 447 ddfveglsfarsggnwaecfa 467

RESULT 12

AAB20531
 ID AAB20531 standard; Protein; 467 AA.
 XX
 AC AAB20531;
 DT 05-DEC-2000 (first entry)
 XX
 DE Consensus phytase 3 thermo 11 Q50T protein SEQ ID NO:91.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 temperature stability; pH profile; temperature profile; reaction rate;
 specific activity; substrate specificity; substrate cleavage pattern;
 substrate binding; position specificity; phytate degradation rate;
 food; feed; phytate; manure.

Synthetic.
 XX
 PN WO200043503-A1.
 XX
 PD 27-JUL-2000.
 XX
 PF 21-JAN-2000; 2000WO-DK00025.
 XX
 PR 22-JAN-1999; 99DK-0000092.
 PR 21-SEP-1999; 99DK-0001340.
 XX
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Lehmann M;

WPI: 2000-491161/43.
 DR N-PSDB: AAA73290.
 XX
 PT Novel phytases with improved properties such as temperature stability,
 pH stability and substrate specificity, for use in pharmaceuticals and
 compound foods and feeds -
 XX
 PS Disclosure; Fig 22a-c; 240pp; English.

CC The present invention describes improved phytases, preferably with
 CC increased thermostability, and methods for producing them. The methods
 CC can be used for producing phytases with improved properties e.g.
 CC temperature stability, pH stability, pH profile, temperature profile,
 pH stability and substrate specificity, for use in pharmaceuticals and
 compound foods and feeds -

CC specific activity, substrate specificity, substrate cleavage pattern,
 CC substrate binding, position specificity, the velocity and level of
 CC release of phosphate from corn, reaction rate, phytate degradation rate,
 CC and end level of released phosphate. The phytases can be used to produce
 CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.
 CC The present sequence represents a phytase sequence from the present
 CC invention.
 XX
 XX Sequence 467 AA;

Query Match 95.5%; Score 2236; DB 21; Length 467;
 Best Local Similarity 95.2%; Pred. No. 6.5e-218;
 Matches 420; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 NSHSCDVADGGYQCFPEITSHLWGTYSPPFFSLADESALSPDPKGRVTFVQVLSRHGARY 60
 DB 27 nshscdvtvdygqcfpeishlwgtyspffsladesalsdpdpkdcrtvfvqlsrhgary 86
 QY 61 PTSSASKAYSALIEAIQKNAFAKGYAFKTYNTLGGADLTTPFGEGQOMVNSGKIFYR 120
 DB 87 ptssaskaysalieleaigknaafkgyafktyntlgadlttptfgengmvsugikfyrr 146
 QY 121 YKALARKIVPFIRASGSDRVIAAEKFIQFQSAKLADFGANPHQASPVINVIIEGAGY 180
 DB 147 ykalararkivpfirassgdrviaseakfiqfqsakladpgsqphqaspvinvilpegsy 206
 QY 181 NNTLDHGLCTAFESSELGGDDVEANFTAVFAPPFIRARLEAHLPGVNLTDDEVVNLMDMCPF 240
 DB 207 nntldhgtctafeselselgddveanftalfapairleadlpgvntltdevvylmdmcpf 266
 QY 241 DTVARTSDATQSPFCDLTFHDEWIOYDYLQSLGKYYGYGAGNPLGPAQGVGVNELIAR 300
 DB 267 dtvartsdatselpfcalfthdewiqdyqlslgkygygagnpplgpaqgvgfaneliar 326
 QY 301 LTHSPVQDHTSNHTLDSNPATFPLNATLYADFSHDNTMVSIFPFGALGYNKFKPLSTTSV 360
 DB 327 lthspvqdhstsnhtldsnpatfplnatlyadfsdntmvsiffalgyngtkplsttsv 386
 QY 361 ESIEETDGYASWTVPFAARAYVEMMQCEAEKEPLRVRLVNDRVVPLHGGCGVDKLGRCR 420
 DB 387 esieetdgyaswtvpfaarayvemmqcqaekplrvrlvndrvvplhgcavdklgrckr 446
 QY 421 DDFVEGLSFARSGGNWECFA 441
 DB 447 ddfveglsfarsggnwaecfa 467

RESULT 13

AAI69568
 ID AAY69568 standard; protein; 467 AA.
 XX
 AC AAY69568;

DT 19-APR-2000 (first entry)
 XX
 DE Mutant phytase-1, phytase-1-thermo[8]-Q50T-K91A.
 XX
 KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
 KW thermostable; animal feed; monogastric animal; phytate phosphorus;
 KW phosphate availability; consensus; mutant; mutein.

XX Aspergillus terreus 9A1.
 OS Aspergillus terreus cbs16.46.
 OS Aspergillus niger var. awamori.
 OS Aspergillus niger T213.
 OS Aspergillus niger str. NRRL3135.
 OS Aspergillus fumigatus ATCC13073.
 OS Aspergillus fumigatus ATCC32722.
 OS Aspergillus fumigatus ATCC58128.
 OS Aspergillus fumigatus ATCC26906.

Thu Oct 18 11:34:55 2001

OS Aspergillus fumigatus ATCC32239.
OS Emericella nidulans.
OS Talaromyces thermophilus ATCC20186.
OS Myceliophthora thermophila.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..26
FT /note= "Phytase signal peptide from Aspergillus terreus
FT cbs16.46"
FT Protein 27..467
FT /note= "Mature phytase-1-thermo[8]-Q50T-K91A"
XX
XX EP969089-A1.
XX
XX 05-JAN-2000.
XX
XX 23-JUN-1999; 99EP-0111949.
XX
XX 29-JUN-1998; 98EP-0111960.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Bruggen R, Lehmann M, Wyss M;
XX WPI; 2000-099429/09.
DR N-PSDB; AAZ59715.
XX
XX New stabilised enzyme formulation, useful for feed compositions for
XX monogastric animals -
XX
XX Example 5; Fig 19; 101pp; English.
XX
XX The invention relates to a novel stabilised dry or liquid enzyme
XX formulation, comprising phytase (myo-inositol hexakisphosphate
XX phosphohydrolase) and one or more stabilising agents including
XX xylitol or ribitol; polyethylene glycols with a molecular weight of 600
XX to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
XX glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
XX The stabilised phytase formulation is used in a method for preparing a
XX feed composition for monogastric animals (e.g., pigs, poultry) and
XX provides a monogastric animal with its dietary requirements of
XX phosphorus. Although a large amount of phosphate is present in animal
XX feed in the form of phytate phosphorus, monogastric animals are unable
XX to utilise this form of phosphate, resulting in the addition of extra
XX phosphate to the feed of such animals. Phytase enhances the nutritional
XX value of plant material without the need for adding additional phosphate
XX to the feed. The level of phosphate pollution in the environment is
XX reduced by adding phytase to animal feed, as the animal can make use of
XX the inorganic phosphate liberated from phytate phosphorus using the
XX enzyme. The phytase formulation of the invention has an improved
XX thermostability and can therefore remain stable during long-term storage
XX and can withstand feed processing methods such as extrusion, expansion
XX and pelleting. The present sequence represents a mutant phytase-1
XX consensus sequence, phytase-1-thermo[8]-Q50T-K91A, which has a
XX temperature optimum and melting point 7 degrees Celsius higher than that
XX of phytase-1 (AAV69558).
XX
XX Sequence 467 AA;
XX
Query Match 95.5%; Score 2236; DB 21; Length 467;
Best Local Similarity 95.2%; Pred. No. 6.5e-216;
Matches 420; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
QY 1 NNSHCDTVGGYQCFPEISHLNGTTSYPPFSLADESAISDPVPGKGRVTFVQLSRHGRY 60
DB 27 nshscdtvgdygcfeishlwtgyspyfsladesaisdpvdpdcrtvfvqlsrhgary 86
QY 61 PTSSASKAYSALTEATOKNATAFKGYALFKYNTYLTGADDLTPFGCEQOMVNSGKFKFYR 120
DB 87 ptssaskaysalteaoknatafkgyafktyntylgaddltptfgengmvsngikfyrr 146

QY 121 YKALARKIVPFIIRASSDRVIASAEKFTIEGFSAKLADPGANPHQASPVINVIPEGAGY 180
DB 147 YKALARKIVPFIIRASSDRVIASAEKFTIEGFSAKLADPGANPHQASPVINVIPEGAGY 206
QY 181 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPFIRARLEAHLPGVNLTDDEVDVNLMDMCPF 240
DB 207 nntldhgtctafedseelgddveanftalafapairarleadipgvtltddedvvyldmcpf 266
QY 241 DIVARTSDATQISPCDLTFHDEWIQDYLOSLGKYGYGAGNPLGPAAGVGCFVNELIAR 300
DB 267 dtvartsdatslpcalfthdewiqdyloslgkygygagnpplgpaagvgcfvaneliar 326
QY 301 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFFAALGYNKTPLSSTTSV 360
DB 327 lthspvqdhsthtltdsnpatfplnatlyadfsdntlmisifalglyngtkplsttsv 386
QY 361 ESTEETDGYSGASWTVPFAARAVEMMQCEAEKPELVRVLVNDRVVPLHCCGVDKLGRCKR 420
DB 387 esleetdgyssaswtvpfaarayvemmqcqekeplvrvlvndrvvplhgcavdklgrckr 446
QY 421 DDFVEGLSFARSGGNWCECA 441
DB 447 ddfveglsfarsgggnwaecca 467
RESULT 14
AAW93382
ID AAW93382 standard; Protein; 467 AA.
XX
XX AAW93382;
XX
XX 11-JUN-1999 (first entry)
XX
XX Fungal consensus phytase protein mutant Q50T.
XX
XX Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food;
KW feed additive; variant; mutein; feed; pharmaceutical.
XX
XX Fungi.
XX Synthetic.
XX
XX EP897985-A2.
XX
XX 24-FEB-1999.
XX
XX 15-JUL-1998; 98EP-0113176.
XX
XX 24-JUL-1997; 97EP-0112688.
XX
XX (HOFF) HOFFMANN LA ROCHE AG F.
XX Lehmann M;
XX
XX WPI; 1999-134647/12.
XX
XX Preparation of a consensus protein, especially a phytase - using
XX programs to compare evolutionary similarity of sequences
XX
XX Claim 9; Page -: 30pp; English.
XX
XX This invention describes a novel process for the preparation of a
XX consensus protein. The specific example given in the specification is
XX that of a fungal phytase (myo-inositol hexakisphosphate) which
XX hydrolyses phytase to valuable feed additives, with a fully defined amino
XX acid sequence given in the specification, or variant or mutein. The
XX method is useful for improving protein properties by altering their
XX sequence. The consensus protein and mutein are useful in food, feed or
XX pharmaceutical compositions. This sequence is a mutant phytase protein
XX the invention which does not appear in the specification but has been
XX created from the protein represented in AAW93380.
XX
XX Sequence 467 AA;
XX

Query Match 93.4%; Score 2188; DB 20; Length 467;
 Best Local Similarity 93.2%; Pred. No. 4.8e-213;
 Matches 411; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 NSHSCDVGQYOCFPEISHLWGTYSPPFFSLADESAISPDVPRKCRVTFVQVLSRHGARY 60
 Db 27 nshscdvdggyqcfpeishlwtyspyfsladesaispdpddcrvtfvqlsrhgary 86
 QY 61 PTSSASKAYSALIEAOKNATAFKGYAFKTYNYTLGADDLTPFGQQMVNSGKIFYRR 120
 Db 87 ptsskaysalieleaqlkntafkgyafktyntylgaddltptfgqmvnsgikfyrr 146
 QY 121 YKALARKIVPFIIRASGSDRVIAAEKFIIEGFSQAKLADPGANPHQASPVINVIIEGAGY 180
 Db 147 ykalarakivpfirasgsdrviasaekfiegsakladpgsqphaspidvilpegsy 206
 QY 181 NNTLDHGLCTAFEESELGDDVEANFTAFAPTRARLEAHLPGVNLTDDEVVNLDMCPF 240
 Db 207 nntldhgtctafeseldgddveanftalfapairarleadlpgvltltdedvvyldmcpf 266
 QY 241 DTVARTSDATQSPFCDLFTHEWIOYDYLQSLGKYGYGAGNPLGPAQGVFVNLIELAR 300
 Db 267 etvartsdatselpfcalfthdewrtydylqslgkygygagnpigpaqgvfaneliar 326
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDNTMVSIFFAFGLYNGTKPLSTTSV 360
 Db 327 ltrspvqdhstntnhtlidsnpatfplnatlyadfsdnsmisiffalglyngtcaplsttsv 386
 QY 361 ESTEETDGYASWTVPFAARAYVENMQCEAEKPELVRLVNDRVVPLHGCVDKLGRCR 420
 Db 387 esieetdgyaswtvpfagarayvenmqcaekeplrvlrvlndrvvplhgcavdklgrckr 446
 QY 421 DDFVEGLSFARSGGNWEECFA 441
 Db 447 ddfveglsfarsggnwaeefa 467

RESULT 15
 AAB20514 standard; Protein; 441 AA.
 AC AAB20514;
 DT 05-DEC-2000 (first entry)
 XX Consensus phytase SEQ ID NO:14.
 DE Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.
 OS Synthetic.
 XX WO2000043503-A1.
 XX 27-JUL-2000.
 XX 21-JAN-2000; 2000WO-DK00025.
 XX 22-JAN-1999; 99DK-0000092.
 XX 21-SEP-1999; 99DK-0001340.
 XX (NOVO) NOVO NORDISK AS.
 XX Lehmann M;
 XX WPI; 2000-491161/43.
 XX Novel phytases with improved properties such as temperature stability,
 PT pH stability and substrate specificity, for use in pharmaceuticals and

compound foods and feeds -
 Example 9; Fig 1a-d; 240pp; English.
 The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present invention.

XX Sequence 441 AA;
 SQ

Query Match 93.2%; Score 2182; DB 21; Length 441;
 Best Local Similarity 93.0%; Pred. No. 1.8e-212;
 Matches 410; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 1 NSHSCDVGQYOCFPEISHLWGTYSPPFFSLADESAISPDVPRKCRVTFVQVLSRHGARY 60
 Db 1 nshscdvdggyqcfpeishlwtyspyfsladesaispdpddcrvtfvqlsrhgary 60
 QY 61 PTSSASKAYSALIEAOKNATAFKGYAFKTYNYTLGADDLTPFGQQMVNSGKIFYRR 120
 Db 61 ptsskaysalieleaqlkntafkgyafktyntylgaddltptfgqmvnsgikfyrr 120
 QY 121 YKALARKIVPFIIRASGSDRVIAAEKFIIEGFSQAKLADPGANPHQASPVINVIIEGAGY 180
 Db 121 ykalarakivpfirasgsdrviasaekfiegsakladpgsqphaspidvilpegsy 180
 QY 181 NNTLDHGLCTAFEESELGDDVEANFTAFAPTRARLEAHLPGVNLTDDEVVNLDMCPF 240
 Db 181 nntldhgtctafeseldgddveanftalfapairarleadlpgvltltdedvvyldmcpf 240
 QY 241 DTVARTSDATQSPFCDLFTHEWIOYDYLQSLGKYGYGAGNPLGPAQGVFVNLIELAR 300
 Db 241 etvartsdatselpfcalfthdewrtydylqslgkygygagnpigpaqgvfaneliar 300
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDNTMVSIFFAFGLYNGTKPLSTTSV 360
 Db 301 ltrspvqdhstntnhtlidsnpatfplnatlyadfsdnsmisiffalglyngtcaplsttsv 360
 QY 361 ESTEETDGYASWTVPFAARAYVENMQCEAEKPELVRLVNDRVVPLHGCVDKLGRCR 420
 Db 361 esieetdgyaswtvpfagarayvenmqcaekeplrvlrvlndrvvplhgcavdklgrckr 420
 QY 421 DDFVEGLSFARSGGNWEECFA 441
 Db 421 ddfveglsfarsggnwaeefa 441

Search completed: October 16, 2001, 17:49:22
 Job time: 20971 sec

us-09-488-265-31_copy_27_467.rag

Thu Oct 18 11:34:55 2001

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 17:47:43 ; Search time 7358.5 Seconds
(without alignments)
1699.548 Million cell updates/sec

Title: US-09-488-265-30_COPY_79_1401

Perfect score: 1323

Sequence: 1 aactctactctctgtgacac.....actgggaagaatgttcgcct 1323

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

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3: gb_est3:*
4: gb_est4:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	152.6	11.5	802	227	AQ324539	mgxb0019C
2	117.8	8.9	837	226	AQ255459	mgxb0014M
3	109	8.2	581	104	AJ274007	AJ274007
4	83.8	6.3	753	225	AQ163004	mgxb0021D
5	81.2	6.1	699	225	AQ162040	mgxb0010F
6	75.4	5.7	810	225	AQ161556	mgxb0008K
7	74.6	5.6	769	227	AQ361474	mgxb0004I
8	73.6	5.6	669	227	AQ361495	mgxb0004K
9	43.6	3.3	1016	221	CNS04ESQ	AL287459 Tetraodon
10	41.8	3.2	341	109	AV054552	AL287459
11	41.8	3.2	481	225	AQ020816	AQ202816 RPI11-48
12	41.8	3.2	545	224	AQ140737	AQ140737 HS_3124_A
13	41.2	3.1	231	25	AV129427	AV129427 AV129427
14	41.2	3.1	234	109	AV064132	AV064132 AV064132
15	41.2	3.1	236	109	AV054718	AV054718 AV054718
16	41.2	3.1	247	28	AV293643	AV293643 AV293643
17	41.2	3.1	264	108	AV002759	AV002759 AV002759
18	41.2	3.1	269	109	AV077122	AV077122 AV077122
19	41.2	3.1	278	25	AV114552	AV114552 AV114552
20	41.2	3.1	285	109	AV081956	AV081956 AV081956
21	41.2	3.1	297	109	AV060181	AV060181 AV060181
22	41.2	3.1	300	109	AV053884	AV053884 AV053884
23	41.2	3.1	306	25	AV118366	AV118366 AV118366
24	41.2	3.1	342	109	AV047696	AV047696 AV047696
25	40.4	3.1	468	151	BF637070	BF637070 NF049F02L
26	40.4	3.1	482	30	AV423243	AV423243 AV423243
27	40.2	3.0	265	109	AV049962	AV049962 AV049962
28	40.2	3.0	295	26	AV212676	AV212676 AV212676
29	40.2	3.0	512	107	AU039641	AU039641 AU039641
30	39.6	3.0	227	25	AV161297	AV161297 AV161297
31	39.6	3.0	249	109	AV056003	AV056003 AV056003
32	39.6	3.0	266	109	AV091633	AV091633 AV091633
33	39.6	3.0	268	109	AV049564	AV049564 AV049564
34	39.6	3.0	270	109	AV079904	AV079904 AV079904
35	39.6	3.0	280	109	AV078019	AV078019 AV078019
36	39.6	3.0	285	109	AV100697	AV100697 AV100697
37	39.6	3.0	289	25	AV120593	AV120593 AV120593
38	39.6	3.0	289	109	AV055109	AV055109 AV055109
39	39.6	3.0	290	109	AV053894	AV053894 AV053894
40	39.6	3.0	291	25	AV151459	AV151459 AV151459
41	39.6	3.0	296	109	AV058485	AV058485 AV058485
42	39.6	3.0	297	109	AV050799	AV050799 AV050799
43	39.6	3.0	298	109	AV067677	AV067677 AV067677
44	39.6	3.0	300	109	AV054136	AV054136 AV054136
45	39.6	3.0	303	25	AV118481	AV118481 AV118481

ALIGNMENTS

RESULT 1
 LOCUS AQ324539/c
 DEFINITION mgxb0019C01R CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0019C01R, DNA sequence.
 ACCESSION AQ324539
 VERSION 1
 KEYWORDS GSS.
 SOURCE Magnaporthe grisea.
 ORGANISM Magnaporthe grisea.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinsowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome

JOURNAL COMMENT

Unpublished (1998)
 Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: GGAAACAGCTATGACCATG
 Class: BAC ends
 High quality sequence stop: 408.
 Location/Qualifiers
 1. .802

FEATURES

source
 /organism="Magnaporthe grisea"
 /strain="70-15"
 /db_xref="taxon:148305"
 /clone="mgxb0019C01R"
 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII; Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."
 166 a 218 c 209 g 208 t 1 others

BASE COUNT

166 a 218 c 209 g 208 t 1 others

Query Match

Best Local Similarity 11.5%; Score 152.6; DB 227; Length 802;
 Matches 343; Conservative 0; Mismatches 265; Indels 12; Gaps 2;

QY 666 aggtgttaactgactgacgaagcgtgtgttaactgacgtgacacgtgtgtcattgcacac 725
 Db 614 AGGGTGAACCTCAGCGCAAGCGGTGCAGATCATGAGCTTCTGCCGTTTGAGAC 555
 QY 736 tttgtctagaactctgacgtactactcaattgtctcattctgtgactgttgcactcacga 785
 Db 554 CGTGGCAGATCCNCAAGCCAC-----CCTGTCCGAGTCTGTGCACGCTGTTCACGAAG 501
 QY 786 cgaatgattcaatcacgactacttgcgaactcttgggttaagtactacgttgcgtgtctg 845
 Db 500 AGACTGGGAGGCATATGACATATCTCCAGACACTGGGGAAGTGTGTATGGTACGGCAATGG 441
 QY 846 taacctatgggtccagctcaaggtgtgtgttgcgttaacgaattgattgattgac 905
 Db 440 CAACCCCTGGGCTCCACGCAAGGGGTGGGTTCGTCAACGAGCTCATCGCGAGGCTGTGT 381
 QY 906 tcactctccagtttcaagacacacacttctactaacacactttggactctaaacccagctac 965
 Db 380 CCRAAAACCCGTTGACAGCACACAAATACCAACTCGACGCTCGACAGCGACCCCATCGAC 321
 QY 966 ttteccattgaacgctactttgttacgctgactctctctcagcacaacactatggtttctat 1025
 Db 320 GTTCCCACTAGACAAAAGCTGTACGCCGACTTTAGCCCATGATACGATATGCTGGGCAT 261
 QY 1026 ttcttcgcttgggtttgtataaagggttactaagccattgtctactactcttctgtgaatc 1085
 Db 260 CTAGCGCGCGCTGGGATTTACAAAGCCAGCCGCCCGGATTCGGTCCGCAAAAGGAGAG 201
 QY 1086 ta-----ttgaagaactgcaggttactctcttctgtgactgttccattcgtgctag 1139
 Db 200 AAGGAGCGCGCAGGAGCTCAGCGGGTTCCTGTCACAGCTGGGGGGTACCGTTCGGAGCGAG 141
 QY 1140 agcttcgttgaatgatgcaatgtgaagctgaaaggaaccattggttagagtttgggt 1199

718 +ccacactattactaacactctgaactactcaattgtctccattctgtgacttcttca
778

QY 244 gcttcaagggttaagctcttctgaagacttacactacacttgggtgctgaagac 303
 Db 340 GACTATGGGAAGGCTTCAGATTCTCAAGATTACAGTATACCTAGGTTCTGAGCAG 399
 QY 304 tgaactccattgggtgaacacaaatggttaactctgttataagttctacagaagatac 363
 Db 400 CTACCCCTTGGGAGCAGGAAATGTCAGTCTGGAAAAAGTTCTTCAAGCGCTAT 459
 QY 364 aagcgtcttgctagaaaa---gattgtccattcattagagcttctgttctgacagagtt 420
 Db 460 CAGAGTTAGCGGAGGATTCAGCCCATCCCTTTGTCAGGCTCGGGCTCTGAAAGAGTC 519
 QY 421 attgctctgcgtgaagaagttcattgaagtttccaatctgctaag 465
 Db 520 GTCATGTACGCAAGATTTTTCATGGCTCTACAAAGCAAG 564

RESULT 4
 LOCUS AQ163004 753 bp DNA GSS 09-SEP-1998
 DEFINITION clone mgxb0021D19r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
 ACCESSION AQ163004
 VERSION AQ163004.1 GI:3559405
 KEYWORDS GSS.
 SOURCE Magnaporthe grisea.
 ORGANISM Magnaporthe grisea.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 1 (bases 1 to 753)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 Unpublished (1998)
 Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seg primer: GGAACAGCTATGACCATG
 Class: BAC ends
 High quality sequence stop: 448.
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 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25X genome coverage. High density colony filters
 are available upon request."
 208 a 180 c 156 g 206 t 3 others

BASE COUNT 208 a 180 c 156 g 206 t 3 others
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Query Match 6.3%; Score 83.8; DB 225; Length 753;
 Best Local Similarity 50.7%; Pred. NO. 2.7e-13;
 Matches 227; Conservative 0; Mismatches 215; Indels 6; Gaps 1;

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 ACCESSION AQ162040
 VERSION AQ162040.1 GI:3558441
 KEYWORDS GSS.
 SOURCE Magnaporthe grisea.
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 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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 1 (bases 1 to 699)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome
 Unpublished (1998)
 Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
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 High quality sequence stop: 285.
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 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25X genome coverage. High density colony filters
 are available upon request."
 208 a 180 c 156 g 206 t 3 others

BASE COUNT 208 a 180 c 156 g 206 t 3 others
 ORIGIN

Query Match 6.3%; Score 83.8; DB 225; Length 753;
 Best Local Similarity 50.7%; Pred. NO. 2.7e-13;
 Matches 227; Conservative 0; Mismatches 215; Indels 6; Gaps 1;

a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

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Db	651	ACGGGTTCFCGCCAGTTGGCGGTACCGTTCGCAGCGAGAATGTTGTGAAAAATGA	592		
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Qy	1220	tgcacggttggtggtttacaaagttgggttagatgataagagagacgacttcggttgaaggtt	1279		
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Qy	1280	tgtcttctcgctagatctcgttggttaactgggaagaatgttcg	1321		
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ACCESSION	AQ161556
VERSION	AQ161556.1 GI:3557957
KEYWORDS	GSS.
SOURCE	Magnaporthe grisea.
ORGANISM	Magnaporthe grisea
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
AUTHORS	1 (bases 1 to 810) Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE	A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome
JOURNAL	Unpublished (1998)
COMMENT	Contact: Dean RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson University, Clemson, SC 29634 Tel: 864 656 5737 Fax: 864 656 4293 Email: rdeane@clemson.edu Seq primer: GGAAACAGCTATGACCATG Class: BAC ends High quality sequence stop: 321. Location/Qualifiers 1..810
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source	

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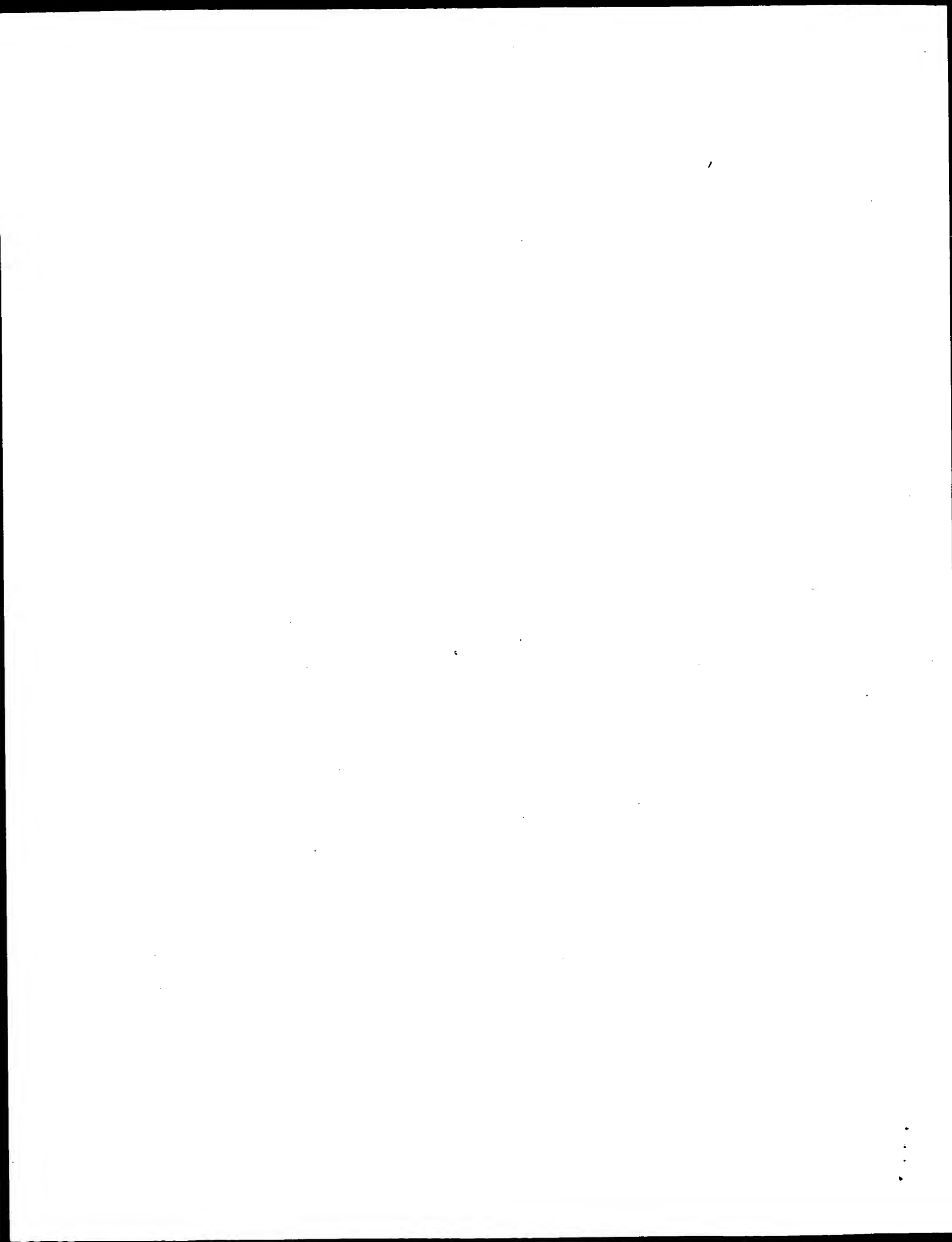
a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

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VERSION	AQ361474.1 GI:4211313
KEYWORDS	GSS.
SOURCE	Magnaporthe grisea.
ORGANISM	Magnaporthe grisea Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 769) Yu., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M, Wing, R.A. and Dean, R.A. A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome
REFERENCE	Unpublished (1998)
AUTHORS	Contact: Dean RA
TITLE	Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson University, Clemson, SC 29634
JOURNAL	Tel.: 864 656 5737
COMMENT	Fax: 864 656 4293 Email: rdean@clemson.edu Seq primer: TAATACGACTCATATAGGG Class: BAC ends High quality sequence start: 51 High quality sequence stop: 416. Location/Qualifiers
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high quality sequences	NCBI
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Rice blast is one of the most devastating fungal diseases	

2




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RESULT 2
US-08-151-574-33

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; Sequence 33, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seltien
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151.574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688, 578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29, 959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 33:
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; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
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RESULT 3
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; Patent No. 5593963
; GENERAL INFORMATION:
; APPLICANT: VAN OIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,424
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: 44615-20011.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
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; US-08-146-424-19

Query Match 45.4%; Score 600; DB 1; Length 1404;
Best Local Similarity 66.1%; Pred. No. 3.4e-165;
Matches 867; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

QY 12 ttgtgaactgtgacggtgtttaccatgtttccagaaattttccagaaattttccaggttac 71
Db 90 TTGGCATCGGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATCTTTGGGTCA 149
QY 72 atactctccattctctcttggctgacgaatctgtctatttctccagacttccaaaggg 131
Db 150 ATACGCACCGTCTCTCTCTGGCAACGAATCGGTATCTCCCTCGAGGTGCGCGCGG 209
QY 132 ttgttagacttcttcttgaagttttgtctagacacggtgtctagatcccaactcttc 191
Db 210 ATGCAGAGTCACTTTCGCTCAGGTCTCTCCGTCATCGAGCGCGGTATCGACCGACTC 269
QY 192 tgcgtcctaagcgtactctgttttgaattgaagctattcaaaagaacgactgcttcaa 251
Db 270 CAAGGGCAAGAAATACCTCCGCTCTCATTTGAGGAGATCCAGCAGAACGACACTTTGA 329
QY 252 gggtaagtcagcttcttgaagacttacaactacactttgggtgctgaagacttgaactcc 311

Db 330 CGGAAATATGCTTCCCTGAACACATACAACTACAGCTTGGGTGCAGATGACCTGACTCC 389
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Db 390 CTTGGGAGAAAGGAGCTAGTCAACTCCGGCATCAAGTTCTACCAAGCGGTACGAATCGCT 449
QY 372 ggtcgaagaagattgttcattcattagagctctggttctgacagagttattgctctgc 431
Db 450 CACAAGGAACATCGTTCCATTTCATCCGATCTCTGGCTCCAGCCGGTGATCGCTCCGG 509
QY 432 tgaagaattcattgaaggtttccaaactctgcttaagttgggtgcccaggtgcttaaccaca 491
Db 510 CRAAGAAATTCATCGAGGGCTTCCAGAGCACCAAGCTGAAGGATCTCGTGCACAGCCGG 569
QY 492 ccaaggtctccagttatttaagcttattattccagaaggtgctggttacaacaacattt 551
Db 570 CCAATCGTGGCCCAAGATGAGCTGGTGTATTTCCGAGGCCAGCTCATCCAAACACACTCT 629
QY 552 gacacaggttctgactgcttgaagaatctgaattgggtgacgacgttgaagctaa 611
Db 630 CGACCCAGGACCTGCACCTGCTTCCAGACACAGCAATGGCCGATACCGTCAAGCCAA 689
QY 612 cttcactgctgttttgcgtccaccattagagctagattggaagctcactgtccaggtgt 671
Db 690 TTTACCGCCGACGTTGCTCCCTCCATTCGTCACCTCTGGAGAACGACCTGTCGGGTGT 749
QY 672 taactgactgaagaagaagttgttaactgtgacatgttccattcgacacactgttc 731
Db 750 GACTCTCACAGACACAGAAGTGAACCTACCTCATGGAGATGTCTCTCGACACCATCTC 809
QY 732 tagaactctgacgtactcaattgtctcacttctgactgttcaactcaacgaagaatg 791
Db 810 CACCAGCACGCTGCACACCAAGCTGTCCCTCTCTGTGACCTGTTTCAACCCATGACGAATG 869
QY 792 gattcaatcagctacttgcatttcttgggttaagtactcaggttaaggtgctggttaaccc 851
Db 870 GATCACTAGGACTAGCTCCAGTCTTGAAGAAAGTATTACGGCCATGTTGTCAGAGTAAACC 929
QY 852 attgggtccagctcaaggttgggttcttaacgaattgattgctagattgactcaactc 911
Db 930 GCTCGGCCGACCCAGGCGTCCGGTACGCTACGCTACGAGCTCATGCCCGCTGACCCACTC 989
QY 912 tccagttcaagaacacacttctactaacacacacttggacttaacccagctacttccc 971
Db 990 GCCTGTCCACGATCACACACAGTTCCAAACACACTTTGGACTCGAGCCCGCTACCTTTCC 1049
QY 972 attgaacgtacttctgactgaacttctctcagacaacactatggttctctatttctt 1031
Db 1050 GCTCAACTCTACTCTACCGGACATTTCCGATGACACGGCATCATCTCCATCTCTCTT 1109
QY 1032 cgttttgggttctgacacggtactaagccattgtctactacttctgttgaattctatga 1091
Db 1110 TGCTTTAGGCTGTACAAAGGCACTAAGCCGCTATCTACCCAGCCGTGGAGAATATCAC 1169
QY 1092 agaaactgaaggttactctcttcttggactgttccattcgtctgtagagcttaactga 1151
Db 1170 CCAGACAGATGGATTCGCTCTGCTGGACGGTTCGGTTTGGCTTCGGCTTTGTACGTCGA 1229
QY 1152 aatgatcaatgtgaagctgaaggaaccattggttagagtttgggttaacagacagagt 1211
Db 1230 GATGATGAGTGTACGGGAGACGAGAGCCGCTGGTCCGTGCTTGGTTAATGATCGCGT 1289
QY 1212 tgttccattgacggttctggttctgacaaagtgggttagattgaagagagacacttctgt 1271
Db 1290 TGTCCCGTGCATGGGTGTCGGGTGTGATGCTTTGGGGAGATGTACCCGGGATAGCTTTGT 1349
QY 1272 tgaaggttcttctcactgactgctgtgataactggaagaagtgttctcgt 1323
Db 1350 GAGGGGTTGAGCTTTGCTAGATCTGGGGTGATTTGGCCGGAGTGTCTTTGCT 1401

RESULT 4

US-08-693-709-1
; Sequence 1, Application US/08693709
; Patent No. 5770413
; GENERAL INFORMATION:
; APPLICANT: VAN OOLJEN, ALBERT J.J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,709
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,424
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20011.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1401
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: 70...1401
; OTHER INFORMATION:
; NAME/KEY: Signal Sequence
; LOCATION: 1...72
; OTHER INFORMATION:
US-08-693-709-1

Query Match 45.4%; Score 600; DB 1; Length 1404;
Best Local Similarity 66.1%; Pred. No. 3.4e-165;
Matches 867; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

QY 12 ttgtacactgttgacggtggttaccaatgtttccagaaaattttcactgttgggttac 71
Db 90 TTGGCATCGGTGATCAGGGGTATCATGTCTTCCGAGACTTCGCATCTTTGGGGTCA 149
QY 72 atactctcattctctctcttgggtgacgaatctgtctatttctcagacgtttccaaagg 131
Db 150 ATAGCACCGTCTTCTCTCTCTGCAAGCAATCGGTCTATCTCCCTGAGTGCCTCCGG 209
QY 132 ttgtagagttactttcgttcaagtttcttagacacggtgcttagataccacacttctc 191

Db 210 ATGCAGAGTCACTTTCCGCTCAGGCTCCTCCCGTATCGAGCGGTTATCCGACCGACTC 269
QY 192 tgcgtcaagcgctactctgttttgaagctattcaaaagacgtactgttttcaa 251
Db 270 CAAGGCGCAAGAATACTCCGCTCTCATTTAGGAGATCCAGCAGAACGCGACCACTTTGA 329
QY 252 gggtaagtacgctttcttgaagacttaacacttaacttttgggtgctgaagacttgactcc 311
Db 330 CGGAAAAATATGCTTCTTGAAGACATACACTACAGCTTGGTGCAGATGACCTTGACTCC 389
QY 312 attcgggtgaacacaaaaaggtaactctggttattaaagttctacagaagatacaaggcttt 371
Db 390 CTTCCGAGAACAGGAGCTAGTCAACTCCGGCATCAAGTTCTACAGCGGTACGAATCGCT 449
QY 372 ggcgaagaagtgttccattcattagagcttctggttctggaagagttattgtcttctgc 431
Db 450 CACAAGGAACATCGTTCATTCACCGATCTCTGGCTCCAGCGCGGTGATCGCTCCCG 509
QY 432 tgaagaagttcaaggtttccaatctgcttaagtgtgctgacccaggtgctaacccaca 491
Db 510 CAAGAAATTCATCGAGGCTTCCAGAGCACCACAGCTCAAGATCCTCGTGCCCGCCCG 569
QY 492 ccaagcttccagttattaaagttattattccagaaggtgctggtttacaacaacacttt 551
Db 570 CCAATCGTCGCCAAGATCGAGCTGGTCAATTCGAGGCCAGCTCATCCAAACACTCT 629
QY 552 ggaacacgggttgtactgctttccagaagactgtaattggtgagacggtgaaagctaa 611
Db 630 CGACCGAGCCACCTGCATCTTCGAGACAGCGGAATTCGCCGATACCGTTCGAAGCCAA 689
QY 612 cttaactgtgttttgcctccacaacttagagctagtagtggaagctcaactgcccaggtgt 671
Db 690 TTTCAACGCCACCTGCTGCTCCCTCCATTCGTAACGCTCTGAGAACGACCTGTCCGGTGT 749
QY 672 taactgactgaagaagactgttgaactgtggaactgtggaagctcaactgcccaggtgt 731
Db 750 GACTCTCACAGACACAGAAGTGACCTACCTATGGACATGTGCTCTCGACACCACTCTC 809
QY 732 tagaacttgaagctactcaattgtctcacttctgacttctcaactcagcagcaatg 791
Db 810 CACCAGACCGCTGCACACCAAGCTTCCCTCTCTGTGACCTGTTCACCCATGACGAATG 869
QY 792 gattcaatgactacttgaactcttttggtaagtaagtaactcaggttaagctgtaaccc 851
Db 870 GATCAACTAGACTACTCTCCAGTCTCTGAAAGAGTATTACGCCATGTGTGACGTAACCC 929
QY 852 atgggttccagctcaaggtgtgttctgcttaacgaattgattgctagatgaactcactc 911
Db 930 GCTCGGCCGACCCAGGCGTCCGCTACGCTAACGAGCTATCGCCCGCTGACCCACTC 989
QY 912 tccagttcaagacacacttctactaaccacacttggacttaaccagactactttccc 971
Db 990 GCCTGTCCAGGATGACACAGCTTCAACACACTTTGGACTCGAGCCCGGTACTCTTCC 1049
QY 972 attgaacgtacttttgaacttctcactcagcaacactatggtttctatttttt 1031
Db 1050 GCTCAACTCTACTCTACGCGGACTTTTCGCATGACACACGCAATCATCTCCATCTCTT 1109
QY 1032 cgttttgggtttgtacaacggttactaaagccattgtctacttctgttgaacttatga 1091
Db 1110 TGCTTTAGGTCTGTACACCGGCACATAAGCCGCTATCTACACGACCGTGGAGATATCAC 1169
QY 1092 agaaactgacggttactctgtcttctgactgttccactcgtcgtagacttcaagttga 1151
Db 1170 CCAGCAGAGGATGCTCTGCTGTGACGCTTCCGCTTCCGCTTGTGTAGCTCGA 1229
QY 1152 aatgatgaatggaagctgaaagaaacacttattgattagatttttgggttaacgacagat 1211
Db 1230 GATGATGAGTGTACGGCGGACGAGACCGCTGTGCTGCTGTGTGTTAATGATCGCGT 1289
QY 1212 tgttccattgacggttgggttgggttggacaagttgggttagatgtaagagacgacttcgt 1271
Db 1290 TGTCCCGCTGCATGGGTGTCCGGTTGATGCTTTGGGGAGATGTACCCGGGATAGCTTTGT 1349

QY 1272 tgaaggtttgtcttccgctaagactgtggtggttaacttgggaagaatgtttcgtc 1323
Db 1350 GAGGCGGTGAGCTTTGCTAGATCTGGGGGTGATTTGGCGGAGTGTGTTTGT 1401

RESULT 5

US-08-419-448-33
; Sequence 33, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,448
; FILING DATE: 10-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; US-08-419-448-33

Query Match 45.4%; Score 600; DB 2; Length 1404;
Best Local Similarity 66.1%; Pred. No. 3.4e-165;
Matches 867; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

QY 12 ttgtgacactgttgacggtggttaccatgtttcccaagaatttctcacttgggtgac 71
Db 90 TTGGCATACGGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCCGATCTTTGGGTCA 149
QY 72 atactctcattcttctcttgggtgacgaatctgctatttctccagacttccaaagg 131
Db 150 ATACCGACCGTCTCTCTCTGGCAACGAATCGGTATCTCCCTGAGTGCCCGCG 209
QY 132 ttgtagacttcttctcaagttttgtctagacacggtgctagatacccaacttctc 191
Db 210 ATGCAGAGTCACTTTGCTCAGGCTCTCTCCGTCATGGAGCGGTATCCGACCGACTC 269

QY 1272 tgaaggtttgtcttcgttagatctggttaactggggaagaatgtttcgt 1323
 Db 1350 GAGGGGTGAGCTTGTCTAGATCTGGGGGTGATTGGCGGAGTGTCTTGTCT 1401

RESULT 6

US-08-151-574-31
 ; Sequence 31, Application US/08151574
 ; Patent No. 5436156
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert F.M. Van Gorcom
 ; APPLICANT: Willem Van Hartingsveldt
 ; APPLICANT: Petrus A. Van Paridon
 ; APPLICANT: Annemarie E. Veenstra
 ; APPLICANT: Rudolf G.M. Luttin
 ; APPLICANT: Gerardus Selten
 ; TITLE OF INVENTION: Cloning and Expression of Microbial
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster
 ; STREET: 545 Middlefield Road, Suite 200
 ; CITY: Menlo Park
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94025-3471
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/151,574
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/688,578
 ; FILING DATE: 24-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murashige, Kate H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 24615-20026.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-327-7250
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6756 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Aspergillus ficuum (Aspergillus niger)
 ; STRAIN: NRRL 3135
 ; IMMEDIATE SOURCE:
 ; LIBRARY: lambda AF
 ; CLONE: pAF2-3, pAF2-6, pAF2-7
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 210..253
 ; FEATURE:
 ; NAME/KEY: intron
 ; LOCATION: 254..355
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 356..1715
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: join(210..253, 356..1715)
 ; OTHER INFORMATION: /codon_start= 210

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 Db 450 CACAAGGAACATCGTTCCATTATCCGATCTCTGGCTCCAGCCGCGTGTATCGCTCCGG 509
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 Db 510 CAAAGAAATTCAGGAGGCTTCCAGACCAAGCTGAAGATCTCTGTCGCCAGCCCGG 569
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 Db 630 CGACCCAGGACCTGCACCTGTCTTGAAGACAGCAAGTTGGCCGATACCGTGAAGCCAA 689
 QY 612 cttcactgctgttttgcctcccaattagagcttagattgggaagctcacttgccagggtgt 671
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 QY 672 taacttgactgaagaagcgtttgtaacttgatgacatgtgtcattcgcacactgttgc 731
 Db 750 GACTCTCAGACACACAGAGTACCTTACCTCATGTGACATGTCTCTCGACACCATCTC 809
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 Db 1050 GCTCAACTACTCTCTACCGGACTTTTCGATGACACAGGATCATCTCCATCTCTT 1109
 QY 1032 cgtttgggtttgataacggtactaagcattgtctactacttctgttgaatctattga 1091
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 QY 1092 agaaactgaaggttactctcttcttggactgttccattcgtgcttagagcttaacttga 1151
 Db 1170 CCAGACAGATGGATTCGTCTGCTTGGAGGTTTCCGTTTGTCTCGGCTTTGTACGTCGA 1229
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 QY 1212 tgttccattgacaggtttggtgttgacaagttgggttagatgtaagaagagacgacttcgt 1271
 Db 1290 TGTCCCGTGCATGGGTGTCGGTTGTGCTTTGGGAGATGTACCCGGGATAGCTTTGT 1349

OTHER INFORMATION: /product= "Phytase"
 FEATURE: sig_peptide
 NAME/KEY: LOCATION: 210...380
 FEATURE: mat_peptide
 NAME/KEY: LOCATION: 381...1712
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /function= "inositol phosphate"
 OTHER INFORMATION: /product= "Phytase"
 OTHER INFORMATION: /evidence= EXPERIMENTAL
 US-08-151-574-31

Query Match 45.4%; Score 600; DB 1; Length 6756;
 Best Local Similarity 66.1%; Pred. No. 6.7e-165;
 Matches 867; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

QY 12 ttgtgacactgttgacggttggttaccaatgtttcccaagaattttctcactgtgggttac 71
 DB 401 TTCCGATACGGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCAATCTTTGGGGTCA 460

QY 72 atactccattctcttcttgggtgacgaatctgtctatttctccagacgttccaaaggg 131
 DB 461 ATACGACCGTCTCTCTCTCGCAAGCAATCGGTCTATCTCCCTGAGGTGCCCGCGG 520

QY 132 ttgtgagttactttctgacgtttgttcttagacacgtgtgtctagatcccaactttctc 191
 DB 521 ATSCAGAGTCACCTTGGCTCAGGTCTCTCCCGTCATCGAGCGGGTATCCGACCGACTC 580

QY 192 tgcgttaaggcgtactctgtttgattgaagctattccaaagaacgtactgttttcaa 251
 DB 581 CAAGGCAAGAAATACCTCGCTCTCATTTGAGGAGATCCAGCAGAACGGACCCACTTTGA 640

QY 252 gggtaagtacgttctctgaagaactacaaactacactttgggtgctgacactgtgactcc 311
 DB 641 CGGAAATATGCTTCTCTGAGACATCAACTACAGCTTGGGTGACAGTACCTGACTCC 700

QY 312 attcgttgacacacaaatgttgaactctgttattgaagttctacagaagatacaagcttt 371
 DB 701 CTTTCGAGAACAGGAGGTAGTCAACTCGGGATCAAGTTCTACCGCGGTACGAATCGCT 760

QY 372 gctgaaagattgttcattcattagagcttctgttctgacagagttattgtcttctgc 431
 DB 761 CACAAGGAAATCGTTCATTCATCCGATCTCTGCTCCAGCGGTGATCCCTCCG 820

QY 432 tgaagttcattgaagtttcccaactctgaagttctgaagttctgaagttctgaagttct 491
 DB 821 CAAGAAATTCATCGAGGCTTCCAGAGACCAAGCTGAAGGATCCTCGTCCCGACCGCG 880

QY 492 ccaagcttctccagttattacgttatttccagaaggtgctggttacaacaacacttt 551
 DB 881 CCAATCGTCGCGCAAGATCGAGGTGCTATTTCGAGGCCAGCTCATCCACCAACTCT 940

QY 552 gacacaggtttgtactgttctgaagaactgaattggtgacagagttgaagactaa 611
 DB 941 CGACCCAGGACCTGCACTGTTCTGAGAGACAGCAATTTGGCGGATACCGTGAAGCCAA 1000

QY 612 ctccactgtgtttctcctcccaacttagagcttagagttggaagctcacttgcaggtgt 671
 DB 1001 TTTACCGCCACGTTCGTCCCTCCATTCGTCACAGCTTGGAGAACGACTGTCGGGTG 1060

QY 672 taacttgactgacgaagactgttgaactgtatggacatgtgtccattgcacactgttgc 731
 DB 1061 GACTCTCACAGACACAGAAGTGACCTACCTCATGGACATGTGCTCTCGACACCATCTC 1120

QY 732 tagaactctgacgactactcaattctctcattctgtactgttctcactcaagaatg 791
 DB 1121 CACCAGCACCGTCACACCAAGTGTCCCTCTGTGACCTGTTCACCCATGACGAATG 1180

QY 792 gattcaatacacttctgaactcttttgggaagtactacggttgcgtgtgtaacc 851
 DB 1180 gattcaatacacttctgaactcttttgggaagtactacggttgcgtgtgtaacc 851

DB 1181 GATCACTAGCACTACTCTCCAGTCTTTGAAAAAGTATTACGGCCATTGGTGCAGGTAACCC 1240
 QY 852 atgggttccagctcaaggtgttgggttggtaacgaattgtagtagtaactc 911
 DB 1241 GCTCGGCCCCACCCAGGGGTGCGGTACGCTAACGAGCTCATCGGCCGCTTACGCCACTC 1300

QY 912 tccagttcaagacacacacttctactaacacacactttggacttaaccagactacttccc 971
 DB 1301 GCCTGTCCAGATGACACAGTTCCAAACACACTTTGGACTCGACCGGCTACCTTTCC 1360

QY 972 attgaagctactttgtacgtgacttctctcaccacacactatggttttctattttct 1031
 DB 1361 GCTCAACTCTACTCTCTACGCGGACTTTTCGATGACAACGGCATCATCTCCATTCTCT 1420

QY 1032 cgttttgggtttgtacaacggtacttaagcattgtctactactacttctgtgaactatga 1091
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QY 1092 agaaactgacggttactctgtcttcttggactgttccactcgtctagagcttactgtga 1151
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RESULT 7

US-08-419-448-31
 ; Sequence 31, Application US/08419448
 ; Patent No. 5863533
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert F.M. Van Gorcom
 ; APPLICANT: Willem Van Hartingsveldt
 ; APPLICANT: Petrus A. Van Paridon
 ; APPLICANT: Annemarie E. Veenstra
 ; APPLICANT: Rudolf G.M. Luttin
 ; APPLICANT: Gerardus Selten
 ; TITLE OF INVENTION: Cloning and Expression of Microbial
 ; TITLE OF INVENTION: Phytase
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster
 ; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20006-1888
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; SOFTWARE:
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/419,448
 ; FILING DATE: 10-APR-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murashige, Kate H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 24615-20026.10
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-887-1500
 ; INFORMATION FOR SEQ ID NO: 31:

Thu Oct 18 11:34:53 2001

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; IMMEDIATE SOURCE:
; LIBRARY: lambda AF
; CLONE: pAF2-3, pAF2-6, pAF2-7
; FEATURE:
; NAME/KEY: exon
; LOCATION: 210..253
; FEATURE:
; NAME/KEY: intron
; LOCATION: 254..355
; FEATURE:
; NAME/KEY: exon
; LOCATION: 356..1715
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Join(210..253, 356..1715)
; OTHER INFORMATION: /codon_start= 210
; OTHER INFORMATION: /product= "Phytase"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 210..380
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 381..1712
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "inositol phosphate"
; OTHER INFORMATION: /phosphatase"
; OTHER INFORMATION: /product= "Phytase"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
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; US-08-419-448-31

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Query Match 45.4%; Score 600; DB 2; Length 6756;
Best Local Similarity 66.1%; Pred. No. 6.7e-165;
Matches 867; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

Qy 12 ttgtgacactgttgacgggtgtaccagtgttcccaagaatttccacttggtgggtac 71
Db 401 TTGGGATACGGTGCATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATCTTTGGGGTCA 460
Qy 72 atactctccattctcttctgtgctgacgaatctgtatttctccagacgttccaaagg 131
Db 461 ATAGCAGCCGTTCTCTCTGCGCAACGATCGGTCTATCTCCCTGAGGTGCGCGCGG 520
Qy 132 ttgtagagtacttcttccgaatttctgtctagacacgggtgtgtatgatacccaactttc 191
Db 521 ATGCAGAGTCACTTCGCTCAGGCTCTCTCCGTCATGAGCGGGGTATCCGACCGACTC 580
Qy 192 tgcctctaagcgtactctgtgttgattgaagctattcaaaagaacgtactgctttcaa 251
Db 581 CAAAGGCAAGAAATACCTCCGCTCTATTGAGGAGATCCAGCAAGACCGGACCACTTTGA 640
Qy 252 gggttaaglacgttcttgaagacttacaactacacttttggtgctgacgacttgactcc 311
Db 641 CGGAATAATATGCTTCTTGAAGACATCAACTACAGCTTGGGTGCGATGACCTGACTCC 700
Qy 312 attcggtgaacaacaaatggttaactctgtgtatttaagtctacagaagatacaaggcttt 371
Db 701 CTTCGGAGAACAGGAGCTAGTCAACTCCGGCATCAAGTTCTTACCAGCGGTACGAATCGCT 760
Qy 372 ggcataagaagtgttccattcattagagcttctgtgtctgacagagttattgtctgc 431
Db 761 CACAAGGAACATCGTGTCTTCCATCCGATCTCTGGCTCCAGCCGCGTATCGCTCCGG 820

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Qy 432 tgaagttcattgaaggttttccaatctgctaagttggctgacccagggtgttaaccaca 491
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Qy 492 ccaagcttctccagttattaaagttattattccagaaggtgtgtgttacaacaacacttt 551
Db 881 CCAATCGTGCCCAAGATCAGCGTGTGTCATTTCCGAGGCGCAGCTCATCCAACAACTCT 940
Qy 552 ggaccacggttgtgtactgtcttcgaagaatctgaattgggtgacgaggttgaagctaa 611
Db 941 CGACCCAGGCACTGTCATCTTCCGAAGACAGCAATTTGGCCGATACCTGCGAAGCCAA 1000
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Qy 912 tccagttcaagacacacacttctacttaaccacacttggactctaacccagctacttccc 971
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Qy 972 attgaacgtacttgtacgctgactctctcaagacaaactatggtttctatttctt 1031
Db 1361 GCTCAACTCTACTCTCTACGGGACTTTTTCGATGACAAACGGCATCATCTCCATCTCTT 1420
Qy 1032 cgttttgggtttgtacaacggtacttaagccattgtctactactcttcttgaactattga 1091
Db 1421 TGTCTTTAGGTCTGTACACGGGCACTTAAGCCGTATCTACCAGACCGTGGAGAATATCAC 1480
Qy 1092 agaaactgaacgttactgtcttctgtgactgttccattcgtctgactgactgactgacttga 1151
Db 1481 CCAGACAGATGGATTCTGCTGTGCTTGGACGGTTCCTGTTGCTTCGCGCTTTGTACGTCGA 1540
Qy 1152 aatgatgaatgaagctgaagaaagaaacattggttagagtttgggttaacacagagag 1211
Db 1541 GATGATGTCAGTGTACGGCGGACAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1600
Qy 1212 tgttccattgcaggtgtgtgtgtgacaaagtgtgggttagatgtaagagacagacttgc 1271
Db 1601 TGTCCCGCTGCATGGGTGTCGGTGTGATCTTTGGGAGATGTACCCGGGATGCTTGTGT 1660
Qy 1272 tgaaggttbtcttctgttagatctggttgtaactgggaagaatatttgc 1323
Db 1661 GAGGGGGTGTGAGCTTTGCTAGATCTGGGGGTGATTGGGGGGAGTGTGTTTGTCT 1712

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RESULT 8
US-07-923-724-7
; Sequence 7, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Toikkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.

```

APPLICANT: Rambosek, John A.
 APPLICANT: Turunen, Marja K.
 APPLICANT: Fagerstr m, Richard B.
 TITLE OF INVENTION: Production of Phytase Degrading Enzymes
 TITLE OF INVENTION: in Trichoderma
 NUMBER OF SEQUENCES: 66

Query Match	45.2%	Score 598.2;	DB 1;	Length 2363;
Best Local Similarity	65.9%;	Pred. No. 1.4e-164;		
Matches 867;	Conservative 0;	Mismatches 448;	Indels 0;	Gaps
QY	9	ctcttgtgaacactgttgacggtggttaccaaatgtttccagagaattttccagaaattttccacttgtggg	68	
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QY	69	tacatacttcacattctctcttggctgcagaactctgctattttccagacgcttccaaa	128	
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QY	129	gggtgtagagttaactttcgatccaaatgtttgtctagacacggtgtagataccaaacttc	188	
Db	712	CGGTTCGAGAGTCACTTTGCGTCTCAGTCTCTCCCGTCTATGGAGCGGGTATCCGACCGA	771	
QY	189	tctgcgctctaaagcgtactctctgtattgaaactattccaaagaacgctactactgttt	248	
Db	772	GTCCAAGGGCAAGAAATACCTCGCTCTCATTTGAGGAGATCCAGCAGAACGTGACCACTT	831	
QY	249	caagsgtaagtcacgtctcttgaagacttacaactacaactttgggtgctgaacacttgac	308	
Db	832	TCATGTGAAATATGCCCTTCTCTGAAGACATACAACTACAGCTTTGGTTCAGATCACTGCAC	891	

QY	309	tccattcgtgaacaacaaatggf	taaactcgtgtattaaagtctacagaagatacaaggc	368
Db	892	TCCTCTCGGAGAGAGAGGAGCTAGTCAACTCCGGCATCAAGTTCTACCGAGTACGAATC	951	
QY	369	tttggctgaagaagattgtccattcattagagcttctggtctctgcacagagttattgcttc	428	
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QY	609	taactcacctgcgttttctgcgtccacaattagagctagattggaagctcaactgtgccagg	668	
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RESULT 9
US-08-609-426A-7
; Sequence 7, Application US/08609426A

Patent No. 5830733
 GENERAL INFORMATION:
 APPLICANT: Nevalainen, Helena K.M.
 APPLICANT: Paloheimo, Marja T.
 APPLICANT: Miettinen-Oinonen, Arja S.K.
 APPLICANT: Torkkeli, Tuula K.
 APPLICANT: Cantrell, Michael
 APPLICANT: Piddington, Christopher S.
 APPLICANT: Rambosek, John A.
 APPLICANT: Turunen, Marja K.
 APPLICANT: Fagerstr m, Richard B.
 APPLICANT: Houston, Christine S.
 TITLE OF INVENTION: Production of Phytase Degrading Enzymes
 TITLE OF INVENTION: in Trichoderma
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,426A
 FILING DATE: 01-MAR-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/923,724
 FILING DATE: 31-JUL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/496,155
 FILING DATE: 19-MAR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/044,077
 FILING DATE: 29-APR-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: UK 8610600
 FILING DATE: 30-APR-1986
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Grant E.
 REGISTRATION NUMBER: P-41,264
 REFERENCE/DOCKET NUMBER: 1050.0080001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2363 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: both
 FEATURE:
 NAME/KEY: CDS
 LOCATION: join(404...447, 550...1906)
 US-08-609-426A-7

Query Match 45.2%; Score 598.2; DB 2; Length 2363;
 Best Local Similarity 65.9%; Pred. No. 1.4e-164;
 Matches 867; Conservative 0; Mismatches 448; Indels 0; Gaps 0;
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 Db 1012 CGCGAGAAATTCATTGAGGCTTCCAGAGCACCAGCTGAAGGATCTCTGTCGCCAGCC 1071
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 Db 1072 GGGCAATCGTGCCTCAAGATCGACGTGGTTCATTTCCGAGGCCAGCTCATCCCAACAC 1131
 Qy 549 ttggagaccaggtttgtgactgtttcgagaatctgaattgggtgacagcttgaagc 608
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 Db 1552 CCGGCTCAACTCTACTCTCTAGCGGACTTTTCCACAGATAACGGCATCATCTCTATCT 1611
 Qy 1029 cttgcgtttgggtttgtacacacggttactaaagcattgtctactactctctgtgaactat 1088
 Db 1612 CTTTGTCTTGGGTCTGTACACGGCACTAAGCCGCTGTCTACACGACCGTGGAGAAATAT 1671
 Qy 1089 tgaagaacactgacggttactctgtcttcttggactgttccattcgtctgctagagcttaogt 1148
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 Db 1732 CGAGATGATGCGATGCGAGGCGGAGCAGGCGGCTGGTGGTCTTGGTTAATGATCG 1791

QY	1209	agttgttcacattgcacggttctgggttgacaaagtctgggttagatgttaagagagacgacct	1368
Db	1792	CGTGTGCCCGCTGCATGGGTGCCAAATTCATGCTTTGGGGAGATGTACCCGGGATAGCTT	1851
QY	1269	cgttgaaagttctcttcgcgtagatctcgttggttaactcgggaaagaaagtttctcgt	1323
Db	1852	TGTGAGGGGGTTGACCTTGTAGATCTGGGGGTCATTTGGCGGAGATGTTCTGCT	1906

RESULT 10

US-08-374-652C-1

: Sequence 1, Application US/08374652C

: Patent No. 5834286

: GENERAL INFORMATION:

: APPLICANT: NEVALAINEN, HELENA K.M.

: APPLICANT: PALOHEIMO, MARJA T.

: APPLICANT: FAGERSTROM, RICHARD B.

: APPLICANT: MIETTINEN-OINONEN, ARJA S.

: APPLICANT: TURUNEN, MARJA K.

: APPLICANT: RAMBOSEK, JOHN A.

: APPLICANT: PIDDINGTON, CHRISTOPHER S.

: APPLICANT: HOUSTON, CHRISTINE S.

: APPLICANT: CANTRELL, MICHAEL A.

: TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,

: TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING

: TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS

: NUMBER OF SEQUENCES: 94

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

: STREET: 1100 NEW YORK AVENUE, SUITE 600

: CITY: WASHINGTON

PHYTATE DEGRADING

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MIT: 09-2000C
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995

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PRIOR APPLICATION DATA: 435
 APPLICATION NUMBER: PCT/US93/07058
 FILING DATE: 27-JUL-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/925,401
 FILING DATE: 31-JUL-1992

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 1050.071001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

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: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 2379 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: both
:   TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
:   NAME/KEY: CDS
:   LOCATION: join(404..447, 550..1906)
: S-08-374-653C-1

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Query Match 45.2%; Score 598.2; DB 2; Length 2379;
Best Local Similarity 65.9%; Pred. No. 1.4e-164;

Matches	867;	Conservative	0;	Mismatches	448;	Indels	0;	Gaps	0;
QY	9	ctcttggacactgttgacggtggttaccaaatgtttccagaaaattctcactgtggg	68						
Db	608	CACCTTCGATACGGTGCATCAAGGTATCAATGCTCTCCGAGACTTCGATCTTTGGGG	667						
QY	69	tacatactctcaattctctcttggctgaagaaatctgtctatttctcagacgttccaaa	128						
Db	668	TCAATACGGCGCGTCTCTCTCGCAAAACGAATCGGCCATCTCCCTGATGTGCGCG	727						
QY	129	gggttagagttactttctgttccaaagtttcttagacacaggtgtctagatacccaattc	188						
Db	728	CGGTTGCAGAGTCACCTTCGTGCTCAGGTCTCTCCCGTCATGGAGCGCGGTATCCGACCGA	787						
QY	189	tctcgctctaaggcgtactctgtcttbtgattgaagctattcaaaagaacgctactgtttt	248						
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QY	249	caagggtaaagtcgtttcttgaagactcaaatcaacttgggtgtgctgacgacttgac	308						
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QY	309	tcattcgggtgaacaaataatggttaactctgggtattaaagttctacagaagaactacaaggc	368						
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QY	369	tttgctagaagaattgttccattcatttagagcttctgttctgacagagtatttgcttc	428						
Db	968	GCTCACAGGAACATCATCTCGCTATCCGATCCTCTGGCTCCAGCGCGGTATCGCGCTC	1027						
QY	429	tgctgaaagtctcatggaagtttccaatctgtctaaagtgtggtgacccaggtgctaacc	488						
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QY	489	acacaaagcttccagttattaacggtattattccagaaggtgctggtttacaacaacac	548						
Db	1088	GGGCCAATCTGTGCGCCCAAGATTCGACGTGGTGTCATTTCCGAGGCCAGCTCATCCAAACACAC	1147						
QY	549	tttgaccacaggtttgttactgcttttcgaagaatactgaattgggtgacagactgaagc	608						
Db	1148	TCTCGACCCAGGCACCTGCACTGCTTTGAAGACAGCGAATTGGCCGATACCGTCTGAAGC	1207						
QY	609	taacttaactgctgttttgcgtccaccaattagagctagattggaagctcaattgcacgg	668						
Db	1208	CAATTTACCCGCCACGTTGCGCCCTCCATCTGCTCAAGCTCTGGAGAACGACCTGTCTGG	1267						
QY	669	tgtaacttgactgaagagacgttgttaactgattgacatgtgtccattgcgaactgt	728						
Db	1268	CGTGACTCTACAGACACAGATGACCTACCTCATGGACATGTGCTCTGACACCAT	1327						
QY	729	tgctagaactctgacgctactcgaattgtgtccattctgtgacttgttctcaactcagcaga	788						
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QY	789	atggattcaatacagctacttgaaactcttgggttaagtactaaggttaacggtgctggtaa	848						
Db	1388	ATGGATCCACTACGATACCTCCAGTCCCTCCGTAATAATACTACGGGCATGGCGCAGGTAA	1447						
QY	849	cccattgggttccagctcaaggtgttggtttcgtttaacgaattgattgctagattgactca	908						
Db	1448	CCCGCTCGGCCGACCCAGGGCTGCGCTAGCGTAAAGAGCTCATGCCCGCTTCACCCA	1507						
QY	909	ctctccaggttcaagacacacttctactaaccaacactttggactcttaacccagctacttt	968						
Db	1508	CTGCGCTGTCCAGTACACACAGCTTCRAACACACTTTGGACTCTGAAACCCAGCTACCTT	1567						
QY	969	cccattgaacgctactttgacgctgacttctctctcaacgacaaactatggtttctatttt	1028						
Db	1568	CCCGCTCAACTCTACTCTCTACGCGGACTTTTCCACGATACGGCATCATCTCTATCCT	1627						
QY	1029	cttcgctttgggtttgtatacaacggttactaagccattgttactactctctgttgaatat	1088						
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COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 50708/819,825
FILING DATE: 18-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-819-825-1

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Query Match	25.28;	Score 346;	DB 2;	Length 2200;
Best Local Similarity	57.2%;	Pred. No. 3.3e-91;		
Matches 753;	Conservative	0;	Mismatches 515;	Indels 48;
Gaps	5;			
QY	49	gaattctcaattctggtgggtacatactctccattctctcttggctgacgaatctgt	108	
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QY	109	atttccaaagcgtttccaaaaggtgttagagttacttcttcgaatttgccttagaac	168	
Db	667	ATCTGCCTTCGGTCCCAAGGGTGTGCTGTCAGTTTGTGAGGTGTCCTCCGGCAC	726	
QY	169	ggtgctagatacccaactctctgcgtctaaagcgtactctgctttgattgaagctatt	228	
Db	727	GGAGCTCGGTACTCTGCTCACAAAGTAGTAAGTCTACGCCGAGTTGCTTCAAAAGATC	786	
QY	229	caaaagaaacgtactgctttcaaaggttaagtaagctttcttgaagcattacaactacat	288	
Db	787	CAGGACACTGCCACCGAGTTCAAGGGCGATTTTGCGCTTTCGCGAGCTATGCTTATCAT	846	
QY	289	ttaggtgctgacgacttgactccatctggtgaacacaaatggttaactctggtattaag	348	
Db	847	CTCGGTGGCGATAATTGACGGCTTTGCGGAGGAGCAGATGATGTAATCGGGCGCCAG	906	
QY	349	tctcagaagatacaaggctttggctgaaagattgttccattcattagagcttcggt	408	
Db	907	TTCTACACCGGTATGTTGAGACGCCGAGAGATTTGCGCATTTTGTGCGTGGCGAGGC	966	
QY	409	tctgacagagtattgcttctgctgaagattcattgaagtttcccaatctgctaagttg	468	
Db	967	TCCGCGGAGTCATTGCGTTCGCGACAGTCTTCACCCGCGGATCCAGGATGCCAAGAC	1026	
QY	469	gctgaccagggtgctaacccacacacagcttctccagttatttaacgttatttccagaa	528	
Db	1027	CGGGATCCCAAGTTCGAACAAAGCAGCAGCGAGCGCTGTATCAACGTATGATCTTCGAA	1086	
QY	529	ggtgctggttacacaacactttgacacaggtttgtgactgctttcgaagaactctgaa	588	
Db	1087	GAACACTGGCAGTAAACAATACTCTGGATGGCTGACGTGCCCGGGCCGAGGA---GGCA	1143	
QY	589	ttaggttgacgacttgaaagctaacttcaactgctgttttcgctccaccaattagagctaga	648	
Db	1144	CCGGAACCCAAACCGCCGAGTTCCTGCAAGTTCCTGGCCCGCGTGTCTTGAAAAG	1203	
QY	649	ttaggaagctcaactgcccaggtgttgaacttgactgacgaagacgtttgtaacttgatgac	708	

Db	1204	ATCAGTAAACACATGCGGGTGTGAACCTCACCTTGAGAGATGTCCCCTGTTTCATGGAT	1263
QY	709	atgtgtccattccagacactgt-----tqtagaactctctgacgttactctoaattgtctctcca	762
Db	1264	CTTTGTCCGTTTGACACGGTGGGTCGAGACCCAGTCTTTTTCACCGGCAGCTCTTC	1323
QY	763	ttctgtgacttgttctactcagcagcaaatggaattcaatacactacttgcaatctttgggt	822
Db	1324	TTTTGTTCACATGTTTCACGGCGGACGATTTGGATGGCCCTACGATTTACTACTACACCTCGAC	1383
QY	823	aagtactacggttacggtgtgttaacccatttgggtccagctcaaggtgttgggtttcgtt	882
Db	1384	AAATACTACAGCCACGGCGGCGAGCGCATTTTGGCCGCTCCCGCGGCTCGGGTTCGTCTC	1443
QY	883	aacgaattgattgtagattgac---tcaactctccagttcaagaacacactcttactaac	939
Db	1444	AACGAGCTGATTGGCGCGTATGACGGGAAATCTCCCGTCAAGGAGCCACACAACTCAAC	1503
QY	940	cacacttggacttaaccagcttacttccattgaacgttactttgtacgtgacttc	999
Db	1504	CACACTCTCGATGACACCCGGAACCTTCCCGTTGGAGCGTCTCTACGCGAGACTTT	1563
QY	1000	tctcagcaacaactatgtttctattttctctgtttgggtttggttgtaacacaggttactaag	1059
Db	1564	TCGCAGGACAACCATGACGGGATCTTTTCCGCAATTGGCCCTGTACACGGCACAAAG	1623
QY	1060	ccattgtctactactctgttgaactc-----attgaagaactgacggttactctgtct	1113
Db	1624	CCGTGTTCGAGCGTCCAGATTACGCTCCGACGGGTGCAGCAGCGATGATATCGGCA	1683
QY	1114	tcttgagactgttccattcgctgctagagcttacgttgaatgatgcaatgtgaagctgaa	1173
Db	1684	TCGTGGACGGTGGCGTTTCGCAGCGAGGGCGTATGTGGAGTTGCTGCGATGTGAGACGAA	1743
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QY	1264	gacttcgtgaaggttgttcttctcgtagatcgtgtgtaactgggaagaatgttt	1319
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US-09-163-642-1			
; Sequence 1, Application US/09163642			
; Patent No. 6221644			
; GENERAL INFORMATION:			
; APPLICANT: Berka, Randy M.			
; APPLICANT: Ray, Michael W.			
; APPLICANT: Klotz, Alan V.			
; TITLE OF INVENTION: Polypeptides Having Phytase Activity			
; TITLE OF INVENTION: And Nucleic Acids Encoding Same			
; NUMBER OF SEQUENCES: 5			
; CORRESPONDENCE ADDRESS:			
; ADDRESS: No. 6221644o No. 6221644disk of No. 6221644th America, Inc.			
; STREET: 405 Lexington Avenue, Suite 6400			
; CITY: New York			
; STATE: New York			
; COUNTRY: U.S.A.			
; ZIP: 10174-6401			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSeq for Windows Version 2.0			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/163,642			
; FILING DATE:			

CLASSIFICATION:

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/819,825

FILING DATE: 18-MAR-1997

ATTORNEY/AGENT INFORMATION.

ATTORNEY/AGENCY INFORMATION:
NAME: Lambiris, Elias J.

NAME: LAMBLIS, ELIAS J.
REGISTRATION NUMBER: 33

REGISTRATION NUMBER: 33, /28
REFERENCE/DOCKET NUMBER: 4758 200-05

REFERENCE/DOCKET NUMBER: 4/
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION
TELEPHONE: 212 867 0123

TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298

TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1

INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
LENGTH. 2200 base pairs

LENGTH: 2200 base pairs
TYPE: nucleic acid

TYPE: nucleic acid
STRANDEDNESS: single

STRANDEDNESS: single
TOPOLOGY: linear

TOPOLGY
; IIS-09-163-642-1

Query Match	26.2%	Score 346;	DB 4;	Length 2200;
Best Local Similarity	57.2%;	pred. No. 3.3e-91;		
Matches 753; Conservative	0;	Mismatches 515;	Indels 48;	Gaps 5;

QY	49	gaattttctcaacttggggtacatactctcaattcttcttcttggctgaagaaatctgct	108
Db	607	GACATTCGCCCGCAGTGGGCCAGTACTCGCCCTTCTTCGCTGGCGAGGTCTCTGAA	666
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Db	667	ATCTCGCCTCGGTGCGCAAGGCGTGTCTGTGAGATTGTGACAGGTGTGTCCGGCGAC	726
QY	169	gggtcttagataccaccaacttctctcggtctaaggcgctactctgtttgattgaagctattt	228
Db	727	GGAGCTCGGTATCTACTGCTCACAGAGTGAAGTCTACGCCGAGTGTCTTCAAAGATC	786
QY	229	caaaagaacgctactgctttccaagggtgaagtcagcttcttctgaagaacttaacaacta	288
Db	787	CAGGACACTGCGACCGAGTTCGAAGGCGATTTTGCTTTTCCGAGACTATGCGCTATCAT	846
QY	289	ttgggtgctgaagacttgaactccattcgggtgaacaacaaatggttaacctgtgtattaag	348
Db	847	CTCGGTGCCGTAATTTGACGCGCTTTTGGCGAGGAGCAGATGATGGAATCGGGCGCCAG	906
QY	349	tttcacagaagatacaaggctttggctgaaagattgttccattcattagagcttctggt	408
Db	907	TTCTACCCCGGTATCGTGAGCAGGCCCGCAGAGATTGTGCCATTGTGCGTGGCGCAGGC	966
QY	409	ctgcacagagttattgctctctgctgtaaaagttcattgaaggtttcccaatctgctaa	468
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QY	469	gctgacccaggtgtctaaaccacacccaagctctccagttattaacgttattattccagaa	528
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Db	1204	ATCACTAAACACATCCCGGGTGTGAACCTCACTTGGAGGATGTCCCGTTGTTTCATGGAT	1263
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Thu Oct 18 11:34:53 2001

; FILING DATE: 07-MAY-1997
 ; APPLICATION NUMBER: 60/046,081
 ; FILING DATE: 09-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gregg, Valeta A
 ; REGISTRATION NUMBER: 35,127
 ; REFERENCE/DOCKET NUMBER: 5101.200-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1320 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-221-654-1

Query Match 9.9%; Score 131.4; DB 3; Length 1320;
 Best Local Similarity 56.9%; Pred. No. 7.3e-29;
 Matches 268; Conservative 0; Mismatches 191; Indels 12; Gaps 1;

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QY	645	tagattggaagctcaacttgcaggtgttaacttgaactgacgaagacgtttgttaacttgat	704
DB	654	GCATTGACGCTGTGCGCGGAGTGCACACCTCTCAGACAGCGGCGCTCACTCTCAT	713
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DB	714	GGATATGTGCCCGTTCGACACTCTCAG-----CTCCGGGACGCCAGCCCTT	761
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DB	762	CTGTGACCTATTTACCGGGAGGAGTATGTGCTGACGAGTACTACTATGACCTCGACAA	821
QY	825	gtactacggttacggtgctggtaaccatttgggtccagctcaagggtgtgttgggttaa	884
DB	822	GTACTATGGCACGGGCCCGGGAACGCTCTCGGTCTCTCCAGGGCGTCGGATACGTCAA	881
QY	885	cgaattgattgtagattgactcaactctccagttcaagaccacacttctactaacacac	944
DB	882	TGAGCTGCTTGCACGCTTGACCGGCCAAGCCGTTTCGAGACGACGACGACGAACCGCAC	941
QY	945	ttaggactctaacccagctacttcccaattgaacgctactttgtacgctgacttctctca	1004
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Search completed: October 16, 2001, 12:08:05
 Job time: 679 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 12:15:15 ; Search time 573.71 seconds
(without alignments)
1447.968 Million cell updates/sec

Title: US-09-488-265-30_COPY_79_1401

Perfect score: 1323

Sequence: 1 aactctactcttgacac.....actgggaagaatgttcgct 1323

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1323	100.0	1404	21	AAZ31521
4	1307	98.8	1404	21	AAZ31521
5	1307	98.8	1426	21	AAZ31521
6	1307	98.8	1426	21	AAZ31521
7	1303.8	98.5	1404	21	AAZ31521
8	1246.2	94.2	1404	20	AAZ31520
9	1246.2	94.2	1404	21	AAZ31523
10	1246.2	94.2	1404	21	AAZ31523
11	1241.4	93.8	1404	21	AAZ31521

12	1238.2	93.6	1404	21	AAZ31521	Consensus phytase
13	1236.6	93.5	1426	20	AAZ27423	Ascomycete consens
14	1236.6	93.5	1426	20	AAZ23022	Fungal phytase gen
15	1236.6	93.5	1426	21	AAZ31521	Consensus phytase
16	1236.6	93.5	1426	21	AAZ31521	DNA encoding phytase
17	1177.4	89.0	1426	20	AAZ31523	Consensus phytase
18	1177.4	89.0	1426	21	AAZ31523	Consensus phytase
19	1177.4	89.0	1426	21	AAZ31523	DNA encoding phytase
20	620.4	46.9	1404	20	AAZ31522	A. fumigatus phytase
21	620.4	46.9	1404	21	AAZ31522	Aspergillus fumigatus
22	620.4	46.9	1404	21	AAZ31522	DNA encoding a mut
23	608.2	46.0	1571	19	AAZ31522	Aspergillus fumigatus
24	608.2	46.0	1571	20	AAZ27422	A. fumigatus phytase
25	600	45.4	1404	12	AAQ11175	Chromosomal phytase
26	600	45.4	1404	18	AAZ65136	Aspergillus fucium
27	600	45.4	1404	20	AAZ27421	A. fucium phytase
28	600	45.4	6756	12	AAQ11174	Sequence, from ove
29	600	45.4	6756	18	AAZ65137	Aspergillus fucium
30	598.2	45.2	2363	15	AAQ58126	Phytase gene. Asp
31	598.2	45.2	2379	15	AAQ56944	A. niger phytase g
32	596.8	45.1	1404	12	AAQ13878	Phytase gene. Asp
33	580.6	43.9	1515	18	AAZ96709	Aspergillus niger
34	576.8	43.6	1931	19	AAQ3142	Aspergillus nidula
35	576.8	43.6	1931	20	AAZ27413	A. nidulans phytase
36	548.8	41.5	1912	17	AAQ3743	Phytase chimeric g
37	536.2	40.5	1845	19	AAQ3143	Talaromyces thermo
38	534.6	40.4	1845	20	AAZ27416	T. thermophilus ph
39	511.2	38.6	1567	19	AAQ3145	Aspergillus terreu
40	511.2	38.6	2327	17	AAQ3736	Phytase gene. Asp
41	511.2	38.6	2327	20	AAZ27414	A. terreus phytase
42	510.2	38.6	1464	22	AAZ77030	P.hordei phytase c
43	510.2	38.6	1584	22	AAZ77029	Part of P.hordei p
44	510.2	38.6	1922	22	AAZ77028	P.hordei phytase D
45	413.6	31.3	4898	22	AAZ77031	P.hordei phytase c

ALIGNMENTS

RESULT 1

AAZ31521

ID AAZ31521 standard; DNA; 1404 BP.

XX

AC AAZ31521;

XX

DT 06-JAN-2000 (first entry)

XX

DE Consensus phytase-10-thermo(3)-Q50T-K91A coding sequence.

XX

KW Phytase; animal feed preparation; thermostable phytase; transgenic plant;

XX

OS consensus sequence; ds.

XX

PN Synthetic.

XX

PN WO948380-A1.

XX

PD 30-SEP-1999.

XX

PF 22-MAR-1999; 99WO-DK00154.

XX

PR 23-MAR-1998; 98DK-0000407.

XX

PR 19-JUN-1998; 98DK-0000806.

XX

PR 18-SEP-1998; 98DK-0001176.

XX

PR 22-JAN-1999; 99DK-0000091.

XX

PR 22-JAN-1999; 99DK-0000093.

XX

PA (NOVO) NOVO-NORDISK AS.

XX

PI Petersen S;

XX

XX WPI; 1999-591030/50.

DR

XX P-PSDB; AAZ43170.

preparing animal feed using a thermostable phytase

Example 3; Fig 10; 71pp; English.

This sequence encodes the consensus phytease-10-thermo(3)-050M-K91A. The invention relates to a process for preparing animal feed by agglomerating feed ingredients with a thermostable phytease, which is added before or during agglomeration. The thermostable phytease is useful for expression in transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytease allows animal feed to be produced more efficiently, in addition to improved phytease-expressing transgenic plants. These plants provide a feed ingredient and a feed additive (phytease) simultaneously.

sequence 1404 BP: 329 A; 309 C; 308 G; 458 T; 0 other;

Query Match 100.0%; Score 1323; DB 20; Length 1404;

Query Match:	100.00%
Best Local Similarity	100.00%; Pred No. 0;

BEST LOCAL SIMILARITY	100.00;	Recat. no.: 87
MATCHES 1323;	Conservative	0; Mismatches
Indels	0; Gaps	0;

1 aactctcactcttgtgacactgttgacggtggttaccaatgtttccagaaatttctcac 60

1

79 aactctcaactcttgacactgttgacggtggttaccaatgtttccagaatttctcac 138

	C	C	F
1	0	0	0
2	0	0	0
3	0	0	0
4	0	0	0
5	0	0	0
6	0	0	0
7	0	0	0
8	0	0	0
9	0	0	0
10	0	0	0
11	0	0	0
12	0	0	0
13	0	0	0
14	0	0	0
15	0	0	0
16	0	0	0
17	0	0	0
18	0	0	0
19	0	0	0
20	0	0	0
21	0	0	0
22	0	0	0
23	0	0	0
24	0	0	0
25	0	0	0
26	0	0	0
27	0	0	0
28	0	0	0
29	0	0	0
30	0	0	0
31	0	0	0
32	0	0	0
33	0	0	0
34	0	0	0
35	0	0	0
36	0	0	0
37	0	0	0
38	0	0	0
39	0	0	0
40	0	0	0
41	0	0	0
42	0	0	0
43	0	0	0
44	0	0	0
45	0	0	0
46	0	0	0
47	0	0	0
48	0	0	0
49	0	0	0
50	0	0	0
51	0	0	0
52	0	0	0
53	0	0	0
54	0	0	0
55	0	0	0
56	0	0	0
57	0	0	0
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61	0	0	0
62	0	0	0
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69	0	0	0
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72	0	0	0
73	0	0	0
74	0	0	0
75	0	0	0
76	0	0	0
77	0	0	0
78	0	0	0
79	0	0	0
80	0	0	0
81	0	0	0
82	0	0	0
83	0	0	0
84	0	0	0
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89	0	0	0
90	0	0	0
91	0	0	0
92	0	0	0
93	0	0	0
94	0	0	0
95	0	0	0
96	0	0	0
97	0	0	0
98	0	0	0
99	0	0	0
100	0	0	0

61 ttgtgggtacatactctccattcttctctttggctgacgaatctgctatttctccagac 120

139 ttgtgggtacatactctccattcttctcttttggctgacgaatctgctatttctccagac 198

[illegible]

121 gttccaaagggttgtagagttacttcgttcaagtttgcctagacacacggtgctagatac 180

100 cttccceccggttctacacttccgttcaagttttgtctagacacggtcctagatac 258

199 gtccaaagggtgtgtagagttactttctgttcaagttttgtctagacacacggctgcctagatcac z38

181 ccaacttcttctacatctaagcgctactctgctttgatctgaagctattcaaaaqaacqct 240

I8I ccaactctctcgcgtctaaagccaccccccgcgcccccccgcccccc

259 ccaacttcttcgcgtctaaaggcgtactctgcctttgattgaaqctattcaaaagaaacgct 318

[illegible]

241 actgctttcaaggqtaagtacgcctttcttgaagacttaacaactacactttgggtgctgac 300

241

319 actgcttcaagggtaagtagcgtttcttgaagacttacaactacactttgggtgctgac 378

.....

301 gacttgactccattcgggtgaacacaaatggttaactctggtattaaagtctctacagaaga 360

379 gacttgactccattcggtagaacacaaatggttaactctggtatttaagttctacagaaga 438

[illegible]

361 tacaaggcttggctagaagattgttccattcattagagcttctggttctgacagagtt 420

[illegible]

439 tacaaggcttggctagaaagattgttccattcattagagcttctggttctgacagagtt 498

DR P-PSDB; AAB20527.

XX Novel phytases with improved properties such as temperature stability,
PT pH stability and substrate specificity, for use in pharmaceuticals and
PT compound foods and feeds -

XX Claim 10; Fig 8a-c; 240pp; English.

CC The present invention describes improved phytases, preferably with
CC increased thermostability, and methods for producing them. The methods
CC can be used for producing phytases with improved properties e.g.
CC temperature stability, pH stability, pH profile, temperature profile,
CC specific activity, substrate specificity, substrate cleavage pattern,
CC substrate binding, position specificity, the velocity and level of
CC release of phosphate from corn, reaction rate, phytate degradation rate,
CC and end level of released phosphate. The phytases can be used to produce
CC pharmaceutical compositions or compound food or feeds. The feed can be
CC used to reduce levels of phytate in animal manure, by converting it
CC into lower inositol phosphates and/or inositol and inorganic phosphate.
CC The present sequence encodes a phytase sequence from the present
CC invention.

XX Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;

Query Match 100.0%; Score 1323; DB 21; Length 1404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aactctcaactctgtgacactgttgacggtgtgacaaatgttccacagaaattctcac 60
DB 79 aactctcaactctgtgacactgttgacggtgtgacaaatgttccacagaaattctcac 138
QY 61 ttgtgggtacatactctccattctcttctgttggtgacgaatctgctattctccagac 120
DB 139 ttgtgggtacatactctccattctcttctgttggtgacgaatctgctattctccagac 198
QY 121 gtccaaaaggtgtgagtagtacttctgttcaagtttctgtctagacacggtgtctagatcac 180
DB 199 gtccaaaaggtgtgagtagtacttctgttcaagtttctgtctagacacggtgtctagatcac 258
QY 181 ccaactctctgcgtctaaagcgctactctgttctgattgaagctattcaaaagacgct 240
DB 259 ccaactctctgcgtctaaagcgctactctgttctgattgaagctattcaaaagacgct 318
QY 241 actgcttcaaggttaagtaacgcttctgtgaagacttaacactacactttgggtgctgac 300
DB 319 actgcttcaaggttaagtaacgcttctgtgaagacttaacactacactttgggtgctgac 378
QY 301 gacttgactccattctgttgacacacaaatgggttaactctgttatttaagttctacagaaga 360
DB 379 gacttgactccattctgttgacacacaaatgggttaactctgttatttaagttctacagaaga 438
QY 361 tacaaggtctgttagaagatttccattcttagagcttctgttctgacagagtt 420
DB 439 tacaaggtctgttagaagatttccattcttagagcttctgttctgacagagtt 498
QY 421 attgctctgtgaaagtctcaaggtttccaaatctgctaaagttgctgacacacggt 480
DB 499 attgctctgtgaaagtctcaaggtttccaaatctgctaaagttgctgacacacggt 558
QY 481 gtaacacacacacaggtctccagttattcaagttatttccagaaggtgctgggttac 540
DB 559 gtaacacacacacaggtctccagttattcaagttatttccagaaggtgctgggttac 618
QY 541 aacaacactttggacacggtttgtgtactctgttccagaatctgaagattgggtgacagac 600
DB 619 aacaacactttggacacggtttgtgtactctgttccagaatctgaagattgggtgacagac 678
QY 601 gtgaagtaacttcaactgctgtttctgctccacacaaattagagcttagattggaagctcac 660
DB 679 gtgaagtaacttcaactgctgtttctgctccacacaaattagagcttagattggaagctcac 738

QY 661 ttgcaggtgttaacttgactgacgaagcgtttgtaacttgatgacatgtgtccattc 720
DB 739 ttgcaggtgttaacttgactgacgaagcgtttgtaacttgatgacatgtgtccattc 798
QY 721 gacactgtgtgacactttgacgctactcaattgtctccattctgtgacttgttcaact 780
DB 799 gacactgtgtgacactttgacgctactcaattgtctccattctgtgacttgttcaact 858
QY 781 cagcagcaatggattcaatacagactacttgcacacttttgggtaagtaactacggttacggt 840
DB 859 cagcagcaatggattcaatacagactacttgcacacttttgggtaagtaactacggttacggt 918
QY 841 gctgtaacacacttgggtccagctcaaggtgtgtgttctgttaacgaattgattgctaga 900
DB 919 gctgtaacacacttgggtccagctcaaggtgtgtgttctgttaacgaattgattgctaga 978
QY 901 ttgactcactctccagtttcaagacacacacttctactaaccacactttgggactctaaoccca 960
DB 979 ttgactcactctccagtttcaagacacacacttctactaaccacactttgggactctaaoccca 1038
QY 961 gctacttccacattgaacgctactttgtacgctgacttctctcacgacacacactatggtt 1020
DB 1039 gctacttccacattgaacgctactttgtacgctgacttctctcacgacacacactatggtt 1098
QY 1021 tctatttcttcogcttgggtttgtacacggttactaagccattgtctactactctgtt 1080
DB 1099 tctatttcttcogcttgggtttgtacacggttactaagccattgtctactactctgtt 1158
QY 1081 gaactctattgaagaaactgacggttactctctctcttctgactgttccattcogctgctaga 1140
DB 1159 gaactctattgaagaaactgacggttactctctctcttctgactgttccattcogctgctaga 1218
QY 1141 gcttacgttgaatgtacgtcaatgtgaagctgaaagacacattggttagagtttgggtt 1200
DB 1219 gcttacgttgaatgtacgtcaatgtgaagctgaaagacacattggttagagtttgggtt 1278
QY 1201 aacgacagaggtgttccattgacggttgcaggttgcaggttgcaggttgcaggttgcaggtt 1260
DB 1279 aacgacagaggtgttccattgacggttgcaggttgcaggttgcaggttgcaggttgcaggtt 1338
QY 1261 gacgactctgtgaaggtttgttcttctgctagatctggttaactggtgaggaagattgttc 1320
DB 1339 gacgactctgtgaaggtttgttcttctgctagatctggttaactggtgaggaagattgttc 1398
QY 1321 gct 1323
DB 1399 gct 1401

RESULT 3

AAZ59716

ID -AAZ59716 standard; DNA; 1404 BP.

XX AAZ59716;

XX AC

XX XX

DT 19-APR-2000 (first entry)

XX XX

DE DNA encoding a mutant phytase-10, phytase-10-thermo[3]-Q50T-K91A.

KW phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
KW thermostable; animal feed; monogastric animal; phytate phosphorus;
KW phosphate availability; consensus; mutant; ds.

XX XX

OS Aspergillus terreus 9A1.

OS Aspergillus terreus cbs16.46.

OS Aspergillus niger var. awamori.

OS Aspergillus niger str. NRRL3135.

OS Aspergillus fumigatus ATCC13073.

OS Aspergillus fumigatus ATCC32722.

OS Aspergillus fumigatus ATCC58126.

OS Aspergillus fumigatus ATCC26906.

OS Emericella nidulans.

OS Talaromyces thermophilus ATCC20186.
OS Myceliophthora thermophila.
OS Paxillus involutus NN005693.
OS Trametes pubescens NN9343.
OS Agrocybe pediades NN009289.
OS Peniophora lycii NN006113.
OS Thermomyces lanuginosa.
OS Synthetic.

XX Key Location/Qualifiers
FH 1..1404
FT CDS
FT /*tag= a
FT /product= "Phytase-10-thermo[3-Q50T-K91A]"

XX EP969089-A1.

XX 05-JAN-2000.

XX 23-JUN-1999; 99EP-0111949.

XX 29-JUN-1998; 98EP-0111960.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Brugger R, Lehmann M, Wyss M;

XX WPI; 2000-099429/09.

XX New stabilized enzyme formulation, useful for feed compositions for monogastric animals -

XX Example 5; Fig 19; 101pp; English.

XX The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilising agents including xylitol or ribitol; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal feed in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents DNA encoding a mutant phytase-10 consensus sequence, phytase-10-thermo[3]-Q50T-K91A, which has a temperature optimum and melting point 4 degrees Celsius higher than that of phytase-10 (AAV69566). Its specific activity with phytate as a substrate is also strongly increased.

XX Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;

Query Match 100.0%; Score 1323; DB 21; Length 1404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aactctcactctgtgacactgttgacggttggttaacaaatgtttccagaaatttctcac 60
|||||

Db 79 aactctcactctgtgacactgttgacggttggttaacaaatgtttccagaaatttctcac 138
|||||

Qy 61 ttgtggggtacatactctcattctctcttctgtgctgacgaactctgtattctccagac 120
|||||

Db 139 ttgtggggtacatactctcattctctcttctgtgctgacgaactctgtattctccagac 198
|||||

Qy 121 gtccaaaagggttgtagagttactttcgtttcaagttttgtctagacacacggtgctagatac 180
|||||

Db 199 gtccaaaagggttgtagagttactttcgtttcaagttttgtctagacacacggtgctagatac 258
|||||

Qy 181 ccaactctctcgtcgtctaaggcgtagctctgtttgattgaagctattcaaaaagaacgct 240
|||||

Db 259 ccaactctctcgtcgtctaaggcgtagctctgtttgattgaagctattcaaaaagaacgct 318
|||||

Qy 241 actgctttcaagggttaagtaacgctttcttgaaagactcaaacactacactttgggtgctgac 300
|||||

Db 319 actgctttcaagggttaagtaacgctttcttgaaagactcaaacactacactttgggtgctgac 378
|||||

Qy 301 gacttgactccattcgttgaaacaaatgtttaactctgtgtattaaagttctctacagaaga 360
|||||

Db 379 gacttgactccattcgttgaaacaaatgtttaactctgtgtattaaagttctctacagaaga 438
|||||

Qy 361 tacaaggctttggctagaagaattgttccattcatttagagcttctggttctgacagatt 420
|||||

Db 439 tacaaggctttggctagaagaattgttccattcatttagagcttctggttctgacagatt 498
|||||

Qy 421 attgcttctgctgaaaagttcattgaagggtttccaactctgctaagttgctgacccaggt 480
|||||

Db 499 attgcttctgctgaaaagttcattgaagggtttccaaactgctaagttgctgacccaggt 558
|||||

Qy 481 gctaacccacacacacgcttctccagttattaaagttattatccagaaggtgctggttac 540
|||||

Db 559 gctaacccacacacacgcttctccagttattaaagttattatccagaaggtgctggttac 618
|||||

Qy 541 aacaaactttggacacacggtttgtgactgctttccagaagaatctgaattgggtgacgac 600
|||||

Db 619 aacaaactttggacacacggtttgtgactgctttccagaagaatctgaattgggtgacgac 678
|||||

Qy 601 gttcaagctaaactcactgctgttttcgctccacaaattagagctagatgtggaagctcac 660
|||||

Db 679 gttcaagctaaactcactgctgttttcgctccacaaattagagctagatgtggaagctcac 738
|||||

Qy 661 ttgcacaggtgttaactgactgacgaagaaggttgttaactgtatggacatgtgtccattc 720
|||||

Db 739 ttgcacaggtgttaactgactgacgaagaaggttgttaactgtatggacatgtgtccattc 798
|||||

Qy 721 gacactgtgtgtagaactcttgacgctactcaaatgtctccattctgactgtgttcaact 780
|||||

Db 799 gacactgtgtgtagaactcttgacgctactcaaatgtctccattctgactgtgttcaact 858
|||||

Qy 781 cagcaggaatgattcacaacacgactacttgcaatctttgggtaagtagactacggttacggt 840
|||||

Db 859 cagcaggaatgattcacaacacgactacttgcaatctttgggtaagtagactacggttacggt 918
|||||

Qy 841 gctggttaacccattgggtccacgctcaagggtgttggtttggttaacgaattgattgctaga 900
|||||

Db 919 gctggttaacccattgggtccacgctcaagggtgttggtttcgttaacgaattgattgctaga 978
|||||

Qy 901 ttgactcactctccagttcaagacacacactctactaacacactttggactctaaaccca 960
|||||

Db 979 ttgactcactctccagttcaagacacacactctactaacacactttggactctaaaccca 1038
|||||

Qy 961 gctactttcccaattgaacgctactttgtacgctgacttctctcagcaaacactatggtt 1020
|||||

Db 1039 gctactttcccaattgaacgctactttgtacgctgacttctctcagcaaacactatggtt 1098
|||||

Qy 1021 tctattttcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1080
|||||

Db 1099 tctattttcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1158
|||||

Qy 1081 gaactcatttgaagaacacgacggttactctctctgtgtgtgtgtgtgtgtgtgtgtgtgt 1140
|||||

Db 1159 gaactcatttgaagaacacgacggttactctctctgtgtgtgtgtgtgtgtgtgtgtgtgt 1218
|||||

Qy 1141 gcttacgttgaatgatgcaatgtgaagctgaaaagggaacacttgggttagaggtttggtt 1200
|||||

Db 1219 gcttacgttgaatgatgcaatgtgaagctgaaaagggaacacttgggttagaggtttggtt 1278
|||||

QY 301 gacttgactccattcggtagaacaacaaatggttaactctggtattaaagtctacagaaga 360
Db 390 gacttgactccattcggtagaacaacaaatggttaactctggtattaaagtctacagaaga 449
QY 361 tacaaggcttggtagaagaatgttccattcattagactctggttctgacagagtt 420
Db 450 tacaaggcttggtagaagaatgttccattcattagactctggttctgacagagtt 509
QY 421 attgcttctgtagaagaatgttccattcattagactctggttctgacagagtt 480
Db 510 attgcttctgtagaagaatgttccattcattagactctggttctgacagagtt 569
QY 481 gctaacccacacaaagcttccagttattacagttattattccagaaggtgctgtttac 540
Db 570 gctaacccacacaaagcttccagttattacagttattattccagaaggtgctgtttac 629
QY 541 aacacacacttggaccacaggttggtagctgtttccgaagaatctgaattgggtgacgac 600
Db 630 aacacacacttggaccacaggttggtagctgtttccgaagaatctgaattgggtgacgac 689
QY 601 gttgaagcttaacttactctgtttccgctccacaaattagagctagattggaagctcac 660
Db 690 gttgaagcttaacttactctgtttccgctccacaaattagagctagattggaagctcac 749
QY 661 ttgcccaggtgttaacttactgacgaagacgttggtagctgtttccgaagaatctgaattgggtgacgac 720
Db 750 ttgcccaggtgttaacttactgacgaagacgttggtagctgtttccgaagaatctgaattgggtgacgac 809
QY 721 gacactgttggtagaacttctgacgctactcaattgtctccattctgtgactgtttcact 780
Db 810 gacactgttggtagaacttctgacgctactcaattgtctccattctgtgactgtttcact 869
QY 781 cagcagcaatgatttcaatacactacttgcgaactcttctggttaagtactacaggtttacggt 840
Db 870 cagcagcaatgatttcaatacactacttgcgaactcttctggttaagtactacaggtttacggt 929
QY 841 gctggttaacccattgggtccagctcaaggtgttgggttctggttaacgaattgattgctaga 900
Db 930 gctggttaacccattgggtccagctcaaggtgttgggttctggttaacgaattgattgctaga 989
QY 901 ttgactcaactctcaattcaagacacacactctactaaccacacacttggactctaaccca 960
Db 990 ttgactcaactctcaattcaagacacacactctactaaccacacacttggactctaaccca 1049
QY 961 gctacttccattgacgctacttctgacgctgacttctctcagcagacacactatggtt 1020
Db 1050 gctacttccattgacgctacttctgacgctgacttctctcagcagacacactatggtt 1109
QY 1021 tctatttcttctgcttgggttggtagaagcgtactaagccattgtctactacttctgtt 1080
Db 1110 tctatttcttctgcttgggttggtagaagcgtactaagccattgtctactacttctgtt 1169
QY 1081 gaactctatgaagaactacaggttactctgcttctgactgttccattcgtcgtcgtaga 1140
Db 1170 gaactctatgaagaactacaggttactctgcttctgactgttccattcgtcgtcgtaga 1229
QY 1141 gcttactgtgaatgatgcaatgtgaagctgaaaggaaccattggttagattttggtt 1200
Db 1230 gcttactgtgaatgatgcaatgtgaagctgaaaggaaccattggttagattttggtt 1289
QY 1201 aacgacagagttgttccattgacggttgggttggtagaagttgggttagatgtagaaga 1260
Db 1290 aacgacagagttgttccattgacggttgggttggtagaagttgggttagatgtagaaga 1349
QY 1261 gacgacttctgtagaaggttcttctcgtctagatctggttgaactgggaagaatgtttc 1320
Db 1350 gacgacttctgtagaaggttcttctcgtctagatctggttgaactgggaagaatgtttc 1409
QY 1321 gct 1323
Db 1410 gct 1412

RESULT 7
AAA73292
ID AAA73292 standard; DNA; 1404 BP.
XX AAA73292;
AC AAA73292;
DT 05-DEC-2000 (first entry)
XX Consensus phytase 10 thermo 5 Q50T polynucleotide SEQ ID NO:94.
XX Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW temperature stability; pH profile; temperature profile; reaction rate;
KW specific activity; substrate specificity; substrate cleavage pattern;
KW substrate binding; position specificity; phytate degradation rate;
KW food; feed; phytate; manure; ds.
XX Synthetic.
OS
XX WO200043503-A1.
XX 27-JUL-2000.
XX PD
XX 21-JAN-2000; 2000WO-DK00025.
XX PF
XX 22-JAN-1999; 99DK-0000092.
XX PR
XX 21-SEP-1999; 99DK-0001340.
XX PA (NOVO) NOVO NORDISK AS.
XX Lehmann M;
XX WPI; 2000-491161/43.
XX P-PSDB; AAB20533.
XX Novel phytases with improved properties such as temperature stability,
PT pH stability and substrate specificity, for use in pharmaceuticals and
PT compound foods and feeds -
XX Disclosure; Fig 24a-c; 240pp; English.
XX The present invention describes improved phytases, preferably with
CC increased thermostability, and methods for producing them. The methods
CC can be used for producing phytases with improved properties e.g. pH
CC temperature stability, pH stability, pH profile, temperature profile,
CC specific activity, substrate specificity, substrate cleavage pattern,
CC substrate binding, position specificity, the velocity and level of
CC release of phosphate from corn, reaction rate, phytate degradation rate,
CC and end level of released phosphate. The phytases can be used to produce
CC pharmaceutical compositions or compound food or feeds. The feed can be
CC used to reduce levels of phytate in animal manure, by converting it
CC into lower inositol phosphates and/or inositol and inorganic phosphate.
CC The present sequence encodes a phytase sequence from the present
CC invention.
XX
SQ Sequence 1404 BP; 331 A; 311 C; 303 G; 459 T; 0 other;

Query Match 98.5%; Score 1303.8; DB 21; Length 1404;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1311; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 aactctcaactcttgcacactgttgacgggtgttaccacatgtttccacagaattttccac 60
Db 79 aattctcaactcttgcacactgttgacgggtgttaccacatgtttccacagaattttccac 138
Qy 61 ttgtgggggtacatactctccattctctcttgggtgacgaattctgtatttccagac 120
Db 139 ttgtgggggtacatactctccattctctcttgggtgacgaattctgtatttccagac 198
Qy 121 gttccaaagggttagagttacttctggttccagttttgtctgacacggtgctagatc 180
Db 199 gttccaaagggttagagttacttctggttccagttttgtctgacacggtgctagatc 258

Db	199	gttcacgacgactgtagagttacttttgctcaagatttgtctotagacacggtgctagatac	258
Qy	181	ccaaacttcttcgcttaagcgctactctgcttttgattgaagctattcaaaagaacgct	240
Db	259	ccaaacttcttcgcttaagcgctactctgcttttgattgaagctattcaaaagaacgct	318
Qy	241	actgctttcaagggttaagtacgctttcttgaagacttacaactacacatttgggtgctgac	300
Db	319	actgctttcaagggttaagtacgctttcttgaagacttacaactacacatttgggtgctgac	378
Qy	301	gacttgactccacttcggtgaacacaacaaatggttaactctggtattaaagtcttcacagaaga	360
Db	379	gacttgactccacttcggtgaacacaacaaatggttaactctggtattaaagtcttcacagaaga	438
Qy	361	tacaaggctttggctagaaaagattgtccattcaattagagcttctggtctgacagatt	420
Db	439	tacaaggctttggctagaaaagattgtccattcaattagagcttctggtctgacagatt	498
Qy	421	attgctcttcgctgaaaagtctcattgaaggtttccaaactcgtcaagtctggctgaccagct	480
Db	499	attgctcttcgctgaaaagtctcattgaaggtttccaaactcgtcaagtctggctgaccaggt	558
Qy	481	gctcaacccacacacagcttctccagttattaaactgtattattccagaaggtgctggttac	540
Db	559	tctcaacccacacacagcttctccagttattaaactgtattattccagaaggtatccggttac	618
Qy	541	aacaacacactttggacacacggttctgctactgctttcgaagaactgaattggtgtgacgac	600
Db	619	aacaacacactttggacacacggttctgctactgctttcgaagaactgaattggtgtgacgac	678
Qy	601	gttgaagctaaacttcactgctgtttctgctccacaaattagagctagattgggaagctcac	660
Db	679	gttgaagctaaacttcactgctgtttctgctccacaaattagagctagattgggaagctgac	738
Qy	661	ttgccaggtgttaacttgactgacgaagacgctgttgaacttgatgacatgctgtccattc	720
Db	739	ttgccaggtgttaacttgactgacgaagacgctgttgaacttgatgacatgctgtccattc	798
Qy	721	gacactgttcttagaactctgaecgctactcaattgtctccattctgtgacttgcttcaact	780
Db	799	gacactgtctgctagaactctgaecgctactgaattgtctccattctgtgcttctcaact	858
Qy	781	caacgacgaatggattccaatcacgactacttgcgaactttttgggttaagtactacggttacggt	840
Db	859	caacgacgaatggattccaatcacgactacttgcgaagctttgggttaagtactacggttacggt	918
Qy	841	gcttggttaaccatttgggtccagctcaaggtgttggtttcgttcaacgaattgattgctaga	900
Db	919	gcttggttaaccatttgggtccagctcaaggtgttggtttcgttcaacgaattgattgctaga	978
Qy	901	ttgactcaactctccagttccaagaccacacttctactaaccacacttgggactctaaccaca	960
Db	979	ttgactcaactctccagttccaagaccacacttctactaaccacacttgggactctaaccaca	1038
Qy	961	gctactttccatttgaacgctactttgtacgctgacttctctcagacaacacatttggtt	1020
Db	1039	gctactttccatttgaacgctactttgtacgctgacttctctcagacaacacatttggtt	1098
Qy	1021	tctattttcttcgctttgggttttgacaacggtactaagccattgctactactctgtt	1080
Db	1099	tctattttcttcgctttgggttttgacaacggtactaagccattgctactactctgtt	1158
Qy	1081	gaatctattgaagaactgaacggttactctgcttttggactgttccattcgtgtgctaga	1140
Db	1159	gaatctattgaagaactgaacggttactctgcttttggactgttccattcgtgtgctaga	1218
Qy	1141	gcttcagctgaagatgatgcaatgtgaagctgaagaagaacacattgggttagagtttttggtt	1200
Db	1219	gcttcagctgaagatgatgcaatgtgaagctgaagaagaacacattgggttagagtttttggtt	1278
Qy	1201	aacgacagagttgttccatttcacggttctggtgttgacaggttgggttagatgaagaaga	1260
Db	1279	aacgacagagttgttccatttcacggttctgctgttgacaagtttgggtatgatataagaaga	1338

Qy	1261	gagcaattcgttgaaggtttgtcttcttcgctagatcgtggtgaactggggaagaatgtttc	1320
Db	1339	gagcaattcgttgaaggtttgtcttcttcgctagatcgtggtgaactgggctgaatgtttc	1398
Qy	1321	gct	1323
Db	1399	gct	1401

RESULT 9

RESOLUTION 3
AAA73233
ID AAA73233 standard: DNA: 1404 BP.

XX	
AC	AAA73233;
XX	
DT	05-DEC-2000 (first entry)

Consensus phyrtase 1 thermo 8 a50t. k91a polynucleotide seo id no:28.

AA phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure; ds.

OS Synthetic.

XX PN WO200043503-A1.

27-JUL-2000

21-JAN-2000: 2000WO-DK000025.

XX
PP
22-JAN-1999.
99DK-00000092

PK ZZ-JAN-1999; 55DK-000003Z;
PB 21-SEP-1999; 99DK-0001340.

XX PA (NOVO) NOVO NORDISK AS

XX Lehmann M.

XX
DB WPT: 2000-491161/A3

DR WPI; 2000-491161/
P-PCDB: AAB20526

XX Novel phytases with improved properties such as temperature stability,
PT pH stability and substrate specificity, for use in pharmaceuticals and
PT compound foods and feeds -
PT

XX
PS
Claim 10: Fig 7a-c: 240pp: English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present invention.

Sequence 1404 BP: 329 A: 319 C: 304 G: 452 T: 0 other: XX

Query Match	94.2%	Score 1246.2;	DB 21;	Length 1404;
Best Local Similarity	96.4%;	Pred. No. 0;		
Matches 1275;	Conservative	0;	Mismatches 48;	Indels 0;
Gaps 0;				

Qy 1 aactctcactctctgtgacactgttgacggtggtattaccaatgtttcccgagaattctcac 60

Db	79	aattctcaactcttgtgacactgttgacggtgtgacggtgttaccaaattgttccacagaatttctccac	139
Qy	61	ttgtggggtacatactctccattctctctctcttctgtgtgacgaatctgctattttccagac	120
Db	139	ttgtggggtacatactctccattctctctctcttctgtgtgacgaatctgctattttccagac	198
Qy	121	gttccaaagggtgtgagagttactttgttccaaagtgttctctagacacggtgtctagatcac	180
Db	199	gttccagagactgtgagagttactttgttccaaagtgttctctagacacggtgtctagatcac	258
Qy	181	ccaaactctcttcgctctaaaggctactctctgtttgattgaagctattccaaagaacgct	240
Db	259	ccaaactctcttcgctctaaaggctactctctgtttgattgaagctattccaaagaacgct	318
Qy	241	actgctttcaagggttaagtagcgtttcttaagagacttacaactacactttgggtgctgac	300
Db	319	actgctttcaagggttaagtagcgtttcttaagagacttacaactacactttgggtgctgac	378
Qy	301	gacttgactccaattcgggtgaacacaaatgggttaactcttggtattaaagtctctacagaaga	360
Db	379	gacttgactccaattcgggtgaacacaaatgggttaactcttggtattaaagtctctacagaaga	438
Qy	361	tacaaggctttggctagaagaattgttccattcattagagcttctgggttctgacagagtt	420
Db	439	tacaaggctttggctagaagaattgttccattcattagagcttctgggttctgacagagtt	498
Qy	421	attgctttctgctgaagggttcattgaaggtttccaatctgctaagtgtggctgaccacaggt	480
Db	499	attgctttctgctgaagggttcattgaaggtttccaatctgctaagtgtggctgaccacaggt	558
Qy	481	gctaaccacacacaaaggttctccagttattaaactgttatttccagagaaggtgctgggttac	540
Db	559	tctcaacacacacaaaggttctccagttattaaactgttatttccagagaaggtgctgggttac	618
Qy	541	aacaacactttggaccacgatttgtactgcttctcgaaagactcgaatctgaattgggtgacgac	600
Db	619	aacaacactttggaccacgatttgtactgcttctcgaaagactcgaatctgaattgggtgacgac	678
Qy	601	gttgaagctaacttcaactgctgttttcgctccaccaaatagagctagatgtggaagctcac	660
Db	679	gttgaagctaacttcaactgctgttttcgctccaccaaatagagctagatgtggaagctcac	738
Qy	661	ttgcacaggtgttaacttgactgacgaagacgttgtttaaacttgatggacatgtgtccattc	720
Db	739	ttgcacaggtgttacttctgactgacgaagacgttgtttaaacttgatggacatgtgtccattc	798
Qy	721	gacactgttctagaacttctgacgctactcaaatgtctccattctgtgacttgttccact	780
Db	799	gacactgttctagaacttctgacgctactcaaatgtctccattctgtgacttgttccact	858
Qy	781	cacgacgaatggattcaatacacgactacttgcaactttttgggtaaagtactacggttacggt	840
Db	859	cacgacgaatggattcaatacacgactacttgcaactttttgggtaaagtactacggttacggt	918
Qy	841	gctgttaacccattgggtccagctcaaggttgttggtttcggttaacgaattgattgctaga	900
Db	919	gctgttaacccattgggtccagctcaaggttgttggtttcggttaacgaattgattgctaga	978
Qy	901	ttgactcactctccagttcaagacacacacttctactaacacacactttggacttaacca	960
Db	979	ttgactcactctccagttcaagacacacacttctactaacacacactttggacttaacca	1038
Qy	961	gtcaactttcccaattgaacgctactttgttaoactgtacttctcacgacacacactatgggt	1020
Db	1039	gtcaactttcccaattgaacgctactttgttaoactgtacttctcacgacacacactatgggt	1098
Qy	1021	tctattttctcgctttgggtttgacaaggttaactaagccaattgtctactactctgtt	1080
Db	1099	tctattttctcgctttgggtttgacaaggttaactaagccaattgtctactactctgtt	1158
Qy	1081	gaatctattgaagaacactgacggttactctgcttcttgactgttccactcgtcgtcgtaga	1140
Db	1159	gaatctattgaagaacactgacggttactctgcttcttgactgttccactcgtcgtcgtaga	1218

phosphohydrolase) and one or more stabilising agents including xylitol or ribitol; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal feed in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents DNA encoding a mutant phytase-1 consensus sequence, phytase-1-thermo[8]-Q50R-K91A, which has a temperature optimum and melting point 7 degrees Celsius higher than that of phytase-1 (AA969558).

XX
SO
Sequence 1404 BP: 329 A: 319 C: 304 G: 452 T: 0 other;

Query Match	94.28;	Score 1246.2;	DB 21;	Length 1404;
Best Local Similarity	96.4%;	Pred. No. 0;		
Matches 1275;	Conservative 0;	Mismatches 48;	Indels 0;	Gaps 0;
Qy 1	aactctactcttgacacgttgacggttgacaaatgtttccagaaatttctcac	60		
Db 79	aattctactctcttgacacgttgacggttgacaaatgtttccagaaatttctcac	138		
Qy 61	tgtgtgggttacatactctccattctctcttttgggtgacgaatctgtatttctccagac	120		
Db 139	tgtgtgggttaactctccatactctctcttttggcagacgaatctgtatttctccagac	198		
Qy 121	gtttccaaaggggttagaggttaacttttgcataagtttctctagacacaggtgtcagatac	180		
Db 199	gtttccagacgacttagaggttaacttttgcataagtttctctagacacggtgtcagatac	258		
Qy 181	ccaaactttctgcgtctaaaggtctactctgtttgtattgaagctattccaaaagaacgct	240		
Db 259	ccaaactttctgcgtctaaaggtctactctgtttgtattgaagctattccaaaagaacgct	318		
Qy 241	actgctttccaaagggtaagtaacgctttcttgaagacttaacactacactttgggtgtcgtac	300		
Db 319	actgctttccaaagggtaagtaacgctttcttgaagacttaacactacactttgggtgtcgtac	378		
Qy 301	gacttgactccacttcggtgaacacaaatggttaactctggtattgaagtctctacagaaga	360		
Db 379	gacttgactccacttcggtgaacacaaatggttaactctggtattgaagtctctacagaaga	438		
Qy 361	tacaaaggctttgggttagaagaattgttccattcatctagagcttctggtctgcagagtt	420		
Db 439	tacaaaggctttgggttagaagaattgttccattcatctagagcttctggtctgcagagtt	498		
Qy 421	atgctcttctgtgaaagttcattgaaggtttccaatctgtaagtggctgaccacaggt	480		
Db 499	atgctcttctgtgaaagttcattgaaggtttccaatctgtaagtggctgaccacaggt	558		
Qy 481	gctaacccacacaaagcttctccagttattaaacgttatattccagaaggtgtggttac	540		
Db 559	tctcaaccacacaaagcttctccagttattaaacgttatattccagaaggtgtggttac	618		
Qy 541	aacaaacactttgacacaggtttgtgactgttttccagaagaactgaattgggtgcacac	600		
Db 619	aacaaacactttgacacaggtttgtgactgttttccagaagaactgaattgggtgcacac	678		
Qy 601	gttgaagctaaacttactctgctgttttgcctccacaaattagatgattggaagctcac	660		
Db 579	gttgaagctaaacttactctgctgttttgcctccacaaattagatgattggaagctcac	738		

Query Match	93.5%	Score 1236.6	DB 20	Length 1426
Best Local Similarity	95.9%	Fred. No. 0		
Matches 1269	Conservative	0	Mismatches 54	Indels 0
Gaps	0			
1	aactctcaactctgtgacacactgttgacgggtgtaccacatgtttccccagaaaatttctcac	60		
y				
b				
90	aattctcaactctgtgacacactgttgacgggtgtaccacatgtttccccagaaaatttctcac	149		
y				
b				
61	tgttggtgggtcacatactctccattctctctttgggtgcagaaatctgtctatttctccagac	120		
y				
b				
150	tgttggtgggtcaatactctccatactctcttttggaagacgaactctgtctatttctccagac	209		
y				
b				
121	gttccaaaagggtgttagagctactcttcttcgaagttttgtcttagacacagggtctagatac	180		
y				
b				
210	gttccagacagactgagagctactcttcgttccaagttttgtcttagacacagggtctagatac	269		
y				
b				
181	ccaaactcttctccgtctcfaagcgtactctctgttgattggaagcctatttccaaaagacgct	240		
y				
b				

Db	1350	gacgacactcgttggaaggtttgttcttcgtagactgctggtgtaactgggctgaatgttc	1400
Qy	1321	gct 1323	
Db	1410	gct 1412	
RESULT	15		
AAAY3231			
ID	AAA73231	standard; DNA; 1426 BP.	
XX			
AC	AAA73231.		
XX			
DT	05-DEC-2000	(first entry)	
XX			
DE		Consensus phytase polynucleotide sequence SEQ ID NO:15.	
XX			
KW		Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure; ds.	
KW			
KW			
XX			
OS		Synthetic.	
XX			
PN	W0200043503-A1.		
XX			
PD		27-JUL-2000.	
XX			
XX		21-JAN-2000; 2000WO-DK00025.	
PF			
XX			
PR		22-JAN-1999; 99DK-0000092.	
PR		21-SEP-1999; 99DK-0001340.	
XX			
XX		(NOVO) NOVO NORDISK AS.	
PA			
XX			
PI		Lehmann M;	
XX			
DR		WPI; 2000-491161/43.	
XX		P-PSDB; AAB20515.	
DR			
XX			
PT		Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -	
PT			
XX			
PS		Example 9; Fig 2a-c: 240pp; English.	
XX			
CC		The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present invention.	
CC			
XX			
XX		Sequence 1426 BP; 338 A; 311 C; 308 G; 469 T; 0 other;	
Query Match		93.5%;	
Best Local Similarity		Score 1236.6; DB 21; Length 1426;	
Matches 1269; Conservative		0; Mismatches 54; Indels 0; Gaps	
Qy	1	aactctcaactctgtgacactgttgacggtgttaccagtgtttcccgagaattctcac	60
Db	90	aattctcaactctgtgacactgttgacggtgttaccagtgtttcccgagaattctcac	149
Qy	61	ttgtggggtacatactctccattctcttcttttggctgcgaatctgctattcttccagac	120

Db 1230 gcttgcgttgaaatgatgcaaatgtcaagctgaaaggaaccattgggttagagttttggtt 1289
QY 1201 aacgacagagttgttccattgcaogttgtgtgtgttgacaagttgggttagatgtaagaga 1260
Db 1290 aacgacagagttgttccattgcaogttgtgtgtgttgacaagttgggttagatgtaagaga 1349
QY 1261 gacgacttcgttgaaagttgttcttctcgtatgactgtgtgtaactggggaagaatgtttc 1320
Db 1350 gacgacttcgttgaaagttgttcttctcgtatgactgtgtgtaactggggtgaatgtttc 1409
QY 1321 gct 1323
Db 1410 gct 1412

Search completed: October 16, 2001, 12:15:53
Job time: 1147 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 15:49:37 ; Search time 12806.7 Seconds
(without alignments)
1597.903 Million cell updates/sec

Title: US-09-488-265-30_COPY_79_1401
Perfect score: 1323
Sequence: 1 aactctcaactctgtgacac.....actgggaagaatgttcgct 1323

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba1:*
- 2: gb_ba2:*
- 3: gb_ba3:*
- 4: gb_in1:*
- 5: gb_in2:*
- 6: gb_in3:*
- 7: gb_om:*
- 8: gb_ov:*
- 9: gb_pat1:*
- 10: gb_pat2:*
- 11: gb_ph:*
- 12: gb_pl1:*
- 13: gb_pl2:*
- 14: gb_pl3:*
- 15: gb_pl4:*
- 16: em_ba1:*
- 17: em_ba2:*
- 18: em_fun:*
- 19: em_htgo_hum:*
- 20: em_htgo_inv:*
- 21: em_htgo_rod:*
- 22: em_htg_hum1:*
- 23: em_htg_hum2:*
- 24: em_htg_hum3:*
- 25: em_htg_hum4:*
- 26: em_htg_hum5:*
- 27: em_htg_hum6:*
- 28: em_htg_hum7:*
- 29: em_htg_hum8:*
- 30: em_htg_inv1:*
- 31: em_htg_inv2:*
- 32: em_htg_other:*
- 33: em_htg_rod:*
- 34: em_hum1:*
- 35: em_hum2:*
- 36: em_hum3:*
- 37: em_hum4:*
- 38: em_hum5:*
- 39: em_hum6:*
- 40: em_hum7:*
- 41: em_in:*
- 42: em_om:*
- 43: em_or:*

44: em_ov:*

45: em_pat:*

46: em_ph:*

47: em_pl:*

48: em_ro:*

49: em_sts:*

50: em_sy:*

51: em_un:*

52: em_vi:*

53: gb_sts1:*

54: gb_sts2:*

55: gb_sts3:*

56: gb_sy:*

57: gb_un:*

58: gb_vil:*

59: gb_vil2:*

60: gb_htg1:*

61: gb_htg2:*

62: gb_htg3:*

63: gb_htg4:*

64: gb_htg5:*

65: gb_htg6:*

66: gb_htg7:*

67: gb_htg8:*

68: gb_htg9:*

69: gb_htg10:*

70: gb_htg11:*

71: gb_htg12:*

72: gb_htg13:*

73: gb_htg14:*

74: gb_htg15:*

75: gb_htg16:*

76: gb_htg17:*

77: gb_htg18:*

78: gb_htg19:*

79: gb_htg20:*

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83: gb_htg24:*

84: gb_htg25:*

85: gb_pr1:*

86: gb_pr2:*

87: gb_pr3:*

88: gb_pr4:*

89: gb_pr5:*

90: gb_pr6:*

91: gb_pr7:*

92: gb_pr8:*

93: gb_pr9:*

94: gb_roi:*

95: gb_ro2:*

96: gb_in4:*

97: gb_pr10:*

98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1236.6	93.5	1426	9 AX021809	AX021809 Sequence
2	780.6	59.0	1350	56 AF295325	AF295325 Synthetic
3	608.2	46.0	1571	9 AX000634	AX000634 Sequence
4	608.2	46.0	1812	15 SFU59804	U59804 Aspergillus
5	600	45.4	1404	9 A19452	A19452 phytase cDN
6	600	45.4	1404	10 I13430	I13430 Sequence 33
7	600	45.4	1404	10 I33881	I33881 Sequence 19
8	600	45.4	2000	13 ANPHYAG	Z16414 A.niger phy


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DEFINITION Aspergillus fumigatus phytase gene, complete cds.
ACCESSION U59804
VERSION U59804.1 GI:2108353
KEYWORDS Aspergillus fumigatus.
SOURCE Aspergillus fumigatus.
ORGANISM Aspergillus fumigatus.
REFERENCE 1 (bases 1 to 1800)
AUTHORS Pasamontes, L., Halker, M., Wyss, M., Tessier, M. and van Loon, A. P.
TITLE Gene cloning, purification, and characterization of a heat-stable
JOURNAL phytase from the fungus Aspergillus fumigatus
MEDLINE Appl. Environ. Microbiol. 63 (5), 1696-1700 (1997)
REFERENCE 2 (bases 1 to 1812)
AUTHORS Pasamontes, L.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1996) Luis Pasamontes, VFCEB, F. Hoffmann-La Roche
AG., Basel 4070, Switzerland
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Best Local Similarity 66.9%; Pred. No. 2.5e-149;
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QY 63 gtgggtacatactcacttctctctctctctctctctctctctctctctctctcagaagt 122
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QY 123 tccaaagggttagagttacttctctcagaagtttctgtagacacgtgctagatacc 182
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QY 243 tcttctcaagggttagagttctctcagaagtttctgtagacacgtgctagatacc 302
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RESULT 5
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 DEFINITION Phytase cDNA fragment.
 ACCESSION A19452
 VERSION A19452.1 GI:583195
 KEYWORDS

PAT 10-JUN-1994

SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 1404).
 AUTHORS van Gorcom, R.F.M., van Hartingsveldt, W., van Paridon, P.A., Veenstra, A.E., Luiten, R.G.M. and Sellen, G.C.M.
 TITLE Cloning and expression of microbial phytase
 JOURNAL Patent: EP 0420358-A 41 03-APR-1991;
 GIST-BROCADES N.V.
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 Best Local Similarity 66.1%; Pred. No. 3.6e-147;
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 ACCESSION I13430
 VERSION I13430.1 GI:910771
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1404)
 AUTHORS Van Gorcom, R.F.M., Van Hartingsveldt, W., Van Paridon, P.A., Veenstra, A.E., Luiten, R.G.M. and Sellen, G.C.M.
 TITLE Cloning and expression of phytase from aspergillus
 JOURNAL Patent: US 5436156-A 33 25-JUL-1995;
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Query Match 45.4%; Score 600; DB 10; Length 1404;
Best Local Similarity 66.1%; pred. NO. 3.6e-147;
Matches 867; Conservative 0; Mismatches 445;

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QY	312	attcgggtgaacaacaaatgggttaactcgtgtattaaagttctacagaagatacaaggcttt	371
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DEFINITION	133881	1404 bp DNA	PAT
ACCESSION	133881	Sequence 19 from patent US 5593963.	06-FEB-1997
VERSION	133881.1	GI:1824672	
KEYWORDS		Unknown.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1. (bases 1 to 1404)	
AUTHORS		Van Ooijen,A.J.J., Rietveld,K., Hoekema,A., Pen,J., Sijmons,P.C.	
TITLE		Expression of phytyase in plants	
JOURNAL		Patent: US 5593963-A 19 14-JAN-1997;	
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Best Local Similarity		66.1%;	Pred. No. 3.6e-147;
Matches 867; Conservative		0; Mismatches 445; Indels	0; Gaps

Query Match 45.4%; Score 600; DB 10; Length 1404;
Best Local Similarity 66.1%; Pred. No. 3.6e-147;
Matches 867. Concentration 0.

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QY	72	atacttcacattctcttttggctgaacaatctgctatttcttcagacggttccaaaggg	131
Db	150	ATACCGACGGTCTCTCTCTGGCAACGAATCGTCACTCCCTGAGGTGCCGCCGG	209
QY	132	ttgtgagttacttcttcgaatttgtctagacacggtgtagatacccaactcttc	191
Db	210	ATGCAGAGTCACTTTCGCTCAGGTCTCTCCCGTCTATGAGCGCGGTATCCGACCGGACT	269
QY	192	tycgtctaaggcgttaactctgtttgattgaagctattcaaaagaacgtactgtttcaa	251
Db	270	CAAGGGCAAGAAATACTCCGCTCTCATTTGAGGAGATCCAGCAGAAGCGGACCACCTTTGA	329
QY	252	gggttaagtacgctttcttgaagacttacaaactacactttgggtgtgacgacttgactcc	311
Db	330	CGGAAATATGCCCTTCCTGAAGACATACAACATACAGCTTGGGTGCAGATGACCTGACTCC	389
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QY	372	ggtcaagaagattgttccattcattagagcttctgttctgaacagagttattgtctgc	431
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QY	432	tgaagaattcattgaaggtttccaatctgctgaattggtgacccaggtgtctaaacccaca	491
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QY	492	ccaagcttccagttattaaagttattattccagaaggtgctgttcaacaaacacattt	551
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QY	552	ggacacaggttctgactgcttccgaagaattctgaattggtgacagcgttgaagctaa	611
Db	630	CGACCCAGGACCTGCACCTGTCTCGAAGACAGCGAATTTGGCCGATACCGTCCGAAGCCNA	689
QY	612	cttcaactgtcttcttccccaattagagctagattggaagctcacttccaggtgtt	671
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DEFINITION	A.niger phyA gene.		06-OCT-1992
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VERSION	Z16414.1		
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SOURCE	Aspergillus niger.		

ORGANISM	Aspergillus niger			
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.			
AUTHORS	1 (bases 1 to 2000) van Hartingsveldt, W., Van Zeijl, C.M.J., Harteveld, M.G., Gouka, R.J., Suykerbuyk, M.E.G., Luiten, R.G.M., Van Paridon, P.A., Selten, G.C.M., Veenstra, A.E., Van Gorcom, R.F.M. and Van Den Hondel, C.A.M.J.			
TITLE	Cloning, molecular characterization and overexpression of the phytase gene (phyA) of Aspergillus niger			
JOURNAL	Gene (1992) In press			
REFERENCE	2 (bases 1 to 2000) van Hartingsveldt, W.			
AUTHORS	Direct Submission			
TITLE	Submitted (05-OCT-1992) Van Hartingsveldt W., TNO Medical			
JOURNAL	Biological Laboratory, Lange Kleiweg 139, Rijswijk, the Netherlands			
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VERSION M94550.1 GI:166520
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ORGANISM Aspergillus niger
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 2665)
AUTHORS Mullaney,E.J., Gibson,D.M and Ullah,A.H.
TITLE Positive identification of a lambda gt11 clone containing a region of
fungal phytase gene by immunoprobe and sequence verification
Appl. Microbiol. Biotechnol. 35, 611-614 (1991)
REFERENCE 2 (bases 1 to 2665)
AUTHORS Mullaney,E.J.
TITLE Sequence of the Aspergillus niger (ficus) phytase gene
Unpublished (1992)
JOURNAL JOURNAL
MEDLINE
REFERENCE 2 (bases 1 to 2665)
AUTHORS Mullaney,E.J.
TITLE Sequence of the Aspergillus niger (ficus) phytase gene
Unpublished (1992)
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Matches 867; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

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Thu Oct 18 11:34:52 2001

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 AUTHORS Veenstra, A.E., Luiten, R.G.M. and van Hartingsveldt, W., van Paridon, P.A.,
 Cloning and expression of microbial phytase
 TITLE Patent: EP 0420358-A 40 03-APR-1991;
 JOURNAL GIST-BROCADES N.V.
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 Db 1661 GAGGGGTGACCTTTGCTAGATCTGGGGGTGATTGGCGGAGTGTTTGTCT 1712

RESULT 11
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 LOCUS I13429 6756 bp DNA PAT 26-JUL-1995
 DEFINITION Sequence 31 from patent US 5436156.
 ACCESSION I13429
 VERSION I13429.1 GI:910770
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 6756)
 AUTHORS Van Gorcom,R.F.M., Van Hartingsveldt,W., Van Paridon,P.A.,
 Veenstra,A.E., Luiten,R.G.M. and Selden,G.C.M.
 TITLE Cloning and expression of phytase from aspergillus
 JOURNAL Patent: US 5436156-A 31 25-JUL-1995;
 FEATURES Location/Qualifiers
 source l..6756
 BASE COUNT 1615 a 1714 c 1712 g 1715 t
 ORIGIN

Query Match 45.4%; Score 600; DB 10; Length 6756;
 Best Local Similarity 66.1%; Pred. No. 3.9e-147;
 Matches 867; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

QY 12 ttgtgacacgtgtgacggtgttaccactgtttccagaataatttccactgttgggttac 71
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 Db 461 ATACGACCGCTTCTCTCTGTCGCAACGAATCGGTTCATCTCCCTGAGTGCCCGCG 520
 QY 132 tctagaattacttctgttccaaagtttctgtacacaggtgtgtagatacccaactcttc 191
 Db 521 ATCAGAGTCACHTTCTGCTCAGGTCTCTCCGCTCATGGAGCGGTATCCGACGACTC 580
 QY 192 tgcgtcaagcgctactctgttggatgaagctatttcaaaagaacgctactgtttcaa 251
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 Db 641 CGGAAATATGCTCTCTGAGACATACACTACAGTTGGGTGCGAGATGACTGACTCC 700
 QY 312 attcgttgaaacaaatggttaactctgttattgaagttctacagaagatacaagcttt 371
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 Db 821 CAAGAAATTCATCGAGGCTTCCAGAGCACCAAGCTGAAGGATCTCTGCTGCGCGCGG 880
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 Db 941 CGACCCAGGACCTGCACHTGCTTGGAGACAGCGAAATGGCCGATACCGTCGAAGCCAA 1000

Query Match		45.2%	Score 598.2;	DB 9;	Length 2363;
Best Local Similarity		65.9%	Pred. No. 1.1e-146;		
Matches 867;		Conservative	0;	Mismatches 448;	Indels 0;
Gaps		0;			
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Qy	69	tacatactctccattctctcttcttggtgacgaatctgctatttctccagacgttccaaa	128		
Db	652	TCAATACGCGCGTTCCTCTCTGCGCAAGAAATCCGCGATCCGATGAGCGGTATCGACCGA	711		
Qy	129	gggttgtagagttacttctcggtcaagttttgtctagacacggtgctagatataccaaetcc	188		
Db	712	CGTTCGAGAGTCACTTCGCTCAGGCTCTCCGCTCATGGAGCGGTATCGACCGA	771		
Qy	189	tctgcgtctaaaggcgtactctggttgattgaagctatttccaaagaacgtactgttt	248		
Db	772	GTCCAAGGGCAAGAAATACTCCGCTCTCATTTGAGGAGATCCAGAGAACTGACACCTT	831		
Qy	249	caagggttaaglacgcttcttgaagacttaacacttctggtgtgctgacgacttgac	308		
Db	832	TGATGGAAATATGCTTCCTTGAAGACATACAATACAGCTTGGTGCAGATGACCTGAC	891		
Qy	309	tccattcgttgaaacaaaatgggttaactctggttatttaagtctacagaagatacaaggc	368		
Db	892	TCCTTCGAGAGCAGGAGCTAGTCACTCGGCTATCAAGTTCACAGCATACGAATC	951		
Qy	369	tttgctgaaagattgtccattcattagagcttctggttctgacagagtattgtctc	428		
Db	952	GCTCAAGAAACATCATTCGCTTCATCCGATCCGATCTCTGCTCCAGCGCGTGTGCTC	1011		
Qy	429	tgtctaaagttcattgaaggtttccaaatctgtaagtgtggtgctaccaggtgttaaccc	488		
Db	1012	CGCGGAGAAATTCATTGAGGCTTCAGAGACCAAGCTGAAGTATCTGTCGCCAGCC	1071		
Qy	489	acaccaagttctccagttattaaagttattattccaaaggtgtggttacaacacac	548		
Db	1072	GGGCCAATCTGCGCCCAAGATCGAGCTGTCTATTTCCGAGGCCAGCTCTATCCAAACAC	1131		
Qy	549	tttgacacaggtttgttactgtcttgaagaatctgaattgggtgacgacgttgaagc	608		
Db	1132	TCTCGACCCAGGACCTGCACGTCTTTTGAAGACAGCGAATTTGCCGATACCGTGAAGC	1191		
Qy	609	taacttcaactgtgttttgcgtccaaatagagactagattgggaagctcaacttccagg	668		
Db	1192	CAATTTTACCGCCAGCTTCGCCCTCCATTCGTCAACGCTCTGAGAACGACCTGCTGCG	1251		
Qy	669	tgtaacttgactgacgaagacgttgttaacttgatgacatgtgtccattcgcacactgt	728		
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Qy	729	tgtagaactctgacgtactcaattgtctccattctgtgacttggtagttagattgactca	788		
Db	1312	CTCACACGACCGTTCAGACACCAAGCTGTCGCCCTTCTGTGACCTGTTCCACCATGACGA	1371		
Qy	789	atggattcaatacagactacttgcaatctttgggttaagtactcaggttgcgtggttaa	848		
Db	1372	ATGGATCCACTAGACTACTCTCCAGTCCCTGAAATAATCTAGGGCCATGGCGCAGGTAA	1431		
Qy	849	ccatttggttccagctcaaggttgtgttctgtaacgaattgattgtagattgactca	908		
Db	1432	CCGCTCGGCCGCCAGCCAGCGGCTGCGTACGCTAACGAGCTATCGCCGCTCTCACCCA	1491		
Qy	909	ctctcagtttcaagacacacttctactaacacacttggacttgaacttaacacagctactt	968		
Db	1492	CTCGCTGTCCAGATGACACAGCTCCAAACACACTTTGGACTCGAAGCCAGCTACCTT	1551		
Qy	969	ccattgaagcgtacttctgacgtacttctctcagcaacactatggtttctatttt	1028		
Db	1552	CCCGCTCAACTCTACTCTCTACGCGGACTTTTCCACGATTAAGGCATCATCTCTATCCT	1611		
Qy	1029	cttcgcttgggtttgtacaaacggttactaaagcattgtctactacttctgttgaatctat	1088		

Qy	612	cttcaactgctgttttgcgtcccaacttagagcttagattggaagctcacttgcagggtgt	671		
Db	1001	TTTCACCGCAGTTCGTCCTCCCTCCATCTGTCACAGTCTGGAGAACGACCTGTCGGGT	1060		
Qy	672	taacttgaactgaagagaagttgttaacttgatgacatgtgtccattcagacactgttgc	731		
Db	1061	GACTCTCACAGACACAGAAGTACCTACCTACCTATGGACATGTGCTCTCGACACCATCTC	1120		
Qy	732	tagaaacttgaactgaactcaattctccattctgctgacttgcactcagcagaatg	791		
Db	1121	CACACAGACCGTTCGACACCAAGCTGTCGCCCTCTCTGTGACCTGTTCCACCCATGACGAATG	1180		
Qy	792	gattcaatcagactacttgcgaactcttgggtgaagtactcaggttgaaggtgctgtaaccc	851		
Db	1181	GATCACTACGACTACTCTCAGTCTTTGAAAGATATTACGGCCATGGTGCAGGTAACCC	1240		
Qy	852	attgggttccagctcaaggtgtgttctgtaacgaattgattgtagactcaactc	911		
Db	1241	GCTCGGCCCGACCGGCTCGGCTACGCTAACGAGCTCATCGCCGCTGTGACCCACCTC	1300		
Qy	912	tccagttcaagacacacttctactaacacacacttgggactctaaacccagctacttcc	971		
Db	1301	GCCTGTCCAGATCACACACAGTTCCAAACACACTTTGGACTCGAGCCGSGCTACCTTTCC	1360		
Qy	972	attgaacgctacttctgacgtgacttctctcagcaacactatggtttctatttt	1031		
Db	1361	GCTCAACTCTACTCTCTACGCGGACTTTTCGCATGACACGGGATCATCTCCATCTCTT	1420		
Qy	1032	cgtttgggttgcacacggtactaagcattgctactactctctgtgaactctattga	1091		
Db	1421	TGCTTTTGGTCTGTACAAACGCGCTAACCGCTATCTACACAGCCGTGGAGATATCAC	1480		
Qy	1092	agaaactgacgttactctgttcttggactgttccattcgtgctgtagaagcttcaagttga	1151		
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Qy	1152	aatgatcaatgtgaagctgaaagaaacacattggttagagtttgggttgaacagacagt	1211		
Db	1541	GATGACAGTGTGAGCGGAGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1600		
Qy	1212	tggtccatgacaggttgggtgttgacaagttgggttagatgtaagagagacacttctgt	1271		
Db	1601	TGTCCTGCTGATGGGTGCTGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1660		
Qy	1272	tgaaggttcttctgctagatctggtgttaactgggaagaaatgtttcgt	1323		
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RESULT 12					
AR018076	AR018076	2363 bp	DNA	PAT	05-DEC-1998
LOCUS	Sequence 7 from patent US 5780292.				
DEFINITION	AR018076				
ACCESSION	AR018076.1	GI:3973679			
VERSION	Unknown.				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2363)				
AUTHORS	Nevalainen, H.K.M., Paloheimo, M.T., Miettinen-Oinonen, A.S.K., Torkkeli, T.K., Cantrell, M., Piddington, C.S., Rambosek, J.A., Turunen, M.K. and Fagerstrom, R.B.				
TITLE	Production of phytate degrading enzymes in trichoderma				
JOURNAL	Patent: US 5780292-A 7 14-JUL-1998;				
FEATURES	Location/Qualifiers				
source	1..2363				
BASE COUNT	559 a 732 c 510 g 562 t				
ORIGIN	/organism="unknown"				

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Qy	489	acacaaagctctccagttattaaagttattattccagaaggtgtggtttacaacaacac	548
Db	1072	GGGCCAATCGTCGCCCAAGATCGAGTGTCATTTCGAGGCCAGCTCATCCACACACAC	1131
Qy	549	tttggaccacggtttgttactgctttcagaagaattgaaattgggtgacgacgttgaagc	608
Db	1132	TCTCGACCCAGGCACCTGCACATGCTTTTGAAGACAGCGAAATGGCCGATACCTCGTGAAGC	1191
Qy	609	taacttcaatgctgttttctgctccaccattagactagattggaagctcaacttgcgcag	668
Db	1192	CAATTTCACCGGCACGGTTGCGCCCTCCATTTCGTAACGTCCTGGAGAACGACCTGTCTGG	1251
Qy	669	tgttaacttgaactgacgaagcgtgttaacttgtatggagaaatgtgtccatgcacactgt	728
Db	1252	CGTGACTCTCAGACACAGAAAGTGACCTACTCATGGACATGTGCTCTTGACACCAT	1311
Qy	729	tgttagaacttctgacgtactcaattgtctccattctgtgaacttgttcaactcacacaa	788
Db	1312	CTTCCACCAAGCAGCTCGACACCAAGCTGTGCCCTTCTGTGACCTGTTCACCATGACCA	1371
Qy	789	atggattcaatacagactacttgcgaattcttgggttaagtactacggttaoagtgctggttaa	848
Db	1372	AUGGATCCACTACGACTACCTCCAGTCCCTTGAAAAAATACTACGGCCATGGCGCAGGTAA	1431
Qy	849	ccatttgggtccagctoaaggtgtgtgttcttcgttaacgaattgattgctagattgactca	908
Db	1432	CCCGCTCGGCCCGACCCAGGCGCTCGGCTACGCTAAGGAGCTCATCGCCGCTCAQCCA	1491
Qy	909	ctctccagttcaagacacacacttctaacaacacactttggactctaaocagctacttt	968
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Db	1552	CCCGCTCAACTCTACTCTTACGCGGACTTTTCCACGATAACGGCATCATCTCTATCCT	1611
Qy	1029	cttcgcttttgggtttgtacaacggttactaagccattgtctactacttctgttgaatctat	1088
Db	1612	CTTTGCTTTGGGTCTGTACAAACGGCACTAAGCCGCTGTCTACCAAGCCGCTGGAGAAAT	1671
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Db	1792	CGTGTGCCGCTGCATGGGTGTCCAATTCATGCTTTTGGGAGATGTAACCCGGGATAGCTT	1851
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Db	1852	TGTTGAGGGGTGTGACTTTCCTAGATCTGGGGGTGATTGGCGGAGGTCTCTGCT	1906

1 (bases 1 to 2379)
Nevalainen,H.K.M., Paloheimo,M.T., Fagerstrom,R.B.,
Miettinen-Oinonen,A.S.K., Turunen,M.K., Rambossek,J.A.,
Piddington,C.S., Houston,C.S. and Cantrell,M.A.
Recombinant cells that express phytate degrading enzymes in desired
ratios
Patent: US 5834286-A 1 10-NOV-1998;
JOURNAL Location/Qualifiers
FEATURES
source 1..2379
BASE COUNT 561 a 735 c 518 g 565 t
ORIGIN
Query Match 45.2%; Score 598.2; DB 9; Length 2379;
Best Local Similarity 65.9%; Pred. NO. 1.1e-146;
Matches 867; Conservative 0; Mismatches 448; Indels 0; Gaps 0;
QY 9 ctcttgacactgttgacggttggttaccaatgtttccagaaattctcacttgagg 68
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DB 1448 CCCGCTCGCCCGACCCAGCGGCTCGGTACGCTAACGAGCTCATCGCCGCTCTCACCACA 1507
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RESULT 15
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LOCUS Aspergillus niger var awamori phytase gene, complete cds.
DEFINITION L02421
ACCESSION L02421 GI:166518
VERSION L02421.1
KEYWORDS phytase.
SOURCE Aspergillus niger (strain ALK0243, sub_species awamori) DNA.
ORGANISM Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE 1 (sites)
AUTHORS Piddington,C.S., Houston,C.S., Paloheimo,M., Cantrell,M.,
Miettinen-Oinonen,A., Nevalainen,H. and Rambossek,J.
TITLE The cloning and sequencing of the genes encoding phytase (phy) and
ph 2,5-optimum acid phosphatase (aph) from Aspergillus niger var.
awamori
JOURNAL Gene 133 (1), 55-62 (1993)
MEDLINE 94040796
REFERENCE 2 (bases 1 to 2379)
AUTHORS Carter,J.R., Franden,M.A., Abersold,R.H. and McHenry,C.S.
TITLE Molecular cloning, sequencing and overexpression of the gene
encoding the psi subunit of E. coli DNA polymerase III holoenzyme
Unpublished (1992)
JOURNAL Location/Qualifiers
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source 1..2379
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566..1925
exon
BASE COUNT 561 a 735 c 518 g 565 t
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/note="putative"
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Query Match 45.2%; Score 598.2; DB 13; Length 2379;
Best Local Similarity 65.9%; Pred. No. 1.1e-146;
Matches 867; Conservative 0; Mismatches 448; Indels 0; Gaps 0;
QY 9 ctctgtgacactgttgacggtgttaccgaattgttccagaaattctccattgtgggg 68
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Job time: 14041 sec

us-09-488-265-30_copy_79_1401.rge

Thu Oct 18 11:34:52 2001

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 17:47:36 ; Search time 7358.5 seconds
(without alignments)
1799.748 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 20456230

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %			ID	Description
		Match	Length	DB		
C	1	152.6	10.9	802	227	AQ324539 mgx00019C
	2	117.8	8.4	837	226	AQ234549 mgx00014M
	3	109	7.8	581	104	AJ274007 AJ274007
	4	83.8	6.0	753	225	AQ163004 mgx00021D
	5	81.2	5.8	699	225	AQ162040 mgx00010F
	6	75.4	5.4	810	225	AQ161556 mgx00008K
	7	74.6	5.3	769	227	AQ361474 mgx00004I
	8	73.6	5.3	669	227	AQ361495 mgx00004K
	9	43.6	3.1	1016	221	CNS04ESQ
	10	41.8	3.0	341	109	AV034352
C	11	41.8	3.0	481	225	AQ202816
	12	41.8	3.0	545	224	AQ140737
	13	41.2	2.9	231	25	AV129427
	14	41.2	2.9	234	109	AV064132
	15	41.2	2.9	236	109	AV054718
	16	41.2	2.9	247	28	AV293643
	17	41.2	2.9	264	108	AV002759
	18	41.2	2.9	269	109	AV077122
	19	41.2	2.9	278	25	AV114552
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	23	41.2	2.9	306	25	AV118366
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	25	40.4	2.9	468	151	BF637070
	26	40.4	2.9	482	30	AV423243
	27	40.2	2.9	265	109	AV049962
	28	40.2	2.9	295	26	AV212676
	29	40.2	2.9	512	107	AU039641
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	32	39.6	2.8	266	109	AV091633
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	34	39.6	2.8	270	109	AV079904
	35	39.6	2.8	280	109	AV078019
	36	39.6	2.8	285	109	AV100697
	37	39.6	2.8	289	25	AV120593
	38	39.6	2.8	289	109	AV055109
	39	39.6	2.8	290	109	AV053894
	40	39.6	2.8	291	25	AV151459
C	41	39.6	2.8	296	109	AV058485
	42	39.6	2.8	297	109	AV050799
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ALIGNMENTS

RESULT	1	
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DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
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REFERENCE		
AUTHORS		
TITLE		
Genome		

JOURNAL
COMMENT

Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 408.

FEATURES

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/organism="Magnaporthe grisea"
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/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;"
</RADIII><p>Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome ($n=7$) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome-wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request.

BASE COUNT	166 a	218 c	209 g	208 t	1 others
ORIGIN	are available upon request."				

Query Match 10.9%; Score 152.6; DB 227;
Best Local Similarity 55.3%; Pred. No. 1.4e-33;
Matches 242.

QY	744	agggtgtaactgactgacgaagacgtgtgtaactgtagacactgtgtccattccacac	803
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QY	804	tgtgtcagaacctctgacgctactcgaattgtctccattgtgtgactttgcactcagca	863
Db	554	CGTGGCAGATCCNCAAGCCAC-----CCTGTGCGAGTTCTGCACGCTGTTTACGCAACG	501
QY	864	cgaaatggattccaataagactactctgcaactcttctgggtaagtactcaaggttaacggtctgg	923
Db	500	AGACTGGGAGGCATATGACTATCTCCAGACACTGGGGGAAGTGGTATGGTTTACGGCAATGG	441

Oy 924 taaccattgggtccagctcaagggtggttggttaacgaattgattgtagattaac 983
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Db 440 CAACCCCTGGGTTCACGCAAGGGTGGGCTTGCTCACAGCCTCATCGGAGGCTGT 381

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Db 380 CCAAAGCCCGTTGAAGACCAACAATAACCAACTCGACGCTCGACAGGCCACCCATCGAC 321

QY 1044 ttctccattgaacgctactttgtacgctgacttctctcacgacaacactatggtttctat 1103

Dbb 320 GTTCCCACTAGACAAAAAGCTGTACGGCGACTTTAGCCATGATACGATATCTGGGCAT 261

Qy 1104 ttcttcgcgtttgggtttgtacaaacggtactaaagccattgtctactactctctgttgaatc 1163

Db 260 CTACGCCGCTGGGGATTACAGCCACGGCCCGGATTCGTCGCCAAAAGGAG 201

Qy 1164 ta-----ttgaagaactgacggttactctgttcttggactgttccattcgctgctag 1217

200 AAGGAGCGCGCAGGAGCTCAGCGGGTCTCGTCCAGCTGGCGGGTACCGTTCCGACGCGAG 141

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[illegible]


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DEFINITION clone mgxb0021D19r, DNA sequence.
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VERSION AQ163004.1 GI:3559405
KEYWORDS GSS.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
REFERENCE 1 (bases 1 to 753)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasnowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCATGACCATG
Class: BAC ends
High quality sequence stop: 448.
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/lab_host="E. coli DH10B"
/notes="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
BASE COUNT 208 a 180 c 156 g 206 t 3 others
ORIGIN

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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
REFERENCE 1 (bases 1 to 699)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasnowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCATGACCATG
Class: BAC ends
High quality sequence stop: 285.
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/notes="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with

```

```

Query Match 6.0%; Score 83.8; DB 225; Length 753;
Best Local Similarity 50.7%; Pred. No. 2e-13;
Matches 227; Conservative 0; Mismatches 215; Indels 6; Gaps 1;

```

Thu Oct 18 11:34:51 2001

a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."

BASE COUNT 175 a 191 c 148 g 185 t
ORIGIN

Query Match 5.8%; Score 81.2; DB 225; Length 699;
Best Local Similarity 60.4%; Pred. No. 1.1e-12;
Matches 134; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 1178 acggttactctgtcttctgactgttccattcgctgtagacttgaatgaaatgatgc 1237
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 651 ACGGGTTCCTCGTACGTTGGCGGGTACCGTTCGCAGCGAGAAATGTTGTTGAAAAATGA 592
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

QY 1238 aatgtgaagctgaaaggaaccattggttagagttttggttaacgacagagattgttccat 1297
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 591 CTTCGCCAGGCGACAGCAGGAGCTTGTGAGAAATCTGTCAACGACAGGGTGCACGCCG 532
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

QY 1298 tgcacggttgggtgtgtgacagttgggttagatgtaagagagacgaacttcgttaagtt 1357
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 531 TGCAGAACTCGATGCGCGACAGTATGGGTGCTGCACGCTGAGCAAGTTCGTTGAGACT 472
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

QY 1358 tgccttcgttagatctgtggttaactggaagaatgtttcg 1399
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 471 TAAGCTTTGCGAGAGTGGAGTTCGCTGGATCAATGTTTG 430

RESULT 6
LOCUS AQ161556/c 810 bp DNA GSS 09-SEP-1998
DEFINITION mgxb0008K02r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0008K02r, DNA sequence.

ACCESSION AQ161556
VERSION AQ161556.1 GI:3557957
KEYWORDS GSS.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 810)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 321.
Location/Qualifiers
1. .810
/organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0008K02r"
/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="protoplasts"
/lab_host="E. coli DH10B"
/note="vector: pBACWICH; Site.1: HindIII; Site.2: HindIII; Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with

FEATURES
source

a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."

BASE COUNT 196 a 219 c 188 g 207 t
ORIGIN

Query Match 5.4%; Score 75.4; DB 225; Length 810;
Best Local Similarity 58.8%; Pred. No. 5.9e-11;
Matches 130; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1179 cggttactctgtcttctgactgttccattcgctgtagacttgaatgaaatgatgc 1238
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 650 CGGGTTCCTCGTACGTTGGCGGGTACCGTTCGCAGCGAGAAATGTTGTTGAAAAATGAC 591
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

QY 1239 atgtgaagctgaaaggaaccattggttagagttttggttaacgacagagttgttccat 1298
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 590 TTGCGCAGGCGACAGCAGGAGCTTGTGAGAAATCTGTCAACGACAGGGTGCACGCCGCT 531
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

QY 1299 gcaaggttgggtgtgtgacagttgggttagatgtaagagagacgaacttcgttaagtt 1358
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 530 GCAGAACTCGATGCGCGACAGTATGGGTGCTGCACGCTGAGCAAGTTCGTTGAGACTT 471
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

QY 1359 gttcttcgttagatctgtggttaactggaagaatgtttcg 1399
||||| ||| | ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 470 AGCTCTGCGAGAGTGGAGTTCGCTGGATCAATGTTTG 430

RESULT 7
LOCUS AQ361474 769 bp DNA GSS 03-FEB-1999
DEFINITION mgxb0004I12f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0004I12f, DNA sequence.

ACCESSION AQ361474
VERSION AQ361474.1 GI:4211313
KEYWORDS GSS.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 769)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 51
High quality sequence stop: 416.
Location/Qualifiers
1. .769
/organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0004I12f"
/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="protoplasts"
/lab_host="E. coli DH10B"
/note="vector: pBACWICH; Site.1: HindIII; Site.2: HindIII; Rice blast is one of the most devastating fungal diseases

FEATURES
source

[illegible]

RESULT 11
 LOCUS AQ0202816 481 bp DNA GSS 20-APR-1999
 DEFINITION RPC111-48J14.TK RPCI-11 Homo sapiens genomic clone RPCI-11-48J14, DNA sequence.
 ACCESSION AQ0202816
 VERSION AQ0202816.1 GI:3613607
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 481)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
 TITLE Use of human BAC End Sequences for Sequence-Ready Map Building
 JOURNAL Unpublished (1998)
 COMMENT Other_GSSs: RPC111-48J14.TJ
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/human/bac_end_search/bac_end_search.html
 Class: BAC ends.
 FEATURES
 Location/Qualifiers
 1..481
 /organism="Homo sapiens"
 /db_xref="GDB:751827"
 /db_xref="taxon:9606"
 /clone="RPCI-11-48J14"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPC111 Human Male BAC Library"
 BASE COUNT 150 a 99 c 81 g 151 t
 ORIGIN

Query Match 3.0%; Score 41.8; DB 225; Length 481;
 Best Local Similarity 45.5%; Pred. No. 0.35;
 Matches 148; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 966 attgattgctagattgactcactctccagttccaaagaccacacttctactaacacacattt 1025
 |||||
 Db 58 ATTATTATTGCTTGAAATTCTCGAGAGTACCTGATTTTCGCTCCACCCCACTCT 117
 |||||
 QY 1026 ggaacttaacacagctactctccactgaacgctactttgtacgctgaactctctcaca 1085
 |||||
 Db 118 ATACACTTCCCGCCCTCCATTTCCRAATTAAAGTGGTAATCTAGCCACTTACTGAATCTTCC 177
 |||||
 QY 1086 caacactatggtttctattttcttcgctttgttggtttgtacacgggtactaagccattgctc 1145
 |||||
 Db 178 AGATAAAGAGCTCCTTAAGATGGTCCACCCCGCTTTTAAACACCACTATCAGAAAGTTCG 237
 |||||
 QY 1146 tactactctcttgaactattgaagaacactgacgggttactctgctcttcttggaactgtcc 1205
 |||||
 Db 238 TTATATTACACTGAAGCCTCTCGAAATGAGGATGATGAAAGTTCAAGATGTACTTTTAC 297
 |||||
 QY 1206 attcgtctagagcttactcgttgaaatgatgcaatgtgaagctgaaagaaacattggt 1265
 |||||
 Db 298 CTGCGTACTCTTTGTTATCACTTGGCTGAAGAACTAGTCAGACGCTTTGAAACAAAGTA 357
 |||||
 QY 1266 tagagtttggtaacgacagatt 1290
 |||||

Db 358 AAAGGTATCTTTTAGTAAAGATTT 382
 RESULT 12
 LOCUS AQ140737 545 bp DNA GSS 24-SEP-1998
 DEFINITION HS_3124_A2_D10_17 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=20 Row=G, DNA sequence.
 ACCESSION AQ140737
 VERSION AQ140737.1 GI:3531390
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 545)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3124 row: G column: 20
 Class: BAC ends
 High quality sequence stop: 545.
 FEATURES
 Location/Qualifiers
 1..545
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=3124 Col=20 Row=G"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="Male"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"
 BASE COUNT 185 a 90 c 90 g 178 t 2 others
 ORIGIN

Query Match 3.0%; Score 41.8; DB 224; Length 545;
 Best Local Similarity 54.0%; Pred. No. 0.36;
 Matches 129; Conservative 0; Mismatches 107; Indels 3; Gaps 2;

QY 284 actctgcttgattgaagctattcacaagaacgctactcttccaagggttaagtaagctt 343
 |||||
 Db 474 AATCTGATTGGTTTAAATAGTAAAGATACATCGGTGTGAGACATGAGTAAGCATTTCT 415
 |||||
 QY 344 tottgaagacttaacacacttctgggtgctgacgacttgactccat-tcgggtgaacaa 402
 |||||
 Db 414 TATTCAATATATCTCTTAATTTATGTGTAIGACATTTATATCAATGTACAGCTCAG 355
 |||||
 QY 403 caaatggttaactctggttacttaagttctacagaagacgcttggcgtagaagaatt 462
 |||||
 Db 354 TACAAGGTTAAGTAAACCATTTATTTCTATCTGTGAAACAAG--AATAACTAGATATTTA 297
 |||||
 QY 463 gtccattcattagacgtcttggtctgacagagttattgctctgctgaaagtcat 521
 |||||
 Db 296 AGCTATACATTTAGGCTTTCTGTTCTTCAAGGGTTATATCTTCTTCTAGGCTTCAT 238
 |||||

RESULT 13
 LOCUS AV129427 231 bp mRNA EST 01-JUL-1999
 DEFINITION AV129427 Mus musculus c57BL/6J 11-day embryo Mus musculus CDNA clone 270006B02, mRNA sequence.


```

ACCESSION AV129427
VERSION AV129427.1 GI:5315662
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

TITLE 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
JOURNAL RIKEN Mouse ESTs
COMMENT Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory

RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES
location/Qualifiers
source 1..231
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="2700068B02"
/clone_lib="Mus musculus C57BL/6J 11-day embryo"
/sex="mixed"
/dev_stage="11-day embryo"
BASE COUNT 59 a 51 c 66 g 55 t
ORIGIN

Query Match 2.9%; Score 41.2; DB 25; Length 231;
Best Local Similarity 52.3%; Pred. No. 0.41;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1154 ctgttgatctattgaagaactgacggttactctgtctgttgactgttccattcgctg 1213
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 40 CAGCTGGACCGGATCCAGCAACTGAAGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 99
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1214 ctagagcttactgttgaaatgatgcaatgtgaagctgaaagaaaccattggttagagttt 1273
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 100 CCGCGCGCCCGAGTGGAGGAAGAAAGTGGAGGCAAGAAAGAGTGTCCGAGGAGTCTG 159
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1274 tgggttaacgacagagttgttccattgacggttgggtgtgttgacaaagttgggta 1327
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 160 AAGATGACATGGGCTCGGCTCTTTTGTGACTAAACTGCTTTTGTAAAGTTGGCTA 213
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
AV064132 234 bp mRNA EST 24-JUN-1999
LOCUS AV064132 Mus musculus small intestine C57BL/6J adult Mus musculus
DEFINITION cDNA clone 2010009L02, mRNA sequence.
ACCESSION AV064132
VERSION AV064132.1 GI:5183960
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 234)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

TITLE 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
JOURNAL RIKEN Mouse ESTs
COMMENT Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory

RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES
location/Qualifiers
source 1..234
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2010009L02"
/clone_lib="Mus musculus small intestine"
/sex="male"
/tissue_type="small intestine"
/dev_stage="adult"
BASE COUNT 55 a 45 c 72 g 62 t
ORIGIN

Query Match 2.9%; Score 41.2; DB 109; Length 234;
Best Local Similarity 52.3%; Pred. No. 0.42;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1154 ctgttgatctattgaagaactgacggttactctgtctgttgactgttccattcgctg 1213
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43 CTGGTGGCGCCGTTCCAGCACCTGGAGCTGGCGCTGTGCTGTGCTGTGCTGTGCTG 102
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1214 ctagagcttactgttgaaatgatgcaatgtgaagctgaaagaaaccattggttagagttt 1273
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 CCGCGCGCCCGAGTGGAGGAAGAAAGTGGAGGCAAGAAAGAGTGTCCGAGGAGTCTG 162
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1274 tgggttaacgacagagttgttccattgacggttgggtgtgttgacaaagttgggta 1327
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 163 AAGATGACATGGGCTCGGCTCTTTTGTGACTAAACTGCTTTTGTAAAGTTGGCTA 216
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

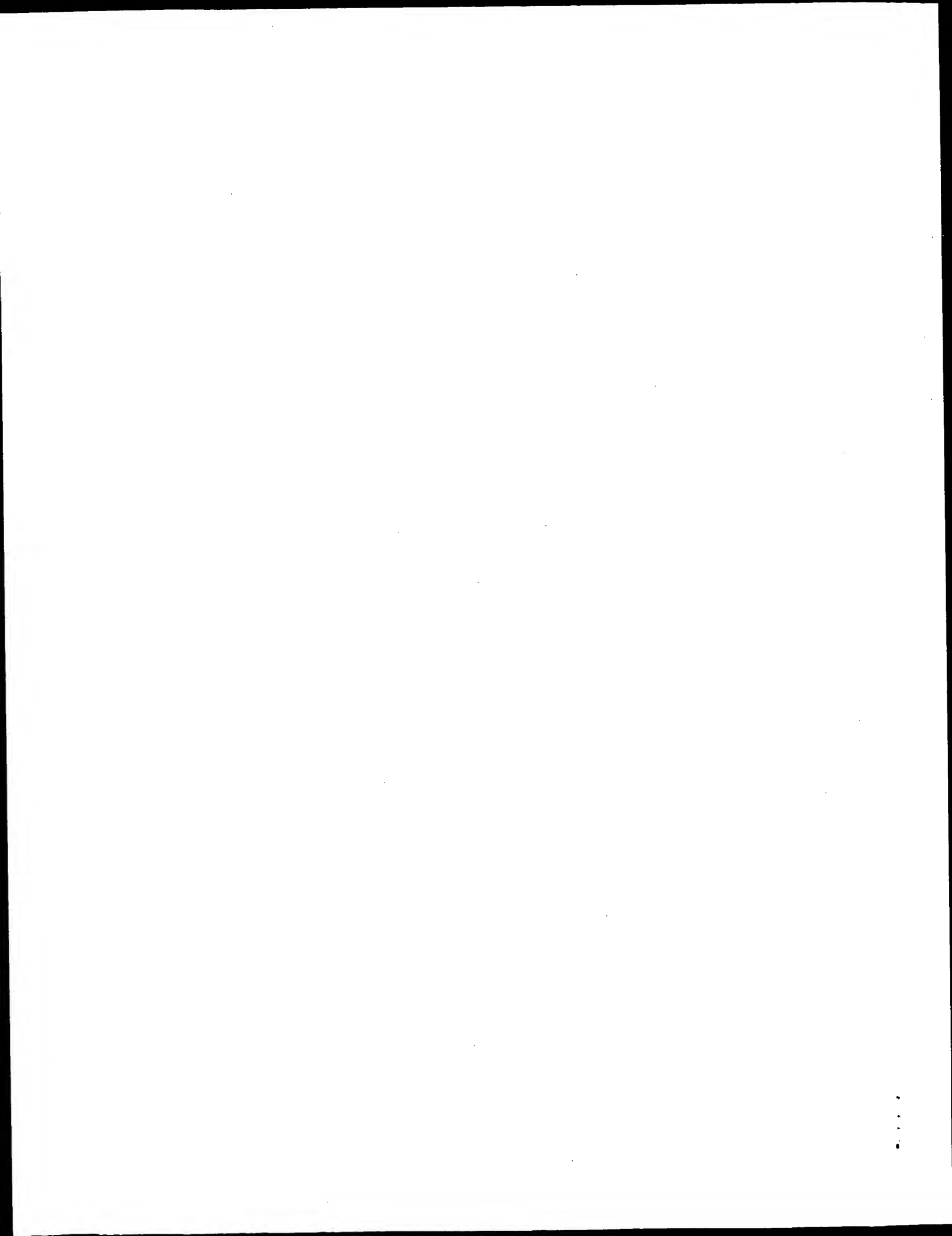
RESULT 15
AV054718 236 bp mRNA EST 23-JUN-1999
LOCUS AV054718 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA
DEFINITION clone 1810032D19, mRNA sequence.
ACCESSION AV054718
VERSION AV054718.1 GI:5154465
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 236)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,

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TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1980, Vol. 83, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Technology	1981, Vol. 5, No. 2, pp. 11-20
3. The Importance of Parental Involvement	Journal of Educational Psychology	1982, Vol. 74, No. 3, pp. 21-30
4. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1983, Vol. 86, No. 4, pp. 31-40
5. The Role of the School in the Community	Journal of Educational Research	1984, Vol. 87, No. 5, pp. 41-50
6. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	1985, Vol. 88, No. 6, pp. 51-60
7. The Role of the Teacher in the Classroom	Journal of Educational Research	1986, Vol. 89, No. 7, pp. 61-70
8. The Impact of Technology on Education	Journal of Educational Technology	1987, Vol. 11, No. 3, pp. 71-80
9. The Importance of Parental Involvement	Journal of Educational Psychology	1988, Vol. 80, No. 4, pp. 81-90
10. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1989, Vol. 92, No. 5, pp. 91-100
11. The Role of the School in the Community	Journal of Educational Research	1990, Vol. 93, No. 6, pp. 101-110
12. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	1991, Vol. 94, No. 7, pp. 111-120
13. The Role of the Teacher in the Classroom	Journal of Educational Research	1992, Vol. 95, No. 8, pp. 121-130
14. The Impact of Technology on Education	Journal of Educational Technology	1993, Vol. 17, No. 4, pp. 151-160
15. The Importance of Parental Involvement	Journal of Educational Psychology	1994, Vol. 86, No. 5, pp. 161-170
16. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1995, Vol. 98, No. 6, pp. 171-180
17. The Role of the School in the Community	Journal of Educational Research	1996, Vol. 99, No. 7, pp. 181-190
18. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	1997, Vol. 100, No. 8, pp. 191-200
19. The Role of the Teacher in the Classroom	Journal of Educational Research	1998, Vol. 101, No. 9, pp. 201-210
20. The Impact of Technology on Education	Journal of Educational Technology	1999, Vol. 23, No. 5, pp. 211-220
21. The Importance of Parental Involvement	Journal of Educational Psychology	2000, Vol. 92, No. 6, pp. 221-230
22. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	2001, Vol. 104, No. 7, pp. 231-240
23. The Role of the School in the Community	Journal of Educational Research	2002, Vol. 105, No. 8, pp. 241-250
24. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2003, Vol. 106, No. 9, pp. 251-260
25. The Role of the Teacher in the Classroom	Journal of Educational Research	2004, Vol. 107, No. 10, pp. 261-270
26. The Impact of Technology on Education	Journal of Educational Technology	2005, Vol. 29, No. 6, pp. 271-280
27. The Importance of Parental Involvement	Journal of Educational Psychology	2006, Vol. 98, No. 7, pp. 281-290
28. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	2007, Vol. 110, No. 8, pp. 291-300
29. The Role of the School in the Community	Journal of Educational Research	2008, Vol. 111, No. 9, pp. 301-310
30. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2009, Vol. 112, No. 10, pp. 311-320
31. The Role of the Teacher in the Classroom	Journal of Educational Research	2010, Vol. 113, No. 11, pp. 321-330
32. The Impact of Technology on Education	Journal of Educational Technology	2011, Vol. 35, No. 7, pp. 331-340
33. The Importance of Parental Involvement	Journal of Educational Psychology	2012, Vol. 104, No. 8, pp. 341-350
34. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	2013, Vol. 116, No. 9, pp. 351-360
35. The Role of the School in the Community	Journal of Educational Research	2014, Vol. 117, No. 10, pp. 361-370
36. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2015, Vol. 118, No. 11, pp. 371-380
37. The Role of the Teacher in the Classroom	Journal of Educational Research	2016, Vol. 119, No. 12, pp. 381-390
38. The Impact of Technology on Education	Journal of Educational Technology	2017, Vol. 41, No. 8, pp. 391-400
39. The Importance of Parental Involvement	Journal of Educational Psychology	2018, Vol. 110, No. 9, pp. 401-410
40. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	2019, Vol. 122, No. 10, pp. 411-420
41. The Role of the School in the Community	Journal of Educational Research	2020, Vol. 123, No. 11, pp. 421-430
42. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2021, Vol. 124, No. 12, pp. 431-440
43. The Role of the Teacher in the Classroom	Journal of Educational Research	2022, Vol. 125, No. 1, pp. 441-450
44. The Impact of Technology on Education	Journal of Educational Technology	2023, Vol. 47, No. 1, pp. 451-460
45. The Importance of Parental Involvement	Journal of Educational Psychology	2024, Vol. 116, No. 2, pp. 461-470
46. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	2025, Vol. 128, No. 3, pp. 471-480
47. The Role of the School in the Community	Journal of Educational Research	2026, Vol. 129, No. 4, pp. 481-490
48. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2027, Vol. 130, No. 5, pp. 491-500
49. The Role of the Teacher in the Classroom	Journal of Educational Research	2028, Vol. 131, No. 6, pp. 501-510
50. The Impact of Technology on Education	Journal of Educational Technology	2029, Vol. 53, No. 7, pp. 511-520
51. The Importance of Parental Involvement	Journal of Educational Psychology	2030, Vol. 122, No. 8, pp. 521-530
52. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	2031, Vol. 134, No. 9, pp. 531-540
53. The Role of the School in the Community	Journal of Educational Research	2032, Vol. 135, No. 10, pp. 541-550
54. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2033, Vol. 136, No. 11, pp. 551-560
55. The Role of the Teacher in the Classroom	Journal of Educational Research	2034, Vol. 137, No. 12, pp. 561-570
56. The Impact of Technology on Education	Journal of Educational Technology	2035, Vol. 59, No. 1, pp. 571-580
57. The Importance of Parental Involvement	Journal of Educational Psychology	2036, Vol. 128, No. 2, pp. 581-590
58. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	2037, Vol. 140, No. 3, pp. 591-600
59. The Role of the School in the Community	Journal of Educational Research	2038, Vol. 141, No. 4, pp. 601-610
60. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2039, Vol. 142, No. 5, pp. 611-620
61. The Role of the Teacher in the Classroom	Journal of Educational Research	2040, Vol. 143, No. 6, pp. 621-630
62. The Impact of Technology on Education		

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Search completed: October 16, 2001, 17:47:43
Job time: 21057 sec



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RESULT 2
 US-08-151-574-33
 ; Sequence 33, Application US/08151574
 ; Patent No. 5436156
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert F.M. Van Gorcom
 ; APPLICANT: Willem Van Hartingsveldt
 ; APPLICANT: Petrus A. Van Paridon
 ; APPLICANT: Annemarie E. Veenstra
 ; APPLICANT: Rudolf G.M. Luttin
 ; APPLICANT: Gerardus Sellen
 ; TITLE OF INVENTION: Cloning and Expression of Microbial
 ; TITLE OF INVENTION: Phylase
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster
 ; STREET: 545 Middlefield Road, Suite 200
 ; CITY: Menlo Park
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94025-3471
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/151,574
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/688,578
 ; FILING DATE: 24-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murashige, Kate H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 24615-20026.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-327-7250
 ; INFORMATION FOR SEQ ID NO: 33:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1404 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Aspergillus ficuum (Aspergillus niger)
 ; STRAIN: NRRL 3135
 ; US-08-151-574-33

Query Match 43.7%; Score 612.2; DB 1; Length 1404;
 Best Local Similarity 64.8%; Pred. No. 1.9e-172;
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RESULT 4
 US-08-693-709-1
 ; Sequence 1, Application US/08693709
 ; Patent No. 5770413
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN OIJEN, ALBERT J.J.
 ; APPLICANT: RIETVELD, KRIJN
 ; APPLICANT: HOEKEMA, ANDREAS
 ; APPLICANT: PEN JAN
 ; APPLICANT: SIJMONS, PETER C.
 ; APPLICANT: VERMOERD, TEUNIS C.
 ; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 PAGE MILL ROAD
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/693,709
 ; FILING DATE: 07-AUG-1996
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/146,424
 ; FILING DATE: 02-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murashige, Kate H
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 24615-20011.10
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-813-5600
 ; TELEFAX: 415-494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1404 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 1...1401
 ; OTHER INFORMATION:
 ; NAME/KEY: mat.peptide
 ; LOCATION: 70...1401
 ; OTHER INFORMATION:


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; NAME/KEY: Signal Sequence
; LOCATION: 1...72
; OTHER INFORMATION:
US-08-693-709-1

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RESULT 6
US-07-923-724-7
; Sequence 7, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,724
; FILING DATE: 31-JUL-1992

Query Match 43.7%; Score 612.2; DB 2; Length 1404;
Best Local Similarity 64.8%; Pred. No. 1.9e-172;
Matches 908; Conservative 0; Mismatches 493; Indels 0; Gaps 0;
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RESULT      7
US - 08-609-426A-7
; Sequence 7, Application US/08609426A
; Patent No. 5930733
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.N.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.
; APPLICANT: Houston, Christine S.
; TITLE OF INVENTION: Production of

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US-08-609-426A-7

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> Sequence 7, Application US/08609426A
> Patent No. 5,937,733
>
> GENERAL INFORMATION:
>
> APPLICANT: Nevalainen, Helena K.N.N.
> APPLICANT: Paloheimo, Marja T.
> APPLICANT: Miettinen-Oinonen, Arja
> APPLICANT: Torkkeli, Tuula K.
> APPLICANT: Cantrell, Michael
> APPLICANT: Piddington, Christopher
> APPLICANT: Rambossek, John A.
> APPLICANT: Turunen, Marja K.
> APPLICANT: Fagerstr m, Richard B.
> APPLICANT: Houston, Christine S.
> TITLE OF INVENTION: Production of

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US-08-151-574-31
; Sequence 31, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135

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US-08-151-574-31

Query Match 43.4%; Score 608.2; DB 1; Length 6756;
Best Local Similarity 64.9%; Pred. No. 6.2e-171;
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RESULT 10

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US-08-419-448-31
; Sequence 31, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Sellen
; TITLE OF INVENTION: Cloning and Expression of Microbial
; NUMBER OF SEQUENCES: 52

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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,448
; FILING DATE: 10-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6736 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; IMMEDIATE SOURCE:
; LIBRARY: lambda AF
; CLONE: pAF2-3, pAF2-6, pAF2-7
; FEATURE:
; NAME/KEY: exon
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; US-08-419-448-31

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Query Match 43.4%; Score 608.2; DB 2; Length 6756;
Best Local Similarity 64.9%; Pred. No. 6.2e-171;
Matches 901; Conservative 0; Mismatches 488; Indels 0; Gaps 0;
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RESULT 11

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US-09-155-855-5
; Sequence 5, Application US/09155855
; Patent NO. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(45)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (157)..(183)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (184)..(1512)
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; LOCATION: (157)..(1512)
; US-09-155-855-5

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Query Match	42.1%	Score 589.6;	DB 3;	Length 1515;
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RESULT 12

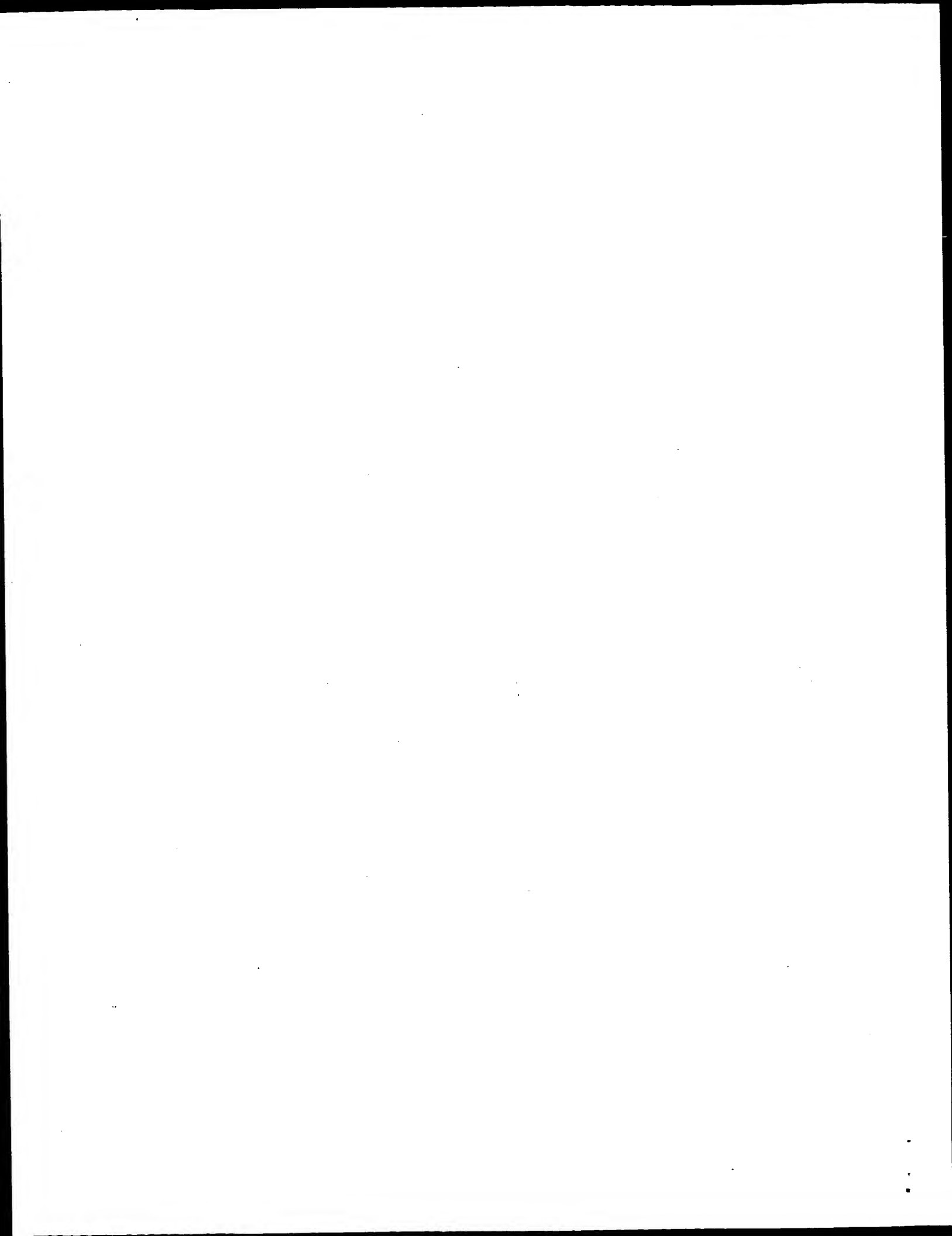
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; Sequence 4, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hideyasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/011175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
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US-09-155-855-4
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Best Local Similarity 65.5%; Pred. No. 1.9e-165;
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; Patent No. 6054306
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren
; APPLICANT: Bech, Lisbeth
; APPLICANT: Fuglsang, Claus
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Ostergaard, Peter
; TITLE OF INVENTION: Peniophora Phytase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6054306 No. 6054306disk of No. 6054306th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/221,654
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,358
FILING DATE: 12-DEC-1997
APPLICATION NUMBER: 0529/97
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5101.200-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-221-654-1
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Best Local Similarity 56.9%; Pred. No. 1.5e-29;
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DB 1002 TGATAACACCAATGGTGGCCCATCTTTTCGCGGCTCGGCTCTTCAACGCCAC 1052
Search completed: October 16, 2001, 12:07:09
Job time: 623 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 12:14:29 ; Search time 573.71 Seconds
(without alignments)
1533.336 Million cell updates/sec

Title: US-09-488-265-30_COPY_1_1401

Perfect score: 1401

Sequence: 1 atggcggttcctgcgtgct.....actgggaagaatgttttcgct 1401

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1401	100.0	1404	21	AAZ73234
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4	1385	98.9	1404	21	AAZ73293
5	1385	98.9	1426	21	AAZ73232
6	1385	98.9	1426	21	AAZ59642
7	1381.8	98.6	1404	21	AAZ73292
8	1324.2	94.5	1404	20	AAZ31520
9	1324.2	94.5	1404	21	AAZ73233
10	1324.2	94.5	1404	21	AAZ59715
11	1319.4	94.2	1404	21	AAZ73291

12	1316.2	93.9	1404	21	AAZ73290
13	1314.6	93.8	1426	20	AAZ27423
14	1314.6	93.8	1426	20	AAZ3022
15	1314.6	93.8	1426	21	AAZ73231
16	1314.6	93.8	1426	21	AAZ59637
17	1255.4	89.6	1426	20	AAZ31523
18	1255.4	89.6	1426	21	AAZ73236
19	1255.4	89.6	1426	21	AAZ59738
20	652.8	46.6	1404	21	AAZ31522
21	652.8	46.6	1404	21	AAZ73235
22	652.8	46.6	1404	21	AAZ59717
23	613.8	43.8	1404	18	AAZ65136
24	612.2	43.7	1404	12	AAQ11175
25	612.2	43.7	1404	20	AAZ27421
26	609.4	43.5	1571	19	AAZ03144
27	609.4	43.5	1571	20	AAZ27422
28	609	43.5	1404	12	AAQ13878
29	608.2	43.4	2363	15	AAQ58126
30	608.2	43.4	2379	15	AAQ56944
31	608.2	43.4	6756	12	AAQ11174
32	608.2	43.4	6756	18	AAZ65137
33	581.6	41.5	1515	18	AAZ96709
34	576.8	41.2	1931	19	AAZ03142
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36	558	39.8	1912	17	AAZ03743
37	539.4	38.5	1845	19	AAZ03143
38	537.8	38.4	1845	20	AAZ27416
39	528.6	37.7	2327	17	AAZ03736
40	528.6	37.7	2327	20	AAZ27414
41	527	37.6	1567	19	AAZ03145
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ALIGNMENTS

RESULT 1

AAZ31521
ID AAZ31521 standard; DNA; 1404 BP.

XX AAZ31521;

AC AAZ31521;

XX 06-JAN-2000 (first entry)

DT Consensus phytase-10-thermo(3)-Q50T-K91A coding sequence.

DE Phytase: animal feed preparation; thermostable phytase; transgenic plant;
KW Consensus sequence; ds.
XX Synthetic.

OS WO9948380-A1.

XX 30-SEP-1999.

PN 22-MAR-1999;

PD 22-MAR-1999;

PF 22-MAR-1999;

PR 23-MAR-1998;

PR 19-JUN-1998;

PR 18-SEP-1998;

PR 22-JAN-1999;

XX 22-JAN-1999;

XX (NOVO) NOVO-NORDISK AS.

XX Petersen S;

XX WPI; 1999-591030/50.

DR P-PSDB; AAZ43170.

XX

OS Aspergillus niger var. awamori.
 OS Aspergillus niger str. NRRL3135.
 OS Aspergillus fumigatus ATCC31073.
 OS Aspergillus fumigatus ATCC32722.
 OS Aspergillus fumigatus ATCC58128.
 OS Aspergillus fumigatus ATCC26906.
 OS Aspergillus fumigatus ATCC32239.
 OS Emericella nidulans.
 OS Talaromyces thermophilus ATCC20186.
 OS Myceliophthora thermophila.
 OS Paxillus involutus NN005693.
 OS Trametes pubescens NN9343.
 OS Agrocybe pediades NN009289.
 OS Peniophora lycii NN006113.
 OS Thermomyces lanuginosa.
 OS Synthetic.

XX Key Location/Qualifiers
 FH 1-1404
 FT CDS
 FT /*tag- a
 FT /product= "Phytase-10-thermo[3-Q50T-K91A"]

EP969089-A1.

05-JAN-2000.

23-JUN-1999; 99EP-0111949.

29-JUN-1998; 98EP-0111960.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

Brugger R, Lehmann M, Wyss M;

WPI; 2000-099429/09.

New stabilized enzyme formulation, useful for feed compositions for monogastric animals.

Example 5; Fig 19; 101pp; English.

The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilising agents including xylitol or ribitol; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal feed in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents DNA encoding a mutant phytase-10 consensus sequence, phytase-10-thermo[3]-Q50T-K91A, which has a temperature optimum and melting point 4 degrees Celsius higher than that of phytase-10 (AAV69566). Its specific activity with phytate as a substrate is also strongly increased.

Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;

Query Match 100.0%; Score 1401; DB 21; Length 1404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 781 atggacatgtgtccattcgcacactgttctagaaacttctgacgctactcaattgtctcca 840
 DB |||||
 QY 841 tctctgacttctcactcagacgaaatggattcaatacactacttgcactcttgggt 900
 DB |||||
 QY 841 tctctgacttctcactcagacgaaatggattcaatacactacttgcactcttgggt 900
 DB |||||
 QY 901 aagttactcaggttactcaggtgctgttaaccatttgggtccagctcaaggtgttgggttctgt 960
 DB |||||
 QY 901 aagttactcaggttactcaggtgctgttaaccatttgggtccagctcaaggtgttgggttctgt 960
 DB |||||
 QY 961 aacgaattgattgcttagattgactcactctcagttcagttcagttcagttcagttcagttc 1020
 DB |||||
 QY 961 aacgaattgattgcttagattgactcactctcagttcagttcagttcagttcagttcagttc 1020
 DB |||||
 QY 1021 actttgacttaacccagctacttccatttccatttccatttccatttccatttccatttccatt 1080
 DB |||||
 QY 1021 actttgacttaacccagctacttccatttccatttccatttccatttccatttccatttccatt 1080
 DB |||||

QY	1081	cacgacacacatggtttctatttcttcgtctttgggtttgtaaacggtactaacgca	1140
Db	1081	cacgacacacatggtttctatttcttcgtctttgggtttgtaaacggtactaacgca	1140
QY	1141	tgtctactactctgttgaatctattgaagaactgacggttactctgtcttttggact	1200
Db	1141	tgtctactactctgttgaatctattgaagaactgacggttactctgtcttttggact	1200
QY	1201	gttcatttcgtcttagagcttaogttgaaatgatgcaatgtgaagctgaaaaggaaacca	1260
Db	1201	gttcatttcgtcttagagcttaogttgaaatgatgcaatgtgaagctgaaaaggaaacca	1260
QY	1261	tfggttagagtttfgtttaacgcacagagttgttccattgcacggttgtgtgtgcacaag	1320
Db	1261	tfggttagagtttfggttaacgcacagagttgttccattgcacggttgtgtgtgcacaag	1320
QY	1321	tfggttagatgataagagagacgacctcgttgaaggtttgtcttcgtctagatctgtggt	1380
Db	1321	tfgggtgagatgaagagagacgacctcgttgaaggtttgtcttcgtctagatctgtggt	1380
QY	1381	aactgggaagaatttttcgt	1401
Db	1381	aactgggaagaatttttcgt	1401

RESULT	4	
ID	AAA73293	
XX	AAA73293 standard; DNA; 1404 BP.	
XX	AAA73293;	
DT	05-DEC-2000 (first entry)	
DE	Consensus phytase 10 thermo 5 Q50T K91A polynucleotide SEQ ID NO:96.	
XX	Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;	
XX	temperature stability; pH profile; temperature profile; reaction rate;	
XX	specific activity; substrate specificity; reaction rate;	
XX	substrate binding; position specificity; substrate cleavage pattern;	
XX	food; feed; phytate; manure; ds.	
XX	Synthetic.	
XX	WO2000043503-A1.	
DD	27-JUL-2000.	
XX	21-JAN-2000; 2000WO-DK00025.	
XX	22-JAN-1999; 99DK-0000092.	
XX	21-SEP-1999; 99DK-0001340.	
XX	(NOVO) NOVO NORDISK AS.	
XX	Lehmann M;	
XX	WPI; 2000-491161/43.	
XX	P-PSDB; AAB20534.	
XX	Novel phytases with improved properties such as temperature stability,	
XX	pH stability and substrate specificity, for use in pharmaceuticals and	
XX	compound foods and feeds -	
XX	Disclosure; Fig 25a-c; 240pp; English.	
XX	The present invention describes improved phytases, preferably with	
XX	increased thermostability, and methods for producing them. The methods	
XX	can be used for producing phytases with improved properties e.g.	
XX	temperature stability, pH stability, pH profile, temperature profile,	
XX	specific activity, substrate specificity, substrate cleavage pattern,	
XX	substrate binding, position specificity, the velocity and level of	
XX	release of phosphate from corn, reaction rate, phytate degradation rate,	
XX	and end level of released phosphate. The phytases can be used to produce	

Thu Oct 18 11:34:50 2001

QY 901 aagttactacggttacggtgctggttaaccattgggtccagctcaaggtggtggttgggt 960
 DB 901 aagttactacggttacggtgctggttaaccattgggtccagctcaaggtggtggttgggt 960
 QY 961 aacgaattgattgctagattgactcaactctccagttcaagaccacactctactaacac 1020
 DB 961 aacgaattgattgctagattgactcaactctccagttcaagaccacactctactaacac 1020
 QY 1021 actttgacttaaccagctacttccattgaaactgacttttgaactgacttctct 1080
 DB 1021 actttgacttaaccagctacttccattgaaactgacttttgaactgacttctct 1080
 QY 1081 cagcaaacactatggtttctattttctgtgttgggtttgttgaacaggttactaacgca 1140
 DB 1081 cagcaaacactatggtttctattttctgtgttgggtttgttgaacaggttactaacgca 1140
 QY 1141 tigtctactacttctgtaactctattgaagaaactgacggttactctgtcttggact 1200
 DB 1141 tigtctactacttctgtaactctattgaagaaactgacggttactctgtcttggact 1200
 QY 1201 gttccattcgtgctagacttactggttgaatgatgcaatgtgaagctgaaagaacaca 1260
 DB 1201 gttccattcgtgctagacttactggttgaatgatgcaatgtgaagctgaaagaacaca 1260
 QY 1261 ttggttagagtttgttaacagacagattgttccattgacggttgggttgggtgacag 1320
 DB 1261 ttggttagagtttgttaacagacagattgttccattgacggttgggttgggtgacag 1320
 QY 1321 ttggttagagtttgaagagacgactcgttgaaggtttgttcttgcctagactggtggt 1380
 DB 1321 ttggttagagtttgaagagacgactcgttgaaggtttgttcttgcctagactggtggt 1380
 QY 1381 aactgggaagaatgttctgct 1401
 DB 1381 aactgggaagaatgttctgct 1401
 RESULT 5
 AAA73232
 ID AAA73232 standard; DNA; 1426 BP.
 XX AC AAA73232;
 XX DT 05-DEC-2009 (first entry)
 XX DE Consensus phytase 10 polynucleotide sequence SEQ ID NO:25.
 XX KW phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 XX KW temperature stability; pH profile; temperature profile; reaction rate;
 XX KW specific activity; substrate specificity; substrate cleavage pattern;
 XX KW substrate binding; position specificity; phytate degradation rate;
 XX KW food; feed; phytate; manure; ds.
 XX OS Synthetic.
 XX PN WO20043503-A1.
 XX PD 27-JUL-2000.
 XX PF 21-JAN-2000; 2000WO-DK000025.
 XX PR 22-JAN-1999; 99DK-00000092.
 XX PR 21-SEP-1999; 99DK-0001340.
 XX PA (NOVO) NOVO NORDISK AS.
 XX PI Lehmann M;
 XX DR WPI; 2000-491161/43.
 XX DR P-PSDB; AAB20524.
 XX PT Novel phytases with improved properties such as temperature stability,
 PT pH stability and substrate specificity, for use in pharmaceuticals and

PT compound foods and feeds -
 XX Claim 8; Fig 5a-c; 240pp; English.
 PS
 XX The present invention describes improved phytases, preferably with
 CC increased thermostability, and methods for producing them. The methods
 CC can be used for producing phytases with improved properties e.g.
 CC temperature stability, pH stability, pH profile, temperature profile,
 CC specific activity, substrate specificity, substrate cleavage pattern,
 CC substrate binding, position specificity, the velocity and level of
 CC release of phosphate from corn, reaction rate, phytate degradation rate,
 CC and end level of released phosphate. The phytases can be used to produce
 CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.
 CC The present sequence encodes a phytase sequence from the present
 CC invention.
 XX
 SQ Sequence 1426 BP; 340 A; 308 C; 310 G; 468 T; 0 other;

Query Match 98.9%; Score 1385; DB 21; Length 1426;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1391; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 atggggtgttgcgtgctgactgctccattgccaactgttgcgttccacatccggtacc 60
 DB 12 atggggtgttgcgtgctgactgctccattgccaactgttgcgttccacatccggtacc 71
 QY 61 gccttgggtcctggtgtaactcactctgtgacactgttgacgttgacgttgacaaatgt 120
 DB 72 gccttgggtcctggtgtaactcactctgtgacactgttgacgttgacgttgacaaatgt 131
 QY 121 ttccagaaatttccacttgggtgtacatactctcattctcttcttcttgggtgacgaa 180
 DB 132 ttccagaaatttccacttgggtgtacatactctcattctcttcttcttgggtgacgaa 191
 QY 181 tctgctatttccagacgttccaaagggttgcgtgactgacttcttgcgttgcgttgcgttgc 240
 DB 192 tctgctatttccagacgttccaaagggttgcgtgactgacttcttgcgttgcgttgcgttgc 251
 QY 241 agacacggtgctagatacccaactcttctgcgttgcgttgcgttgcgttgcgttgcgttgc 300
 DB 252 agacacggtgctagatacccaactcttctgcgttgcgttgcgttgcgttgcgttgcgttgc 311
 QY 301 gctatttcaaaagacgctactgcttccaaagggttgcgttgcgttgcgttgcgttgcgttgc 360
 DB 312 gctatttcaaaagacgctactgcttccaaagggttgcgttgcgttgcgttgcgttgcgttgc 371
 QY 361 tacacttgggtgctgacgactgactcctcattcgtgacacaaatggttaactctggt 420
 DB 372 tacacttgggtgctgacgactgactcctcattcgtgacacaaatggttaactctggt 431
 QY 421 attaatctcagagaatacagaagcttggctagaagaagattgttccattcattagagct 480
 DB 432 attaatctcagagaatacagaagcttggctagaagaagattgttccattcattagagct 491
 QY 481 tctggttctcagacaggttattcttctgctgaaaaagttcattgaaggttccaaatctgct 540
 DB 492 tctggttctcagacaggttattcttctgctgaaaaagttcattgaaggttccaaatctgct 551
 QY 541 aagttggtgacacaggtgctaacccacacacagcttctccagttattataacgttattatt 600
 DB 552 aagttggtgacacaggtgctaacccacacacagcttctccagttattataacgttattatt 611
 QY 601 ccagaagggtgctggtttacaacaacacttggaccacagcttctccagttattataacgttattatt 660
 DB 612 ccagaagggtgctggtttacaacaacacttggaccacagcttctccagttattataacgttattatt 671
 QY 661 tctgaattgggtgacacaggttgaagcactgactgctggttcttgcctccacaaataga 720
 DB 672 tctgaattgggtgacacaggttgaagcactgactgctggttcttgcctccacaaataga 731

XX This sequence encodes the consensus phytase-1-thermo(8)-Q50T-K91A.
 CC The invention relates to a process for preparing animal feed by
 CC agglomerating feed ingredients with a thermostable phytase, which is
 CC added before or during agglomeration. The thermostable phytase is useful
 CC for expression in transgenic plants. These plants are useful in the
 CC preparation of animal feed itself. The thermostable phytase allows animal
 CC feed to be produced more efficiently, in addition to improved
 CC phytase-expressing transgenic plants. These plants provide a feed
 CC ingredient and a feed additive (phytase) simultaneously.
 XX
 SQ Sequence 1404 BP; 329 A; 319 C; 304 G; 452 T; 0 other;

Query Match 94.5%; Score 1324.2; DB 20; Length 1404;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 1353; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 atggggcgttcgtgctactgtccattgcoacttctggttccacatcccggtacc 60
 DB 1 atggggcgttcgtgctactgtccattgcoacttctggttccacatcccggtacc 60
 QY 61 gcttgggttcgtggtgaactctcactcttctgacactgttgacggtgtgtaccatgt 120
 DB 61 gcttgggttcgtggtgaactctcactcttctgacactgttgacggtgtgtaccatgt 120
 QY 121 ttccagaaatttctcacttctggttgacacttctcacttcttcttcttgggtgacgaa 180
 DB 121 ttccagaaatttctcacttctggttgacacttctcacttcttcttcttgggtgacgaa 180
 QY 181 tctgctattctcagacgttccaaagggttgtagacttcttcttcttcttcttcttct 240
 DB 181 tctgctattctcagacgttccaaagggttgtagacttcttcttcttcttcttcttct 240
 QY 241 agacacggtgtagataccacacttcttctgctgaaggtgtagacttcttcttcttcttct 300
 DB 241 agacacggtgtagataccacacttcttctgctgaaggtgtagacttcttcttcttcttct 300
 QY 301 gctattcaaaagacgtactgttcaagggttaagtagacttcttcttcttcttcttcttct 360
 DB 301 gctattcaaaagacgtactgttcaagggttaagtagacttcttcttcttcttcttcttct 360
 QY 361 tacatttgggtgctgacgacttacttcttctgctgaaggttcttcttcttcttcttcttct 420
 DB 361 tacatttgggtgctgacgacttacttcttctgctgaaggttcttcttcttcttcttcttct 420
 QY 421 attaatgtctacagaagatcaacggttggctgtagaagattgttccattcatttagact 480
 DB 421 attaatgtctacagaagatcaacggttggctgtagaagattgttccattcatttagact 480
 QY 481 tctggttctacagaagatttcttctgctgaaggttcttcttcttcttcttcttcttcttct 540
 DB 481 tctggttctacagaagatttcttctgctgaaggttcttcttcttcttcttcttcttcttct 540
 QY 541 aagtttgggtgaccaggttcttcttcttcttcttcttcttcttcttcttcttcttcttct 600
 DB 541 aagtttgggtgaccaggttcttcttcttcttcttcttcttcttcttcttcttcttcttct 600
 QY 601 ccagaaggtgctgtgtacacacacttggaccacggttcttcttcttcttcttcttcttcttct 660
 DB 601 ccagaaggtgctgtgtacacacacttggaccacggttcttcttcttcttcttcttcttcttct 660
 QY 661 tctgaattgggtgacgacgttgaagcacttcttcttcttcttcttcttcttcttcttcttct 720
 DB 661 tctgaattgggtgacgacgttgaagcacttcttcttcttcttcttcttcttcttcttcttct 720
 QY 721 gctagattggaagctcacttgcaggttgaagcacttcttcttcttcttcttcttcttcttcttct 780
 DB 721 gctagattggaagctcacttgcaggttgaagcacttcttcttcttcttcttcttcttcttcttct 780
 QY 781 atggacatgttccattgacactgttctgacactgttctgacactgttctgacactgttctgacact 840
 DB 781 atggacatgttccattgacactgttctgacactgttctgacactgttctgacactgttctgacact 840

QY 841 tctgtgacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 900
 DB 841 tctgtgacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 900
 QY 901 aagtactacggttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 960
 DB 901 aagtactacggttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 960
 QY 961 aacgaattgattgtagattgactcacttccagttcaagcaccacacttcttacttaaccac 1020
 DB 961 aacgaattgattgtagattgactcacttccagttcaagcaccacacttcttacttaaccac 1020
 QY 1021 acttggacttcaaccagcttcttccattgaacgctacttcttcttcttcttcttcttcttcttcttct 1080
 DB 1021 acttggacttcaaccagcttcttccattgaacgctacttcttcttcttcttcttcttcttcttcttct 1080
 QY 1081 cagcacaacactatggttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1140
 DB 1081 cagcacaacactatggttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1140
 QY 1141 ttgtctacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1200
 DB 1141 ttgtctacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1200
 QY 1201 gttccattcgtctgtagagcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1260
 DB 1201 gttccattcgtctgtagagcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1260
 QY 1261 ttggttagagtttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1320
 DB 1261 ttggttagagtttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1320
 QY 1321 ttggttagagtttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1380
 DB 1321 ttggttagagtttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1380
 QY 1381 aactggggaagaattgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1401
 DB 1381 aactggggaagaattgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1401

RESULT 9
 AAA73233
 ID AAA73233 standard; DNA; 1404 BP.
 XX
 AC AAA73233;
 XX
 DT 05-DEC-2000 (first entry)
 XX
 DE Consensus phytase 1 thermo 8 q50t, k91a polynucleotide SEQ ID NO:28.
 XX
 KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure; ds.
 XX
 OS Synthetic.
 XX
 PN WO200043503-A1.
 XX
 PD 27-JUL-2000.
 XX
 PF 21-JAN-2000; 2000WO-DK00025.
 XX
 PR 22-JAN-1999; 99DK-0000092.
 PR 21-SEP-1999; 99DK-0001340.
 XX
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Lehmann M;
 XX

OS Aspergillus fumigatus ATCC32722.
 OS Aspergillus fumigatus ATCC58128.
 OS Aspergillus fumigatus ATCC26906.
 OS Aspergillus fumigatus ATCC32239.
 OS Emericella nidulans.
 OS Talaromyces thermophilus ATCC20186.
 OS Myceliophthora thermophila.
 OS Synthetic.

XX Key Location/Qualifiers
 FH 1..1404
 FT CDS /tag= a
 FT /product= "Phytase-1-thermo[8]-Q50T-K91A"

XX EP969089-A1.

XX 05-JAN-2000.

XX 23-JUN-1999; 99EP-0111949.

XX 29-JUN-1998; 98EP-0111960.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Bruggen R, Lehmann M, Wyss M;

XX WPI; 2000-099429/09.

XX P-PSDB; AAY69568.

XX New stabilized enzyme formulation, useful for feed compositions for monogastric animals -

XX Example 5; Fig 19; 101pp; English.

XX The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilising agents including xylitol or ribitol; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal feed in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents DNA encoding a mutant phytase-1 consensus sequence, phytase-1-thermo[8]-Q50T-K91A, which has a temperature optimum and melting point 7 degrees Celsius higher than that of phytase-1 (AAY69558).

XX Sequence 1404 BP; 329 A; 319 C; 304 G; 452 T; 0 other;

Query Match 94.5%; Score 1324.2; DB 21; Length 1404;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 1353; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 atggcggtgttgctgctactgtccattgccaccctgttcggttcacacccggtacc 60

DB 1 atggcggtgttgctgctactgtccattgccaccctgttcggttcacacccggtacc 60

QY 61 gcttgggtccctcggttaactctcaactctgtgacactgttgacggtgggttaccatgt 120

pb 61 gcttgggtccctcggttaactctcaactctgtgacactgttgacggtgggttaccatgt 120

QY 121 ttccacagaaatttctcaacttgtgggttacatactctccattctctcttcttggcgacgaa 180
 DB 121 ttccacagaaatttctcaacttgtgggttacatactctccattctcttcttggcgacgaa 180
 QY 181 tctgctatttctccagacggttccaaagggttagagttacttctcgttcaagtttctct 240
 DB 181 tctgctatttctccagacggttccaaagggttagagttacttctcgttcaagtttctct 240
 QY 241 agacacggtgctagatataccaaatttctgctgcttaaggcgtactctgcttggattgaa 300
 DB 241 agacacggtgctagatataccaaatttctgctgcttaaggcgtactctgcttggattgaa 300
 QY 301 gctattcaaaagacgctactgcttcaagggttaagtcagcttcttcttgaagacttaaac 360
 DB 301 gctattcaaaagacgctactgcttcaagggttaagtcagcttcttcttgaagacttaaac 360
 QY 361 tacactttgggtgctgacgactgactccattcggtgaacaaacaaatgggttaactctggt 420
 DB 361 tacactttgggtgctgacgactgactccattcggtgaacaaacaaatgggttaactctggt 420
 QY 421 attaaagttctacagaagatacaagccttggctagaagaattgttccattcattagagct 480
 DB 421 attaaagttctacagaagatacaagccttggctagaagaattgttccattcattagagct 480
 QY 481 tctggttctgacagagttattgcttctgctgctgctgctgctgctgctgctgctgctgct 540
 DB 481 tctggttctgacagagttattgcttctgctgctgctgctgctgctgctgctgctgctgct 540
 QY 541 aagttggctgacagagttattgcttctgctgctgctgctgctgctgctgctgctgctgct 600
 DB 541 aagttggctgacagagttattgcttctgctgctgctgctgctgctgctgctgctgctgct 600
 QY 601 ccagagaggtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 660
 DB 601 ccagagaggtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 660
 QY 661 tctgaattgggtgacgacgcttgaagccttaactgctgctgctgctgctgctgctgctgctgctgct 720
 DB 661 tctgaattgggtgacgacgcttgaagccttaactgctgctgctgctgctgctgctgctgctgctgct 720
 QY 721 gctaatggagagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 780
 DB 721 gctaatggagagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 780
 QY 781 atggacatgtgtccattgacacactgttgcagctgctgctgctgctgctgctgctgctgctgctgct 840
 DB 781 atggacatgtgtccattgacacactgttgcagctgctgctgctgctgctgctgctgctgctgctgct 840
 QY 841 tctgtgacttcttccactcacgacgaatggattcaatcacgactacttgcacttcttgggt 900
 DB 841 tctgtgacttcttccactcacgacgaatggattcaatcacgactacttgcacttcttgggt 900
 QY 901 aagttacggtttagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 960
 DB 901 aagttacggtttagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 960
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 Db 1321 ttgggttagatgaagagacgactctcgtttgaagtttatttctcgttagatctgtgt 1380
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 Db 1381 aactgggtgaatgtttcgtct 1401

RESULT 12

AAAT73290
 ID AAA73290 standard; DNA; 1404 BP.

XX AC AAA73290;

XX DT 05-DEC-2000 (first entry)

XX DE Consensus phytase 3 thermo 11 Q50T polynucleotide SFQ ID NO:90.

XX KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure; ds.

XX OS Synthetic.

XX XX WO200043503-A1.

XX PD 27-JUL-2000.

XX PF 21-JAN-2000; 2000WO-DK00025.

XX PR 22-JAN-1999; 99DK-0000092.

XX PR 21-SEP-1999; 99DK-0001340.

XX XX (NOVO) NOVO NORDISK AS.

XX PI Lehmann M;

XX DR WPI; 2000-491161/43.

XX DR P-PSDB; RAB20531.

XX PT Novel phytases with improved properties such as temperature stability,
 PT pH stability and substrate specificity, for use in pharmaceuticals and
 PT compound foods and feeds -

XX PS Disclosure; Fig 22a-c; 240pp; English.

XX CC The present invention describes improved phytases, preferably with
 CC increased thermostability, and methods for producing them. The methods
 CC can be used for producing phytases with improved properties e.g.
 CC temperature stability, pH stability, pH profile, temperature profile,

CC specific activity, substrate specificity, substrate cleavage pattern,
 CC substrate binding, position specificity, the velocity and level of
 CC release of phosphate from corn, reaction rate, phytate degradation rate,
 CC and end level of released phosphate. The phytases can be used to produce
 CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.
 CC The present sequence encodes a phytase sequence from the present
 CC invention.
 XX SQ Sequence 1404 BP; 330 A; 320 C; 302 G; 452 T; 0 other;

Query Match 93.9%; Score 1316.2; DB 21; Length 1404;
 Best Local Similarity 96.2%; Pred. No. 0;
 Matches 1348; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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 Db 1 atggcggttcctcgtcgtactgtccattgcaaccccttgggttccacatccggtacc 60

QY 61 gccttgggtcctcgttgtaactctcaactcttgacactgttgacggttggttaccatgt 120
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QY 121 ttcccagaatttctcacttgggtgtacatctcacttctcacttctccttcttgggtgacgaa 180
 Db 121 ttcccagaatttctcacttgggtgtacatctcacttctcacttctccttcttgggtgacgaa 180

QY 181 tctgctatttccagacggttccaaagggttgtagagttacttctcgttcaagtttctct 240
 Db 181 tctgctatttccagacggttccaaagggttgtagagttacttctcgttcaagtttctct 240

QY 241 agacacggtgtgtagatacccaacttcttctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 300
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 Db 301 gctattcaaaagacgctactgttcttcaagggttaaggtaagtcgcttcttgaagactacaac 360

QY 361 tacactttgggtgctgacgacttgactcctcattcgttgacacacaaatggttaactctggt 420
 Db 361 tacactttgggtgctgacgacttgactcctcattcgttgacacacaaatggttaactctggt 420

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 Db 421 attaggttctacagaagatacaaggcttggctagagaagattgttccattcattagact 480

QY 481 tctggttctgacagagtattgtctctgctgaaagggttcattgaagggttccaaactgct 540
 Db 481 tctggttctgacagagtattgtctctgctgaaagggttcattgaagggttccaaactgct 540

QY 541 aagttggtgacccagggtgttaacccacacacacacacacacacacacacacacacacacac 600
 Db 541 aagttggtgacccagggttctcacaacacacacacacacacacacacacacacacacacacac 600

QY 601 ccagaaggtgctggtttacacacacacacacacacacacacacacacacacacacacacacac 660
 Db 601 ccagaaggtgctggtttacacacacacacacacacacacacacacacacacacacacacacac 660

QY 661 tctgaattgggtgacgacgttgaagcttaactcactgtgttctcgtcgtcgtcgtcgtcgtcgt 720
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QY 721 gctagattggaagcactcattgcccaggtgttaacttgactgacgacgacgacgacgacgacgac 780
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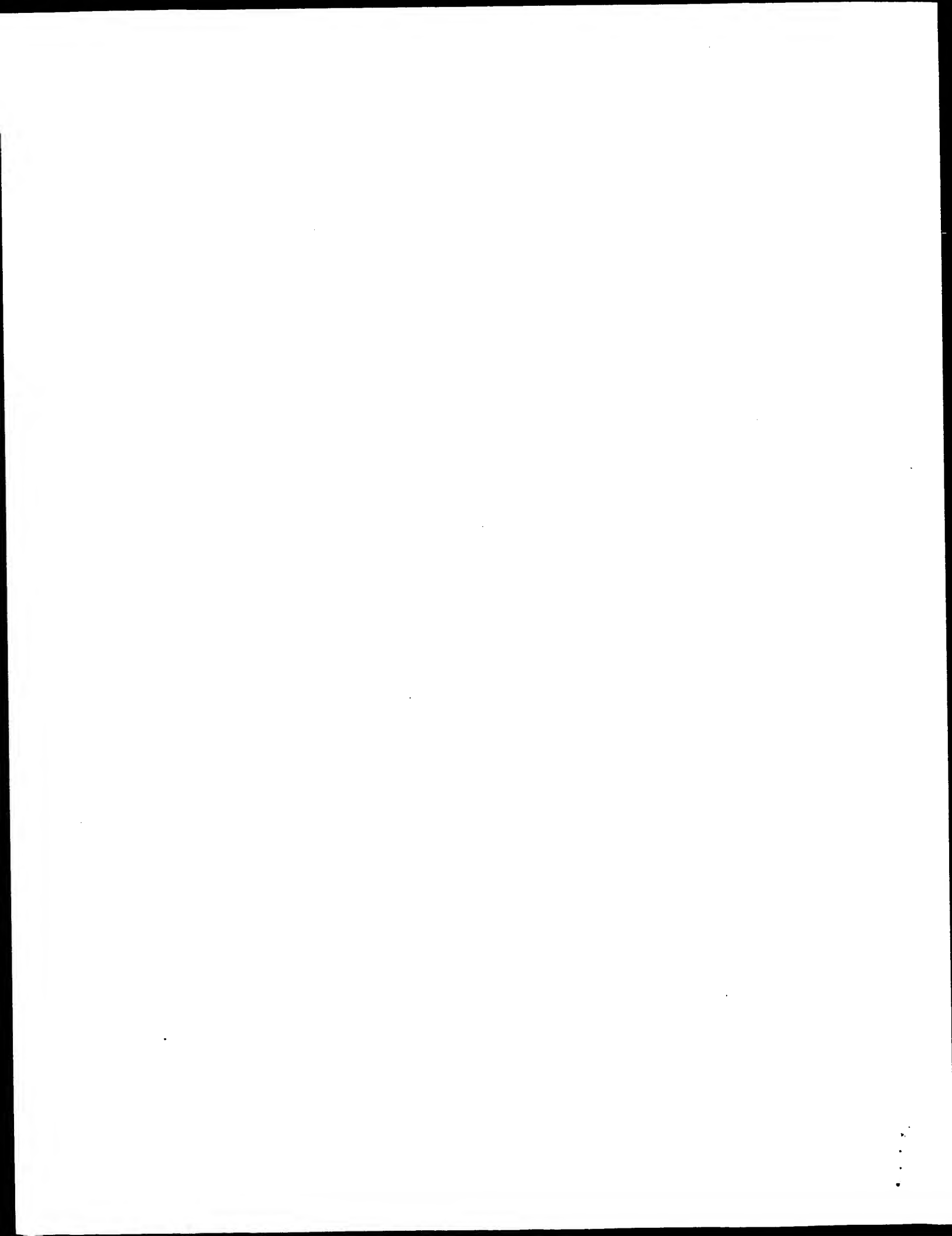
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 Db 781 atggacatgtgtccattcgcacactgttgtagaacttctgacgactactcaattgttctcca 840

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1141	ttgtctactacttctgttgaactatctgaagaactacggttactctctcttctggact	1200
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1212	gttcatttcgctgcagagcttagttgaaatgatgcaatgtgaactgaaagggaacca	1271
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RESULT	14	
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ID	AAAX23022 standard; DNA; 1426 BP.	
XX		
XX	AAAX23022;	
XX		
XX	11-JUN-1999 (first entry)	
DT		
XX		
DE	Fungal phytase gene consensus DNA.	
XX		
KW	phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food;	
KW	feed additive; variant; mutein; feed; pharmaceutical; ds.	
XX		
OS	Fungi.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	12..1415
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FT	
XX	EP897985-A2.
XX	
XX	24-FEB-1999.
XX	
XX	15-JUL-1998; 98EP-0113176.
XX	
XX	24-JUL-1997; 97EP-0112688.
PR	
XX	(HOFF) HOFFMANN LA ROCHE AG F.
XX	
XX	Lehmann M;
PI	
XX	
XX	WPI; 1999-134647/12.
DR	P-PSDB; AAW93380.
DR	
XX	Preparation of a consensus protein, especially a phytase - using
PT	programs to compare evolutionary similarity of sequences
PT	
XX	
XX	Claim 8; Fig 2; 30pp; English.
PS	
XX	
XX	This invention describes a novel process for the preparation of a
CC	consensus protein. The specific example given in the specification is
CC	that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses
CC	phytase to valuable feed additives, with a fully defined amino acid
CC	sequence given in the specification, or variant or mutin. The method is
CC	useful for improving protein properties by altering their sequence. The
CC	consensus protein and mutin are useful in food, feed or pharmaceutical
CC	compositions. This sequence encodes the consensus phytase protein used
CC	in the method of the invention.
XX	
SO	Sequence 1426 BP: 338 A; 311 C; 308 G; 469 T; 0 other;

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	Best Local Similarity	96.1%;	Pred. No. 0;		
	Matches 1347;	Conservative	0;	Mismatches 54;	Indels 0;
	Gaps				
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Db	12	atgggctgttcgtgctactgtccattgcaccttgcgttccacatccggtacc	71		
Qy	61	gccttgggtcctcgttgtaacttcactcttgtgacactgtgaacggtgttaccaatgt	120		
Db	72	gccttgggtcctcgttgtaacttcactcttgtgacactgtgaacggtgttaccaatgt	131		
Qy	121	ttccagaaatttcactgtgggtgacatacttcactctctctcttcttggctgcgaa	180		
Db	132	ttccagaaatttcactgtgggtgacatacttcactctctcttcttgggaacgaa	191		
Qy	181	ttctgtattctccagacgttccaaagggtgtgagagttactctgttccgaagtttgcct	240		
Db	192	ttctgtattctccagacgttccaaagggtgtgagagttactctgttccgaagtttgcct	251		
Qy	241	agacacggtgctagataccacaattcttctggtctgaaggcgtactcgttttgattgaa	300		
Db	252	agacacggtgctagataccacaattcttctgaagtcgaaggttactcgttttgattgaa	311		
Qy	301	gctattccaaagaacgtactcgttccaaagggtgaagtcgcttcttgaagacttacaac	360		
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100

Thu Oct 18 11:34:50 2001

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35	280.2	20.0	860	10	AX085208	AX085208 Sequence
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38	133.4	9.5	950	10	AX085210	AX085210 Sequence
39	92.2	6.6	1117	14	MGR299239	AJ299239 Magnaport
40	64.8	4.6	1404	14	SCU19789	U19789 Saccharomyc
41	64	4.6	1404	14	SCP050A	X01079 Yeast gene
42	64	4.6	1904	10	AX072908	AX072908 Sequence
43	64	4.6	2934	15	SCYBRO93C	Z35962 S.cerevisia
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ALIGNMENTS

RESULT 1	AX021809	LOCUS	AX021809	1426 bp	DNA	PAT	07-SEP-2000
DEFINITION	Sequence 3 from Patent EP0897985.						
ACCESSION	AX021809						
VERSION	AX021809.1 GI:10045052						
KEYWORDS	synthetic construct.						
SOURCE	artificial sequence.						
ORGANISM	Lehmann.M.						
REFERENCE	1 (bases 1 to 1426)						
AUTHORS	Consensus phytases						
TITLE	Patent: EP 0897985-A 3 24-FEB-1999;						
JOURNAL	HOFFMANN LA ROCHE (CH)						
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Query Match	93.8%	Score 1314.6;	DB 9;	Length 1426;
Best Local Similarity	96.1%;	Pred. No. 0;		
Matches 1347;	Conservative	0;	Mismatches 54;	Indels 0; Gaps 0;
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Db 1392 AACTGGGCTGAATGTTTCGCT 1412

RESULT 2
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VERSION AF295325.1 GI:10732782
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 1350)
AUTHORS Yang,L., Chen,Z., Bei,J., Liao,L. and Wang,X.
TITLE Synthetic sequence of phytase gene for expression in Pichia pastoris
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1350)
AUTHORS Chen,Z
TITLE Direct Submission
JOURNAL Direct Submission
Submitted (11-AUG-2000) Animal Science Institute, Guangdong Academy of Agricultural Sciences, Guangzhou, Guangdong 510640, China
REFERENCE 3 (bases 1 to 1350)
AUTHORS Yang,L., Bei,J., Liao,L. and Wang,X.
TITLE Direct Submission
JOURNAL Direct Submission
Submitted (11-AUG-2000) Biopharmaceutical Center, Zhongshan University, Guangzhou, Guangdong 510275, China
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Query Match 43.5%; Score 609.4; DB 9; Length 1571;
Best Local Similarity 66.8%; Pred. No. 8.3e-152;
Matches 884; Conservative 0; Mismatches 436; Indels 3; Gaps 1;

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Pasamontes, L., Haiker, M., Wyss, M., Tessier, M. and van Loon, A.P.
Gene cloning, purification, and characterization of a heat-stable
phytase from the fungus Aspergillus fumigatus
Appl. Environ. Microbiol. 63 (5), 1696-1700 (1997)
97288063
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Best Local Similarity 64.9%; Pred. No. 1.8e-151;
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ACCESSION AR018076
VERSION AR018076.1 GI:3973679
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2363)
AUTHORS Nevalainen,H.K.M., Paloheimo,M.T., Miettinen-Oinonen,A.S.K.,
Turkeli,T.K., Cantrell,M., Piddington,C.S., Rambosk,J.A.,
Turunen,M.K. and Fagerstrom,R.B.
TITLE Production of phytate degrading enzymes in trichoderma
JOURNAL Patent: US 5780292-A 7 14-JUL-1998;
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Query Match 43.4%; Score 608.2; DB 9; Length 2363;
Best Local Similarity 64.9%; Pred. No. 1.8e-151;
Matches 901; Conservative 0; Mismatches 488; Indels 0; Gaps 0;

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RESULT 10
AR051916 2363 bp DNA PAT 29-SEP-1999
LOCUS Sequence 7 from patent US 5830733.
DEFINITION AR051916
ACCESSION AR051916
VERSION AR051916.1 GI:5975280
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2363)
AUTHORS Nevalainen, H. K. M., Paloheimo, M. T., Miettinen-Oinonen, A. S. K.,
Torkkeli, T. K., Cantrell, M., Piddington, C. S., Rambosek, J. A.,
Turunen, M. K., Fagerstrom, R. B., and Houston, C. S.
TITLE Nucleic acid molecules encoding phyase and pH2.5 acid phosphatase
JOURNAL Patent: US 5830733-A 7 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..2363
BASE COUNT 559 a 732 c 510 g 562 t
ORIGIN

Query Match 43.4%; Score 608.2; DB 9; Length 2363;
Best Local Similarity 64.9%; Pred. No. 1.8e-151;
Matches 901; Conservative 0; Mismatches 488; Indels 0; Gaps 0;

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LOCUS Sequence 1 from patent US 5834286.
DEFINITION AR053934
ACCESSION AR053934
VERSION AR053934.1 GI:5978796
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2379)
AUTHORS Nevalainen,H.K.M., Paloheimo,M.T., Fagerstrom,R.B.,
Miettinen-Oinonen,A.S.K., Turunen,M.K., Rambosek,J.A.,
Piddington,C.S., Houston,C.S. and Cantrell,M.A.
TITLE Recombinant cells that express phytate degrading enzymes in desired
ratios
JOURNAL Patent: US 5834286-A 1 10-NOV-1998;
FEATURES Location/Qualifiers
source 1..2379
BASE COUNT 561 a 735 c 518 g 565 t
ORIGIN /organism="unknown"
Query Match 43.4%; Score 608.2; DB 9; Length 2379;
Best Local Similarity 64.9%; Pred. No. 1.8e-151;
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 1 (sites)
 Piddington C.S., Houston C.S., Palohelmo M., Cantrell M.,
 Miettinen-Oinonen A., Nevalainen H. and Rambosek J.

TITLE The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-optimum acid phosphatase (aph) from *Aspergillus niger* var. awamori
 JOURNAL Gene 133 (1), 55-62 (1993)
 MEDLINE 94040796
 REFERENCE 2 (bases 1 to 2379)
 AUTHORS Carter, J.R., Franden, M.A., Aebersold, R.H. and McHenry, C.S.
 TITLE Molecular cloning, sequencing and overexpression of the gene encoding the psi subunit of E. coli DNA polymerase III holoenzyme Unpublished (1992)
 JOURNAL Location/Qualifiers
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 BASE COUNT 561 a 735 c 518 g 565 t
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 Best Local Similarity 64.9%; Pred. No. 1.8e-151;
 Matches 901; Conservative 0; Mismatches 488; Indels 0; Gaps 0;
 QY 13 gtcgtgtaacttccattgacacttgccttgccttgccttgccttgccttgccttgccttgcct 72
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 A19451 6756 bp DNA PAT 10-JUN-1994
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 ACCESSION A19451
 VERSION A19451.1 GI:583193
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 6756)
 AUTHORS van Gorcom,R.F.M., van Hartingsveldt,W., van Paridon,P.A.,
 Veenstra,A.E., Luiten,R.G.M. and Selten,G.C.M.
 TITLE Cloning and expression of microbial phytase
 JOURNAL Patent: EP 0420358-A 40 03-APR-1991;
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 FEATURES
 Location/Qualifiers
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 357..1715
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 /number=2
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 Best Local Similarity 64.9%; Pred. No. 1.9e-151;
 Matches 901; Conservative 0; Mismatches 488; Indels 0; Gaps 0;
 Qy 13 gtcgtgactgtccattgccacattgttgcggtttccacatccggtacgcttgggttccct 72
 Db 324 GTGGGACTACTGATCGCTGACTATCTGTGACAGTCACTCCGAGCTGGCAGTCCCGGCC 383
 Qy 73 cgtggttaactctactcttggacacattgtgacggtgttaccactgttccacagaatt 132
 Db 384 TCGAGAAATCAATCCAGTTCGATACGATCAGGGGTATCAATGCTTCTCCGAGACT 443
 Qy 133 tctcactgtgggtgacatactctccattctcttcttcttggctgacgaatctgctattct 192

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 Qy 193 ccaacggttccaaaggttttagagttacttcttccaaagttttgtctagacaggtgtct 252
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 Qy 253 agatacccaacttctctggtctcaagcggtactctcttctgattgaagctattcaaaag 312
 Db 564 CGGTATCCGACCGATCCAAAGGCAAGAAATACCTCCGCTCTCATTTGAGGAGATCCAGCAG 623
 Qy 313 aacgctactgttccaaaggttaagtcggttcttcttgaagacttacaactacactttgggt 372
 Db 624 AACCGGACCACTTTGACGGGAAATATGCTCTCTGGAAGACATACAACTACAGCTTGGGT 683
 Qy 373 gctgacgactgactcattcgttggaacaaacaaatggttaactctggtattaaagttctac 432
 Db 684 GCAGATGACCTGACTCCTCTCGGAGAACAGAGCTAGTCAACTCCGGCATCAAGTTCTAC 743
 Qy 433 agaagatacagaggtttggtctagaagattgttccattcattagagcttctggtctgac 492
 Db 744 CAGCGGTACGAATCGCTCACAAGGAACATGTTCCATTCATCCGATCCCTGCTCGACG 803
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 Db 864 CTCTGTCGCCACCGCGGCAATCGTCCGCAAGATCGAGGTGCTCATTTCCGAGGCGCAGC 923
 Qy 613 ggttacaacacactttggaccacggtttgttactgtcttccgaagaatctgaattgggt 672
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 Qy 1093 atggtttctatttctgcttgggtttgttacaacggttactaaagccattgtctactact 1152
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 Qy 1393 tgttctgct 1401
 Db 1704 TGTTTGCT 1712

RESULT 15
 LOCUS I13429 6756 bp DNA PAT 26-JUL-1995
 DEFINITION Sequence 31 from patent US 5436156.
 ACCESSION I13429
 VERSION I13429.1 GI:910770
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 6756)
 AUTHORS Van Gorm, R.F.M., Van Hartingsveldt, W., Van Paridon, P.A.,
 Venstra, A.E., Luiten, R.G.M. and Sellen, G.C.M.
 TITLE Cloning and expression of phytase from aspergillus
 JOURNAL Patent: US 5436156-A 31 25-JUL-1995;
 FEATURES Location/Qualifiers
 source I..6756
 BASE COUNT 1615 a 1714 c 1712 g 1715 t
 ORIGIN

Query Match 43.4%; Score 508.2; DB 10; Length 6756;
 Best Local Similarity 64.9%; Pred. No. 1.9e-151;
 Matches 901; Conservative 0; Mismatches 488; Indels 0; Gaps 0;

Qy 13 gtcgtgactgtccattgcccaccttgttcggtttccacacccgtaccgcttggtgct 72
 Db 324 GTGGGACTACTGATCGCTGACTATCTGTCAGAGTCACTCCGGACTGGCAGTCCCCGCC 383
 Qy 73 cgtgtaactctcaactcttctgacactgttgacggtgtgacggtgttaccacatgtttcccaagaatt 132
 Db 384 TCGAGAAATCAATCCAGTTGCGATACGGTTCGATCAGGGGTATCAATGCTTCTCCGAGACT 443
 Qy 133 tctcaactgtgggttaataactctccattctcttcttgggtgacgaatctgtattct 192
 Db 444 TCGCATCTTTGGGGTCAATACGACCGCTTCTCTCTGCGAAACGAATCGGTCTATCTCC 503
 Qy 193 ccagacgttccaaaggtgttagagttacttctcaagtttctgtaacacaggtgct 252
 Db 504 CTTGAGTGTCCCGCGGATGTCAGAGTCACTTCTCAGGTCTCTCCGTCATGGAGCG 563
 Qy 253 agatacccaacttcttctggttctaaagcgtaactctcttctgattgaagctattcaaaag 312
 Db 564 CGGTATCCGACCGACTCCAAGGGCAAGAAATACCTCCGCTCTCATTTGAGGAGATCCAGCAG 623
 Qy 313 aacgctactgttccaaaggttaagtcggttcttcttgaagacttacaactacactttgggt 372
 Db 624 AACCGGACCACTTTGACGGGAAATATGCTCTCTGGAAGACATACAACTACAGCTTGGGT 683
 Qy 373 gctgacgacttactcattcgttggaacaaacaaatggttaactctggtattaaagttctac 432
 Db 684 GCAGATGACCTGACTCCTCTCGGAGAACAGAGCTAGTCAACTCCGCACTCAAGTTCTAC 743
 Qy 433 agaagatacagaggtttggtctagaagattgttccattcattagacttctggttagac 492
 Db 744 CAGCGGTACGAATCGCTCACAAGGAACATGCTTCCATTCATCCGATCCCTGCTCGACG 803

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 16, 2001, 17:56:24 ; Search time 197.94 Seconds
(without alignments)
294.769 Million cell updates/sec

Title: US-09-488-265-29_COPY_27_467

Perfect score: 2336

Sequence: 1 NSHSCDTVDGGYQCPEISH.....DFVEGLSFARSGGNWAECPA 441

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:**
1: sp_archaea:**
2: sp_bacteria:**
3: sp_fungi:**
4: sp_human:**
5: sp_invertebrate:**
6: sp_mammal:**
7: sp_mhc:**
8: sp_organelle:**
9: sp_phage:**
10: sp_plant:**
11: sp_rodent:**
12: sp_unclassified:**
13: sp_vertebrate:**
14: sp_virus:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1857.5	79.5	465	3 000092	000092 aspergillus
2	1826	78.2	467	3 090027	090027 aspergillus
3	1818	77.8	467	3 093838	093838 aspergillus
4	1808	77.4	467	3 09HE00	09HE00 aspergillus
5	1713	73.3	466	3 000100	000100 aspergillus
6	1711.5	73.3	466	3 000096	000096 aspergillus
7	1677.5	71.8	466	3 000085	000085 aspergillus
8	1299.5	55.6	487	3 000107	000107 thielavia h
9	333	14.3	469	3 09Y846	09Y846 kluyveromyc
10	328.5	14.1	442	3 074677	074677 pichia anqu
11	297.5	12.7	463	3 060172	060172 schizosacch
12	203	8.7	460	5 09VW72	09VW72 drosophila
13	192.5	8.2	467	5 096421	096421 drosophila
14	189	8.1	451	11 035217	035217 rattus norv
15	185	7.9	481	11 0922L6	0922L6 mus musculu
16	175.5	7.5	487	4 09UNW1	09UNW1 homo sapien
17	174.5	7.5	487	4 09UNW1	09UNW1 homo sapien
18	173.5	7.4	487	4 09UGA3	09UGA3 homo sapien
19	172.5	7.4	453	5 096420	096420 drosophila

20	171.5	7.3	453	5 09W438	09W438 drosophila
21	170.5	7.3	449	13 092170	092170 gallus gall
22	145.5	6.2	468	10 004509	004509 arabidopsis
23	136.5	5.8	198	3 09UTX1	09UTX1 schizosacch
24	136	5.8	274	11 09JJD5	09JJD5 mus musculu
25	131.5	5.6	374	11 09JMG5	09JMG5 mus musculu
26	129.5	5.5	381	11 09QXG5	09QXG5 mus musculu
27	119	5.1	449	5 019076	019076 caenorhabdi
28	117	5.0	683	5 000838	000838 leishmania
29	117	5.0	707	5 000839	000839 leishmania
30	113	4.8	827	5 047871	047871 eubacterium
31	110.5	4.7	421	4 09UIG6	09UIG6 homo sapien
32	110.5	4.7	428	4 09NPH0	09NPH0 homo sapien
33	108.5	4.6	513	2 046334	046334 comamonas t
34	106.5	4.6	380	5 022525	022525 caenorhabdi
35	106	4.5	853	14 093123	093123 human calic
36	104	4.5	354	5 019709	019709 caenorhabdi
37	103.5	4.4	1013	14 091LX9	091LX9 retroperito
38	103	4.4	1225	5 020330	020330 caenorhabdi
39	101.5	4.3	381	11 09QXH7	09QXH7 mus musculu
40	101.5	4.3	516	5 025327	025327 leishmania
41	101	4.3	452	5 019175	019175 caenorhabdi
42	100.5	4.3	730	5 020826	020826 caenorhabdi
43	100	4.3	1723	2 072194	072194 porphyromon
44	99.5	4.3	758	4 09P2C1	09P2C1 homo sapien
45	99	4.2	3008	14 039929	039929 hepatitis c

ALIGNMENTS

RESULT 1

000092 ID 000092 PRELIMINARY; PRT; 465 AA.
AC 000092;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-
DE PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
DE PHVA.
GN Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
RX NCBI_TaxID=5085;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-37.
RC STRAIN=ATCC 34625;
RX MEDLINE=97288063; PubMed=9143104;
RA Pasamontes L., Haiker M., Wyss M., Tessier M., van Loon A.P.G.M.;
RT "Gene cloning, purification, and characterization of a heat-stable
RT phytase from the fungus Aspergillus fumigatus.";
RL Appl. Environ. Microbiol. 63:1696-1700(1997).
CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC FROM PHYTATE.
CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MISCELLANEOUS: SHOWS HIGH ACTIVITY WITH 4-NITROPHENYL PHOSPHATE AT
CC A PH RANGE OF 3 TO 5 AND WITH PHYTIC ACID AT A PH RANGE OF 2.5 TO
CC 7.5. IT IS ABLE TO WITHSTAND TEMPERATURES UP TO 100 DEGREES
CC CELSIUS OVER A PERIOD OF 20 MIN, WITH A LOSS OF ONLY 10% OF THE
CC INITIAL ENZYMIC ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC EMBL; U59804; AAB96872.1; -.
CC HSP; P34752; 1IHP.
CC InterPro: IPR000560.
CC Pfam: PF00328; acid_phosphat; 1.
CC PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
CC PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
CC Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 26

FT CHAIN 27 465 3-PHYTASE A. 1
FT ACT_SITE 81 81 REQUIRED FOR BINDING SUBSTRATE (BY
FT ACT_SITE 82 82 SIMILARITY).
FT ACT_SITE 359 359 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT DISULFID 30 39 PROTON DONOR (BY SIMILARITY).
FT DISULFID 70 412 BY SIMILARITY.
FT DISULFID 213 463 BY SIMILARITY.
FT DISULFID 262 280 BY SIMILARITY.
FT DISULFID 434 442 BY SIMILARITY.
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 465 AA; 50836 MW; 86FC1D9058C9B2C9 CRC64;

Query Match 79.5%; Score 1857.5; DB 3; Length 465;
Best Local Similarity 78.9%; Pred. No. 6.9e-142;
Matches 347; Conservative 36; Mismatches 56; Indels 1; Gaps 1;

QY 2 SHSCDVTDDGGYQCFPIELHWTGTYSPYFSLADESALSPDVPDDCRVTFVQVLSRHGARYP 61
Db 27 SKSCDVTDDGGYQCFPIELHWTGTYSPYFSLADESALSPDVPDDCRVTFVQVLSRHGARYP 86
QY 62 TSSSKAYKSALEIAOKNATFAKGYAFKTYNYTLGADDLTPFGQELVNSGIRFYOR 121
Db 87 TSSSKAYKSALEIAOKNATFAKGYAFKTYNYTLGADDLTPFGQELVNSGIRFYOR 146
QY 122 KALARKIVPIRASGSDRVIASAEKIEGFQSAKLADPGSQPHQASPVINVIPEGSGYN 181
Db 147 KALARKIVPIRASGSDRVIASAEKIEGFQSAKLADPGSQPHQASPVINVIPEGSGYN 205
QY 182 NTLDHGCTAFEDSELGDDVEANFTALFAPARARLEADLPVTTLTDEDVYVLMDCMCPD 241
Db 206 NTLDHGCTAFEDSELGDDVEANFTALFAPARARLEADLPVTTLTDEDVYVLMDCMCPD 265
QY 242 TVARTSDATSELPFCALFTHDEWIOYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARL 301
Db 266 TVARTSDATSELPFCALFTHDEWIOYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARL 325
QY 302 THSPVDQHTSTNTLDSNPATFPLNATLYADFSHDNTMISIFALGLYNGTKPLSTTSVE 361
Db 326 TRSPVDQHTSTNTLDSNPATFPLNATLYADFSHDNTMISIFALGLYNGTKPLSTTSVE 385
QY 362 SIEETDGYASWTVPFAARAYVEMQCAEKEPLVRVLYNDRVPLHGCVDKLGCRKED 421
Db 386 SAKELDGYASWTVPFAARAYVEMQCAEKEPLVRVLYNDRVPLHGCVDKLGCRKED 445
QY 422 DFVEGLSFARSGGNWAECEFA 441
Db 446 DFVKGLSWARSGGNWAECEFA 465

RESULT 2
Q9U0Z7 PRELIMINARY; PRT; 467 AA.
AC Q9U0Z7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE MYO-INOSITOL HEXAPHOSPHATE PHOSPHORYLASE PRECURSOR (EC 3.1.3.8).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Hongning W., Qi W., Jing X.;
RT *PCR, cloning and characterization of the phytase (phyA) gene of

RT Aspergillus niger (China Strain).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218813; AAF25481.1; --
DR HSSP; P34732; 1IHP.
DR InterPro; IPR000560; --
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Signal; Lyase; Hydrolase.
FT SIGNAL 1 19 POTENTIAL.
FT SEQUENCE 467 AA; 51029 MW; F4300A8F165EBF92 CRC64;

Query Match 78.2%; Score 1826; DB 3; Length 467;
Best Local Similarity 76.9%; Pred. No. 2.4e-139;
Matches 339; Conservative 41; Mismatches 61; Indels 0; Gaps 0;

QY 1 NNSHCDVTDDGGYQCFPIELHWTGTYSPYFSLADESALSPDVPDDCRVTFVQVLSRHGARY 60
Db 27 NQSTCDVTDDGGYQCFPIELHWTGTYSPYFSLADESALSPDVPDDCRVTFVQVLSRHGARY 86
QY 61 PTSSAKAYKSALEIAOKNATFAKGYAFKTYNYTLGADDLTPFGQELVNSGIRFYOR 120
Db 87 PTSSAKAYKSALEIAOKNATFAKGYAFKTYNYTLGADDLTPFGQELVNSGIRFYOR 146
QY 121 YKALARKIVPIRASGSDRVIASAEKIEGFQSAKLADPGSQPHQASPVINVIPEGSGY 180
Db 147 YESLTRNIPIRSGSSSRVIAKGYAFKTYNYTLGADDLTPFGQELVNSGIRFYOR 206
QY 181 NTLDHGCTAFEDSELGDDVEANFTALFAPARARLEADLPVTTLTDEDVYVLMDCMCPD 240
Db 207 NTLDHGCTAFEDSELGDDVEANFTALFAPARARLEADLPVTTLTDEDVYVLMDCMCPD 266
QY 241 TVARTSDATSELPFCALFTHDEWIOYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 300
Db 267 DTISTVDTKLSFPFCDLFTHEWINDYDYLQSLGKYYGYGAGNPLGPTQGVGYANELIAR 326
QY 301 LTHSPVDQHTSTNTLDSNPATFPLNATLYADFSHDNTMISIFALGLYNGTKPLSTTSV 360
Db 327 LTHSPVDQHTSTNTLDSNPATFPLNATLYADFSHDNTMISIFALGLYNGTKPLSTTSV 386
QY 361 ESIEETDGYASWTVPFAARAYVEMQCAEKEPLVRVLYNDRVPLHGCVDKLGCRK 420
Db 387 QNITQTDGFSANWVPFAARLYVEMQCAEKEPLVRVLYNDRVPLHGCVDKLGCRK 446
QY 421 DFVEGLSFARSGGNWAECEFA 441
Db 447 DSFVKGLSFARSGGNWAECEFA 467

RESULT 3
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AC O93838;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE PHYTASE.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SK-57;
RA Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
RT *phytase having high-affinity for phytic acid.*;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB022700; CAB19824.1; --
DR HSSP; F34752; 1IHP.
DR InterPro; IPR000560; --
DR Pfam; PF00328; acid_phosphat; 1.

QY	121	YKALARKIVPIRASGSDRVITASAEKIEGFQSAKLADPGSQPHQASPVINVIPEGSY	180
DB	147	YESTLRNIVPPIRSRSGSVIASGNCKIEGFQSTKLKDPRAQGSQSPKIDVIVSEASTS	206
QY	181	NNTLDHGCTAFEDSELGDDVEANFTALFAPLARLEADLPVLTDEVDVYLMDCPF	240
DB	207	NNTLDPGTGVFDESELADIEANFTATFVPSIRQRLENDLSVSLTDEVTYLMDCSF	266
QY	241	DTVARTSATESLSPFCALFTHDEWIOYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR	300
DB	267	DTISTSTVDTKLSPFCDLFTHEEWINDYLSLNKYYGHCAGNPLGPTQGVGYANELIAR	326
QY	301	LTHSPVDQHTSTNHTLDSNPATPLNATLYADFSDHNTMISIFPALGLYNGTKPLSTTSV	360
DB	327	LTHSPVDHDTSSNHTLDSNPATPLNSTLYADFSDHNGIISILFALGLYNGTKPLSSTTA	386
QY	361	ESIEETDGYASNTVTPFAARAYVEMMQCAKEPLRVLVNDRVPLHGCADVCLKRCR	420
DB	387	ENITQDGFSSARTVPFASRMYYVEMMQCSEQLRVLVNDRVPLHGCADVCLGRCTR	446
QY	421	DDFVEGLSFARSGGNWAECA 441	
DB	447	DSFVKGLSFARSGGDWAECA 467	
RESULT	5		
000100		PRELIMINARY;	PRT; 466 AA.
ID	000100		
AC	000100;		
DT	01-JUL-1997 (TEMBLrel. 04, Created)		
DT	01-JUL-1997 (TEMBLrel. 04, Last sequence update)		
DT	01-MAY-2000 (TEMBLrel. 13, Last annotation update)		
DE	3-PHYTASE PRECURSOR (EC 3.1.1.8) (MYO-INOSITOL-HEXAKISPHOSPHATE 3- PHOSPHOHYDROLASE) (3 PHYTASE) (MYO-INOSITOL HEXAKISPHOSPHATE PHOSPHOHYDROLASE).		
DE	Aspergillus terreus.		
OC	Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;		
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.		
OX	NCBI_Taxid=33178;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=CBS 116.46;		
RA	Paramonates L., Halter M., Henriquez Huecas M., Hug D., Mitchell D.B.,		
RA	Rogers C., van Loon A.P.;		
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE FROM PHYTATE (BY SIMILARITY).		
CC	-1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO- INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.		
CC	-1- SUBCELLULAR LOCATION: SECRETED.		
CC	-1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.		
DR	EMBL; U60412; AA58465.1; -		
DR	HSSP; P34752; 1IHP.		
DR	InterPro; IPR000560; -		
DR	Pfam; PF00328; acid.phosphat.1.		
DR	PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.		
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.		
KW	hydrolase; Glycoprotein; Signal.		
FT	SIGNAL	1	15
FT	CHAIN	16	466
FT	ACT_SITE	82	82
FT			
FT	ACT_SITE	83	83
FT	ACT_SITE	361	361
FT	DISULFID	31	40
FT	DISULFID	71	414
FT	DISULFID	215	465
FT	DISULFID	264	282
FT	DISULFID	436	444
FT	CARBOHYD	27	27
FT	CARBOHYD	105	105
FT	CARBOHYD	120	120
FT			
FT	ACT_SITE	83	83
FT	ACT_SITE	361	361
FT	DISULFID	31	40
FT	DISULFID	71	414
FT	DISULFID	215	465
FT	DISULFID	264	282
FT	DISULFID	436	444
FT	CARBOHYD	27	27
FT	CARBOHYD	105	105
FT	CARBOHYD	120	120
FT			
FT	ACT_SITE	83	83
FT	ACT_SITE	361	361
FT	DISULFID	31	40
FT	DISULFID	71	414
FT	DISULFID	215	465
FT	DISULFID	264	282
FT	DISULFID	436	444
FT	CARBOHYD	27	27
FT	CARBOHYD	105	105
FT	CARBOHYD	120	120
FT			
FT	ACT_SITE	83	83
FT	ACT_SITE	361	361
FT	DISULFID	31	40
FT	DISULFID	71	414
FT	DISULFID	215	465
FT	DISULFID	264	282
FT	DISULFID	436	444
FT	CARBOHYD	27	27
FT	CARBOHYD	105	105
FT	CARBOHYD	120	120
FT			
FT	ACT_SITE	83	83
FT	ACT_SITE	361	361
FT	DISULFID	31	40
FT	DISULFID	71	414
FT	DISULFID	215	465
FT	DISULFID	264	282
FT	DISULFID	436	444
FT	CARBOHYD	27	27
FT	CARBOHYD	105	105
FT	CARBOHYD	120	120
FT			
FT	ACT_SITE	83	83
FT	ACT_SITE	361	361
FT	DISULFID	31	40
FT	DISULFID	71	414

FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 466 AA; 51055 MW; F2AECBC1A7C22C4 CRC64;

Query Match 73.3%; Score 1713; DB 3; Length 466;
 Best Local Similarity 71.4%; Pred. No. 3.3e-170;
 Matches 314; Conservative 49; Mismatches 77; Indels 0; Gaps 0;

QY 1 NNSHCDTVDGGYQCPEIHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
 DB 27 NNSHCDTVDGGYQCPEIHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 86
 QY 61 PTSSASKAYSALIEAOKNATKGYAFKTYNTLGGADLTPEGENOMVNSGKIFVRR 120
 DB 87 PTSSASKAYSALIEAOKNATKGYAFKTYNTLGGADLTPEGENOMVNSGKIFVRR 146
 QY 121 YKALARKIVPFRASGSDRVIASAEKFIQFQSAKLADPGSQHQAQVFNVIIEGSGY 180
 DB 147 YDLTRHINPFRASGSDRVIASAEKFIQFQSAKLADPGSQHQAQVFNVIIEGSGY 206
 QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVTLTDDVYVLMDCPF 240
 DB 207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVTLTDDVYVLMDCPF 266
 QY 241 DTVARTSDATLSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELLAR 300
 DB 267 ETVSLTDDAHTLSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELLAR 326
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 360
 DB 327 LTRSPVHDHTCVNNTLDANPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 386
 QY 361 ESTEETDGYASWTVPFAARAYVEMMQCAEKEPLRVLVNDRVPLHGCAYDKLGRCKR 420
 DB 387 EDITRDTGYAAWTVPFAARAYVEMMQCAEKEPLRVLVNDRVPLHGCAYDKLGRCKR 446
 QY 421 DDFVEGLSFARSGNNAECF 440
 DB 447 DDFVEGLSFARSGNNAECF 466

RESULT 6
 ID 000096 PRELIMINARY; PRT; 466 AA.
 AC 000096;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-
 DE PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
 DE PHOSPHOHYDROLASE A).
 GN PHVA.
 OS Talaromyces thermophilus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Talaromyces.
 OX NCBI_TaxID=28565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 20186;
 RX MEDLINE=98007872; PubMed=9349716;
 RA Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
 RA van Loon A.P.G.M.;
 RT *Cloning of the phytases from *Emmericella nidulans* and the thermophilic
 RT fungus *Talaromyces thermophilus*.
 RL Biochim. Biophys. Acta 1353:217-223(1997).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
 CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.

CC -1- MISCELLANEOUS: HAS POTENTIAL AS FOOD AND FEED ADDITIVE. IT CAN
 CC FACILITATE THE DEGRADATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS
 CC USED AS FOOD FOR MONOGASTRIC ANIMALS.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL; U59802; AAB96873.1; -.
 DR HSSP; P34752; 1IHP.
 DR InterPro; IPR000560; -.
 DR Pfam; PF00328; acid_phosphat; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 14 POTENTIAL..
 FT CHAIN 15 466 3-PHYTASE A.
 FT ACT_SITE 79 79 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 357 357 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 28 37 BY SIMILARITY.
 FT DISULFID 68 410 BY SIMILARITY.
 FT DISULFID 212 461 BY SIMILARITY.
 FT DISULFID 261 278 BY SIMILARITY.
 FT DISULFID 432 440 BY SIMILARITY.
 FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 466 AA; 51450 MW; FC4575B52IA5C929 CRC64;

Query Match 73.3%; Score 1711.5; DB 3; Length 466;
 Best Local Similarity 72.3%; Pred. No. 4.3e-130;
 Matches 319; Conservative 35; Mismatches 86; Indels 1; Gaps 1;

QY 1 NNSHCDTVDGGYQCPEIHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
 DB 24 DSHCNTVEGGYQCPEIHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 83
 QY 61 PTSSASKAYSALIEAOKNATKGYAFKTYNTLGGADLTPEGENOMVNSGKIFVRR 120
 DB 84 PTSSASKAYSALIEAOKNATKGYAFKTYNTLGGADLTPEGENOMVNSGKIFVRR 143
 QY 121 YKALARKIVPFRASGSDRVIASAEKFIQFQSAKLADPGSQHQAQVFNVIIEGSGY 180
 DB 144 YKALARKIVPFRASGSDRVIASAEKFIQFQSAKLADPGSQHQAQVFNVIIEGSGY 203
 QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVTLTDDVYVLMDCPF 240
 DB 204 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVTLTDDVYVLMDCPF 263
 QY 241 DTVARTSDATLSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELLAR 300
 DB 264 ETLARNHTDT-LSPFCALSTQEQEQAQYDYLQSLGKYGYGAGNPLGPAQGVGFANELLAR 322
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 360
 DB 323 MTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 382
 QY 361 ESTEETDGYASWTVPFAARAYVEMMQCAEKEPLRVLVNDRVPLHGCAYDKLGRCKR 420
 DB 383 KSIEETDGYSAWTVPFGGRAYVEMMQCDDSDPEVVRVLRVNDVVRVPLHGCAYDKLGRCKR 442
 QY 421 DDFVEGLSFARSGNNAECF 441
 DB 443 DDFVEGLSFARSGNNAECF 463

RESULT 7
 ID 000085 PRELIMINARY; PRT; 466 AA.
 AC 000085;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-

DE PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
DE PHA.
GN Aspergillus terreus.
OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=33178;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A1.
RX MEDLINE=97177792; PubMed=9025298;
RA Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L., Loon A.P.;
RT "The phytase subfamily of histidine acid phosphatases: isolation of
genes for two novel phytases from the fungi Aspergillus terreus and
Myceliophthora thermophila";
RL Microbiology 143:245-252(1997).
CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
FROM PHYTATE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MISCELLANEOUS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF
2.5 TO 7.5, WITH MAXIMAL ACTIVITY AT PH 5.5. ALSO ACCEPT 4-
NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA SHIFTED TO
MORE ACIDIC PH VALUES.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
DR EMBL; U59805; AAB52507.1; -.
DR HSSP; P34752; 1IHP.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 466 3-PHYTASE A.
FT ACT_SITE 82 REQUIRED FOR BINDING SUBSTRATE (BY
SIMILARITY).
FT ACT_SITE 83 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY).
FT DISULFID 31 40 BY SIMILARITY.
FT DISULFID 71 414 BY SIMILARITY.
FT DISULFID 215 465 BY SIMILARITY.
FT DISULFID 264 282 BY SIMILARITY.
FT DISULFID 436 444 BY SIMILARITY.
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 466 AA; 51093 MW; 21CDCB559C96AE66 CRC64;

Query Match 71.8%; Score 1677.5; DB 3; Length 466;
Best Local Similarity 70.4%; Pred. No. 2.4e-127;
Matches 309; Conservative 55; Mismatches 74; Indels 1; Gaps 1;
QY 3 HS-CDTVGGYQCPEISHLWGTSYSPYFSLADESAISPDVDDCRVTFTVQVLSRHGARYP 61
DB 28 HSDCNSVDHGQCPELSHKGWLPYFSLQDESFPDLDPEDCHITFTVQLAHGARS 87
QY 62 TSSASKAYSALIEAIQNAFAKGYAPLKYNTYTLGADDLTPFGENQVNSGKIFYRY 121
DB 88 THSKTKAYANTIAIQRSATAPFGKYAFQSYNSLDSSELTTPGRNQLDGAQFERY 147
QY 122 KALKARKVPIFRASGRVITASAEKFTGQSADKLADPGSQPHQASVINVIPEGSGYN 181
DB 148 NALTRHINFPVRATDSRVHESAEKFTGQTAQDDHANPHQSPRVDAIPEGSAYN 207
QY 182 NTLDHGTCTAFEDSELGDDVEANFTALFAPAIRLEADLPGVTLTDEDVVYLMDCPF 241
DB 208 NTLHSLCTAFESVTGDDAVANFTAVFAPIAQRLEADLPVQLVSTDDVVNLAMCPFE 267

QY 242 TVARTSDATSLSPFCALFTHDEWIQDYQLQSLGKYGYGAGNPLGPAQGVGFANELIARL 301
DB 268 TVSLTDDAHTLSLSPFCDLFTATETQYNVLLSLDKYGYGGNPLGVPQGVGWANELMARL 327
QY 302 THSPVQDHTSNHLDNSNPATFPFNALYADFSDHNTMISITFFALGYNGKPLSTTSVE 361
DB 328 TRAPVHDHTCVNNTLDASDPATFPFNALYADFSDHNSLVSIFWALGYNGTAPLSQTSVE 387
QY 362 SIETDGYSSASWTVPFAARAYVEMQCAKEPLRVRLVNDRVVPLHGCADVCKLGRCKRD 421
DB 388 SVSOTDGYAAATVPFAARAYVEMQCAKEPLRVRLVNDRVVPLHGCPTDKLGRCKRD 447
QY 422 DFVEGLSFARSGGNWAECP 440
DB 448 AFVAGLSFAQAGGNWADCF 466

RESULT 8
O00107 PRELIMINARY; PRT; 487 AA.
AC O00107;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE 3-PHYTASE A PRECURSOR (EC 3.1.1.3.8) (MYO-INOSITOL-HEXAKISPHOSPHATE 3-
DE PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
DE PHOSPHOHYDROLASE A).
GN PHYA.
OS Thielavia heterothallica.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Chaetomiaceae; Thielavia.
OX NCBI_TaxID=78579;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97177792; PubMed=9025298;
RA Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L.,
RA van Loon A.P.G.M.;
RT "The phytase subfamily of histidine acid phosphatases: isolation of
genes for two novel phytases from the fungi Aspergillus terreus and
Myceliophthora thermophila";
RL Microbiology 143:245-252(1997).
CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
FROM PHYTATE.
CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MISCELLANEOUS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF
3.5 TO 8.5, WITH MAXIMAL ACTIVITY BETWEEN PH 5.5 AND 6.0. ALSO
ACCEPT 4-NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA
SHIFTED TO MORE ACIDIC PH VALUES.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC EMBL; U59806; AAB52508.1; -.
DR HSSP; P34752; 1IHP.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 467 3-PHYTASE A.
FT DOMAIN 267 270 POLY-SER.
FT DOMAIN 423 433 POLY-GLY.
FT ACT_SITE 75 75 REQUIRED FOR BINDING SUBSTRATE (BY
SIMILARITY).
FT ACT_SITE 76 76 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 368 368 PROTON DONOR (BY SIMILARITY).
FT DISULFID 26 35 BY SIMILARITY.
FT DISULFID 64 421 BY SIMILARITY.
FT DISULFID 208 485 BY SIMILARITY.
FT DISULFID 289 289 BY SIMILARITY.
FT DISULFID 456 464 BY SIMILARITY.
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 487 AA; 52537 MW; 97D10EDC83D051DB CRC64;

Query Match 55.6%; Score 1299.5; DB 3; Length 487;
 Best Local Similarity 54.4%; Pred. No. 8.9e-97;
 Matches 254; Conservative 53; Mismatches 131; Indels 29; Gaps 4;

QY 2 SHSCDTGCGYOCFFPEISHLWGTYSPIYSLADESAISPDVDDCRVTFVQVLSRHGARY 61
 DB 23 SRPCTDPLGFCGGAISHFWGQYSPYFVSE--LDASIPDDCEVTPAQVLSRHGARAP 80
 QY 62 TSSASKAYSALIEAQKNATAFKGYAFKLTNY--TLGADDLT-----PF-G 106
 DB 81 TLKRAASYVDLDRHIGAISYGPGEFLRTYDTLGADELTRTQOQOMVNSGKIFYRRY 140
 QY 122 KALARKIVPFIASGSDRVIAAEKFIQFQSAKLADPGSQHQAQSPVINIIPGSGYN 181
 DB 141 RALARKSIPFVITAGDQVHSAENFTGFSALLADRGSTVRPLTPYDMVVIPIETAGAN 200
 QY 182 NTLHDGCTAFED---SELGDDVEANFTALFAPARLEADLPGLVTLTDEDVYVLMDC 238
 DB 201 NTLHNDLCTAFEGEYSTIGDQAQTYLSTFAGPTARVNANLPGANLTADATVALMDLC 260
 QY 239 PFDTVARTS-----DATELSPFCALFTHDEWIQYDYLQSLGKYGYGAGNPLGP 287
 DB 261 PFETVASSSSDPATADAGGNGRPLSPFCRLFSSEWRAVDYLSQVGKYGWYGCNPLGP 320
 QY 288 AQGVGFANELIARLTHSPVDHTSTNHTLDSNPATFPLNATLYADFSDHNTWISIFALG 347
 DB 321 TQGVGFVNELARLAGVPRDGTSTNRLDGDPRFTPLGRPLYADFSDHNDMMGMVLGALG 380
 QY 348 LYNKTKPLSTTSVESTEEDTGSASWTVPFAARAYVEMMQ-----QAQKEP 394
 DB 381 AYDGVPLDKTARRPEELGGYAASWAVPFAARIYVEMKRCSGGGGGGGGEGRQKDEE 440
 QY 395 LVRVLVNDRVPLHGCADVCKLGRCKRDFVEGLSFARSGGNWAECA 441
 DB 441 MVRVLVNDRVMTLKGCGADGEMCTLERIESMAFARGNKWDLCA 487

RESULT 9
 QY846 ID QY846 PRELIMINARY; PRT; 469 AA.
 AC QY846;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE ACID PHOSPHATASE (EC 3.1.3.2).
 GN PHO3.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2360/7;
 RA San Vicente A., Ferminan E., Dominguez A.;
 RT "Isolation and characterization of KIPHO3 a gene encoding a
 RT constitutive acid phosphatase from Kluyveromyces lactis."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ007502; CAB46490.1;
 DR HSSP; P34755; IQFX.
 DR InterPro; IPR000560;
 DR Pfam; PF00328; acid_phosphat; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase.
 FT CHAIN 17 469 ACID PHOSPHATASE.
 SQ SEQUENCE 469 AA; 52560 MW; 5C7ABF62CEA891C CRC64;

Query Match 14.3%; Score 333; DB 3; Length 469;
 Best Local Similarity 24.7%; Pred. No. 1e-18;
 Matches 113; Conservative 69; Mismatches 203; Indels 72; Gaps 15;

QY 9 DGVQCF-----PEISHLWGTYSPIYSLADESAISPDVDDCRVTFVQVLSRHGARY 60
 DB 22 DNTVTCVVALNSSTTDSIPPLNGQGHYDYPQSGIPVEVPDCTVEHVQMLARGERY 81
 QY 61 PTSSASKAYSALIEAQKNATAFKGYAFKLTNY--TLGADDLT-----PF-G 106
 DB 82 PTASKGKLIALWDLKKEFGQYNGPMEVFENDYEFVSNTKYFDQLTNTSDVDPSNPYAG 141
 QY 107 ENQMVNSGKIFYRRYKALARKIVPFIASGSDRVIAAEKFIQFQSAKLADPGSQHQA 166
 DB 142 AKTAQHLGKVIAYNYGDLFSDSNP-VFTSSGRVHTAKYVYVSSLEELDIOQLDQIIQE 200
 QY 167 SPVINVIIPGSGYNNLTLDHGTCTAFEDSELGDDVEANFTALFAPARAR--LEADLP 223
 DB 201 N-----ETSGANSLTPADSCWTY-NGDLGDEYENATLPVLTQIKRWMKKNL-N 250
 QY 224 VTLTDEDVYVLMDCPFDVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYGYGAGN 283
 DB 251 LTLHNDLCTAFEGEYSTIGDQAQTYLSTFAGPTARVNANLPGANLTADATVALMDLC 305
 QY 284 PLGPAQGVGFANELIARLTHSPVDHTSTNHTLDSNPATFPLNATLYADFSDHNTWISIF 343
 DB 306 PMSNPISGVLVNASYNLLTQADELN-----KWLFSFHDTDIOQFI 347
 QY 344 FALGLY-NGTKPLSTTSVESTEEDTGSASWTVPFAARAYVEMMQCAKEPLVRLVND 402
 DB 348 SALGLDNG---VTEVSLDQVDFQNLQOLSMTVPMGGRIFTEKLKC--GNASVRYIIND 402
 QY 403 RVVPLHGCADVCKLGRCKRDF-----VEGLSFARS 432
 DB 403 VIIPVPGCTSGPFCPIEDFDYITNRLNGIDYVSS 439

RESULT 10
 QY467 ID QY467 PRELIMINARY; PRT; 442 AA.
 AC QY467;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE REPRESSIBLE ACID PHOSPHATASE (EC 3.1.3.2).
 GN PHO1.
 OS Pichia angusta (Yeast) (Hansenula polymorpha).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4905;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC34438;
 RX MEDLINE=98386672; PubMed=9720203;
 RA Phongdara A., Merckelbach A., Keup P., Gellissen G., Hollenberg C.P.;
 RT "Cloning and characterization of the gene encoding a repressible acid
 RT phosphatase (PHO1) from the methylotrophic yeast Hansenula
 RT polymorpha."
 RL Appl. Microbiol. Biotechnol. 50:77-84 (1998).
 DR EMBL; AF051161; AAC62537.1;
 DR HSSP; P34755; IQFX.
 DR InterPro; IPR000560;
 DR Pfam; PF00328; acid_phosphat; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 KW Hydrolase.
 SQ SEQUENCE 442 AA; 49370 MW; 7087D91A85B05C31 CRC64;

Query Match 14.1%; Score 328.5; DB 3; Length 442;
 Best Local Similarity 25.1%; Pred. No. 2.2e-18;
 Matches 103; Conservative 63; Mismatches 163; Indels 81; Gaps 15;

QY 40 DVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEATQK-NATAFKGYAFKLTNYTIG 98

Db 55 DTPPHCEIQALPMRHCEREPTKSSGKQYKKFYDKLKKANITDYKGLAFIEDLEYFVP 114
 QY 99 ADDLTPFGENQWVNGI-----KFF-----YRYKAL--ARKIVPFRASGSDRVIASAEKFI 148
 Db 115 DSDNYELETTRGLYSGNLNAFKFGYTRERYDSIVDTSSVLPPIPAAS--EDRVVDVTARSEF 173
 QY 149 EGFQSAKLADPGSOPHASPVINVIPE--GSGYNTLTHGTC---TAFDESELGDDV 201
 Db 174 RGFEF-----PDYATSCSIQVNETDTSKANALITKDCNPTNSFSFYDFSGDEI 224
 QY 202 ---FANFTALPAIRARLEADLTDVYVYLMDCPFDVARTSDATLSPEFAL 258
 Db 225 FQREAD-----RLNELSPGNITADDIITMGTYCAYETNVKGH-----SSFCDA 268
 QY 259 FTHDEWIDYQLSGLKYYGAGNPLGPAQGVCFANELARLTHSPVQDHTSTNHTLDS 318
 Db 269 LSRGAFTALQNNVDVTFYFGPGYNNMSAVAGVYAN----- 305
 QY 319 NPATFPL---NATLYADFSDHNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASWTY 375
 Db 306 --ATAKLLQEDGKLWFSFSDNDLLNVTALGLITDE----LGTEVDVDFHRFKISELY 359
 QY 376 PFAARAVYEMMQCAKEPLVRVLVNDVRVPLHGCAVDKLGCRKRDFFE 425
 Db 360 PQGARLIIEKLNCS--SDTSEFVRTILNDKVVPVPGCSGPGYSCPLEDYLD 407

RESULT 11
 O60172
 ID O60172 PRELIMINARY; PRT; 463 AA.
 AC O60172;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE PROBABLE ACID PHOSPHATASE (EC 3.1.3.2).
 GN SPBC21H7.03C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=972;
 RA Lyne M., Rajandream M.A., Barrell B.G., Xiang Z., Aves S.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
 CC ALCOHOL + ORTHOPHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL; AL023286; CAAL8863.1; -.
 DR HSSP; P34755; 10FX.
 DR InterPro; IPR000560; -.
 DR Pfam; PF00328; acid_phosphat; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein.
 FT ACT_SITE 69 69 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 340 340 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 439 439 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 463 AA; 52758 MW; 6C41AF422C6D624A CRC64;
 Query Match 12.7%; Score 297.5; DB 3; Length 463;
 Best Local Similarity 25.3%; Pred.No. 7.4e-16;
 Matches 114; Conservative 67; Mismatched 203; Indels 15;
 QY 20 HLMGTYS----PYFSLADESAISFDVDDCRVTFVQVLSRHGARYPTS--SASKAYSAA-- 71

Db 35 HL--GTLSPHETPFDDGLDSA-----FPETCEIQVHLLQRHGSRNPTGVDVTDVYSOY 88
 QY 72 -----LIEAIQKNATAFKGYAFKTYNTYL---GADDLTPFGENQWVNGIKFYRR 120
 Db 89 LNNFOEKLKNGSIPVNFSPENPLCFIKQWTPVIDAENADQLSSRGRLFDLGRQLYOR 148
 QY 121 KYALARKIVPFRASGSDRVIASAEKFIQGFQSAKLADPGSOPHASPVINVIPEG--S 178
 Db 149 KYKLEDSYVYDINTABQERWESAKWFTYGLFGDKMYEKTN-----FILISEGKAA 199
 QY 179 GYNTLTDHGTCTAFDESEL---GDRVEANFTALPAIRARLEADL-PGVTLTDEDDVY 233
 Db 200 GANSLSMYACPVFKDNNHFNKATDAHAWRNIFIEPIVNRKAKYFDSYKLTINDVRS 259
 QY 234 LMDMCPFDVARTSDATLSPEFALFTHDEWIDYQLSGLKYYGAGNPLGPAQGVGF 293
 Db 260 LFVICEYEIAIK-----DHSDFCSIFTPSEFLNFEDYDLDQAYGGPVSEWASTLGGAY 314
 QY 294 ANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMISIFFALYNGTK 353
 Db 315 INNLADSL-----RNVTPNPDFDRK-----VFLAFTHDSNIIIPVEAALGFPPDIT 358
 QY 354 PLSTTSVESIEETDGYASWTYVFAARAYVEMMQCAKEPLVRVLVNDVRVPLHGCAVD 413
 Db 359 PQNPPLTDKNITYYSOKTSSFPVFPAGNLITELFFC--SDSKYVVRHLVNOQVYPLDCCGY 417
 QY 414 KLGR-----CKRDDFVEGLSFARSGGNWAEFCF 440
 Db 418 PSGTSDGLCELQAYLNSPIRANSTNGISIF 448
 RESULT 12
 Q9VV72
 ID Q9VV72 PRELIMINARY; PRT; 460 AA.
 AC Q9VV72;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE MIPPI PROTEIN.
 GN MIPPI OR C64123.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.T., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., M.G.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Yao Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003527; AAF49450.1; --
 DR FlyBase; FBgn0026061; Mippl.
 DR InterPro; IPR000560; --
 DR Pfam; PF00328; acid_phosphat; 1.
 DR SEQUENCE 460 AA; 52685 MW; F00B25718E40807D CRC64;

Query Match 8.7%; Score 203; DB 5; Length 460;
 Best Local Similarity 24.0%; Pred. No. 3.2e-08;
 Matches 104; Conservative 60; Mismatches 172; Indels 98; Gaps 21;

QY 45 CRVTFVQVLSRRGARYPTSS-----ASKAYSALIEATKNAFAKFGK-----YAF 90
 DB 56 COPQKMWIFHRHGTLPKSKMINKASRV-AELRDLLIINNYQVARTKPTDLCQTDLIAI 114
 QY 91 KTYNTLGGADLTTPFGENOMVNSGKIFRYRYKALARKIVP-FIRASGSD-----RVIASAE 145
 DB 115 KLWKWN---SSITPDMEEYLTAGYEDLGTAKLYQRYPTVLTANYNDYVYQRTTESFK 171
 QY 146 KTEG-FQSAKLADPGSQPHQ-----ASPVINV-IIPEGSYNTLHGICTAED 194
 DB 172 AFAEGLFGSONAAHPVEIPKQDILLRPDYCSFKFNKYKDEGSEYK-----FHQ 222
 QY 195 SELGDDVEANFTALFAPATRARLEADLPG--VTLTDEDVVYLMDCMCPDVTARTSDATEL 252
 DB 223 SKLYNTLAD-----ISTRL-----GFLYTLLEADIKLMDMCRYE---QAWNVDN 266
 QY 253 SPFCALFTHDEWIQDYLSGLKYYGYGAGNPLGPAQGVGFANELIARLTHSPVODHTST 312
 DB 267 SVWCGAFLPEQITVFEYLEDKYYGYGSGYGFENAHLCRLVQDILLTHLS-NPVSPH--- 322
 QY 313 NHTLDSNPATFFLNATLYADFSDHNTMISIFALGLYNGTKPLSTSVESIEETDGYAS 372
 DB 323 -----VVAHFHGSTGLLTLLTALGIXKDDIKLRADNYDSL-TSRWKSS 365
 QY 373 WTVPFAARAYVEMMOQA--EKEPLRVLVNDRVPLHGCACVDKLGRCKRDFVE----- 425
 DB 366 LIDPFAANFVAVKYDCPADLDREKVV--FFLNQOAVQLDWCNV---GLCKWSDVLEKYKI 421
 QY 426 -----GLSFARSGG 434
 DB 422 ADADCGEYCYRTGG 435

RESULT 13
 O96421 PRELIMINARY; PRT; 467 AA.
 ID O96421
 AC O96421;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAY-2001 (Tremblrel. 16, Last annotation update)
 DE MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE 1.
 GN MIPPI OR C64123.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;

RNA SEQUENCE FROM N.A.
 RA Chi H., Wang J., Romano P.R., O'keefe R.J., Puzas J.E., Rosier R.N.,
 RA Reynolds P.R.; (1998) to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF046913; AAD02436.1; --
 DR FlyBase; FBgn0026061; Mippl.
 DR InterPro; IPR000560; --
 DR Pfam; PF00328; acid_phosphat; 1.
 DR SEQUENCE 467 AA; 53602 MW; 1A0571B9958B2632 CRC64;

Query Match 8.2%; Score 192.5; DB 5; Length 467;
 Best Local Similarity 22.9%; Pred. No. 2.3e-07;
 Matches 101; Conservative 61; Mismatches 174; Indels 105; Gaps 20;

QY 45 CRVTFVQVLSRRGARYPTSS-----ASKAYSALIEATKNAFAKFGK-----YAF 90
 DB 56 COPQKMWIFHRHGTLPKSKMINKASRV-AELRDLLIINNYQVARTKPTDLCQTDLIAI 114
 QY 91 KTYNTLGGADLTTPFGENOMVNSGKIFRYRYKALARKIVPFI-----RASGSD 138
 DB 115 KLWKWN---SSITPDMEEYLTAGYEDLGTAKLYQRYPTVLTANYNDYVYQRTDTQ 171
 QY 139 RVIASAEKFTG-FQSAKLADPGSQPHQ-----ASPVINV-IIPEGSYNTLHDG 187
 DB 172 RTTESFKAFAGLFGSONAAHPVEIPKQDILLRPDYCSFKFNKYKDEGSEYK----- 226
 QY 188 TCATFEDSELGDDVEANFTALFAPATRARLEADLPG--VTLTDEDVVYLMDCMCPDVTAR 245
 DB 227 -----FHOSKLYNTLAD-----ISTRL-----GFLYTLLEADIKLMDMCRYE---Q 266
 QY 246 TSDATELSPFCALFTHDEWIQDYLSGLKYYGYGAGNPLGPAQGVGFANELIARLTHSP 305
 DB 267 AWWVDRNSVWCGAFLPEQITVFEYLEDKYYGYGSGYGFENAHLCRLVQDILLTHLS-NP 325
 QY 306 VQDHTSTNHTLDSNPATFFLNATLYADFSDHNTMISIFALGLYNGTKPLSTSVESIEE 365
 DB 326 VSPH-----VVAHFHGSTGLLTLLTALGIXKDDIKLRADNYDSL-T 365
 QY 366 TDGYSASWTVPFAAR--AYVEMMOQA-EKEPLRVLVNDRVPLHGCACVDKLGRCKRDFD 423
 DB 366 SRRWKSSLIDPFAANFVAVKYDCPADLDREKVV--FFLNQOAVQLDWCNV---GLCKWSDV 421
 QY 424 VE-----GLSFARSGG 434
 DB 422 LEKYKTIADADCGEYCYRTGG 442

RESULT 14
 O35217 PRELIMINARY; PRT; 451 AA.
 ID O35217
 AC O35217;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-AUG-1999 (Tremblrel. 11, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE HEPATIC MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE (EC 3.1.3.-)
 GN MIPPI.
 OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE OF 11-451 FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RC TISSUE=LIVER;
 RA MEDLINE-98028656; PubMed-9359836;
 RA Craxton A., Caffrey J.J., Burkhardt W., Safrany S.T., Shears S.B.;
 RT "Molecular cloning and expression of a rat hepatic multiple inositol
 RL polyphosphate phosphatase.";
 RL Biochem. J. 328:75-81(1997).
 RN [2]
 RP CATALYTIC ACTIVITY.

RX MEDLINE=91358435; PubMed=1653239;
 RA Nogimori K., Hughes P.J., Glennon M.C., Hodgson M.E., Putney J.W. Jr.,
 RA Shears S.B.;
 RT "Purification of an inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase
 RT activity from rat liver and the evaluation of its substrate
 RT specificity.";
 RL J. Biol. Chem. 266:16499-16506(1991).
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INOSITOL 1,3,4,5-
 CC TETRAKISPHOSPHATE TO INOSITOL 1,4,5-TRIPHOSPHATE AND INOSITOL
 CC 1,3,4,5-PENTAKISPHOSPHATE TO INOSITOL 1,4,5,6-TETRAKISPHOSPHATE
 CC AND THEN TO INOSITOL 1,4,5-TRIPHOSPHATE. DEPHOSPHORYLATES
 CC INOSITOL HEXAKISPHOSPHATE WITHOUT SPECIFICITY TOWARDS A PARTICULAR
 CC PHOSPHATE GROUP.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY AND LIVER.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL: AF012714; AAC53453.1; -;
 DR InterPro: IPR000560; -;
 DR InterPro: IPR000886; -;
 DR Pfam: PF00328; acid_phosphat; 2.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 DR PROSITE: PS00616; HIS-ACID_PHOSPHAT_1; FALSE_NEG.
 KW Hydrolase; Glycoprotein; Phosphorylation; Multifunctional enzyme.
 FT AC_SITE 59 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT MOD_RES 65 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 146 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 176 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 201 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 218 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 391 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 412 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 435 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 447 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 447 PHOSPHORYLATION (POTENTIAL).
 FT CARBOHYD - 206 206 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARIANT 3 3 P -> H.
 FT CONFLICT 327 327 S -> P (IN AAC53453).
 FT SITE 448 451 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 451 AA; 51592 MW; EB1C05512A03020B CRC64;

Query Match 8.1%; Score 189; DB 11; Length 451;
 Best Local Similarity 20.7%; Pred. No. 4.2e-07;
 Matches 89; Conservative 66; Mismatches 193; Indels 82; Gaps 16;
 QY 26 SPYFS-----LADESALSPD---VPDPCRYTFVQLSRHGARYPTSSASKAYS 70
 DB 14 SPYFGTKTRYEDVNPWLLGDVPAPRRDPPELLAGTCTPVQLVALLRHGTRYPTTKQIRKLR 73
 QY 71 ALIEAIQKNATAFKGYAFILKTYNTYTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVP 130
 DB 74 QLQGLLOTRESVDGSRVAAALDQWPLWYDD---WMDGQVKEGRQDMQLALRLAALFP 130
 QY 131 --FIR-----ASSDRVIAAEKFIETGFSQAKLADPGSQPHQAS-----PVINVI 173
 DB 131 DLFCRENYGRLLRITSSKRCVDSAAFLQGLW--QHYHPGLPPDPVSDMECDPPRVN-- 186
 QY 174 IPEGSGYNTLDHGTCTAFEDSELGDVDEANFTALF-----APAIRARLE-----ADL 221
 DB 187 ----DKLMRFDDH--CEKFL-----TEVERNATALYHVEAFKTPGEMQVLLKVAATLQV 235
 QY 222 PGVTLTDEVDVYLMDCPFDTVARTSDATSELPFCALFTHDEWIQYDYLQSLGKYGYGA 281
 DB 236 PVNNLNADLIQVAFFTCFSFLAIGVH-----SPWCDVFDVDDAKVLEYLNDLKQYWKRSY 291
 QY 282 GNPGLPAGQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMIS 341
 DB 292 GYATNSRSSCNLFQDIFLHLDKAVEQKQRSQ-----PVSSSVILQFGHAETLLP 340
 QY 342 IFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMQCAKEP-----LVR 397
 DB 341 LLSLMGYFKDKLEPTAYNFEEQVHRE--FRSGHIVPYASNLIFFLYHCDQATPOEKFIQ 399

QY 398 VLVNDRVWVPL 407
 DB 400 MLLNEKVLPL 409
 RESULT 15
 Q922L6 PRELIMINARY; PRT; 481 AA.
 ID Q922L6;
 AC Q922L6;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE.
 GN MINP1 OR MIP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RA Chi H., Wang J., Romano P.R., O'keefe R.J., Puzas J.E., Rosier R.N.,
 RA Reynolds P.R.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF046908; RAD02434.1; -;
 DR MGD; MGI:1336159; Minppl.
 DR InterPro: IPR000560; -;
 DR InterPro: IPR000886; -;
 DR Pfam: PF00328; acid_phosphat; 2.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 481 AA; 54537 MW; 7CE78356B11F4606 CRC64;
 Query Match 7.9%; Score 185; DB 11; Length 481;
 Best Local Similarity 20.9%; Pred. No. 9.6e-07;
 Matches 90; Conservative 63; Mismatches 195; Indels 82; Gaps 16;
 QY 26 SPYFS-----LADESALSPD---VPDPCRYTFVQLSRHGARYPTSSASKAYS 70
 DB 44 SPYFGTKTRYEDANPWLVDVPAPRRDPPELLAGTCTPVQLVALLRHGTRYPTTKQIRKLR 103
 QY 71 ALIEAIQKNATAFKGYAFILKTYNTYTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVP 130
 DB 104 QLQGLLOTRESRDGSGVAAALAEWPLWYGD---WMDGQVKEGRQDMQLALRLAALFP 160
 QY 131 --FIR-----ASSDRVIAAEKFIETGFSQAKLADPGSQPHQAS-----PVINVI 173
 DB 161 DLFSRENYDLRLITSSKRCVDSAAFLQGLW--QHYHPGLPPDPVSDMECDPPRVN-- 216
 QY 174 IPEGSGYNTLDHGTCTAFEDSELGDVDEANFTALF-----APAIRARLE-----ADL 221
 DB 217 ----DKLMRFDDH--CEKFL-----TDVERNATALYHVEAFKTPGEMQVLLKVAATLQV 265
 QY 222 PGVTLTDEVDVYLMDCPFDTVARTSDATSELPFCALFTHDEWIQYDYLQSLGKYGYGA 281
 DB 266 PVNNLNADLIQVAFFTCFSFLAIGVH-----SPWCDVFDVDDAKVLEYLNDLKQYWKRSY 321
 QY 282 GNPGLPAGQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMIS 341
 DB 322 GYATNSRSSCNLFQDIFLHLDKAVEQKQRSQ-----PVSSSVILQFGHAETLLP 370
 QY 342 IFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMQCAKEP-----LVR 397
 DB 371 LLSLMGYFKDKLEPTAYNFEE--QVNRKFRSGHIVPYASNLIFFLYHCDNAQSPFQFIQ 429
 QY 398 VLVNDRVWVPL 407
 DB 430 LLLNEKVLPL 439

Search completed: October 16, 2001, 17:56:25
 Job time: 7529 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 16, 2001, 17:57:28 ; Search time 52.08 Seconds
(without alignments)
290.067 Million cell updates/sec

Title: US-09-488-265-29_COPY_27_467
Perfect score: 2336
Sequence: 1 NSHSCDFVDGGYQCPEISH.....DFVEGLSFARSGGNWAECA 441

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1837	78.6	467	1	PHYA_ASPAW
2	1833	78.5	467	1	PHYA_ASPNG
3	1816.5	77.8	463	1	PHYB_EMENI
4	389	16.7	467	1	PPAB_YEAST
5	389	16.7	467	1	PPAC_YEAST
6	381	16.3	467	1	PPAS_YEAST
7	380	16.3	467	1	PPA3_YEAST
8	354	15.2	468	1	PPAD_YEAST
9	350.5	15.0	468	1	PPAL_PTCPA
10	348.5	14.9	479	1	PHYB_ASPNG
11	347.5	14.9	479	1	PHYB_ASPAW
12	332	14.2	469	1	PHYA_KLULA
13	297	12.7	453	1	PPA5_SCHPO
14	278.5	11.9	463	1	PPA1_SCHPO
15	130	5.6	755	1	PPA2_SCHPO
16	124.5	5.3	421	1	PPAX_CAEEL
17	114.5	4.9	423	1	PPAL_MOUSE
18	112	4.8	423	1	PPAL_RAT
19	112	4.8	874	1	NICA_CAEEL
20	102.5	4.4	423	1	COPG_HUMAN
21	101	4.3	874	1	PPAL_HUMAN
22	98.5	4.2	381	1	COPG_BOVIN
23	96.5	4.1	275	1	UL11_HCMVA
24	96.5	4.1	386	1	PPAP_HUMAN
25	96	4.1	411	1	PPAY_CAEEL
26	96	4.1	413	1	PPAW_CAEEL
27	94.5	4.0	580	1	UL25_HSV11
28	94.5	4.0	602	1	PEHX_ERWCH
29	94	4.0	754	1	MBPL_KLULA
30	93.5	4.0	2077	1	TEGU_HSV6G
31	93.5	4.0	2077	1	TEGU_HSV6U
32	92.5	4.0	417	1	AGP_PRORE
33	92.5	4.0	844	1	YD25_SCHPO

34 92 3.9 680 1 NCPR_CANNA
35 92 3.9 764 1 METE_SOLSC
36 91 3.9 551 1 AMYB_THETU
37 89.5 3.8 526 1 CLOS_CLOHI
38 89.5 3.8 848 1 YAM6_SCHPO
39 89.5 3.8 2208 1 POLN_MANCV
40 89 3.8 823 1 AXL2_YEAST
41 88.5 3.8 913 1 AGLU_BETVU
42 88.5 3.8 1014 1 NANH_CLOSE
43 88 3.8 873 1 PCL_HUMAN
44 87.5 3.7 693 1 LYSI_YEAST
45 87 3.7 680 1 NCPR_CANTR

ALIGNMENTS

RESULT 1

PHYA_ASPAW
ID PHYA_ASPAW STANDARD; PRT; 467 AA.
AC P34753;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
DE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
DE PHOSPHOHYDROLASE A).
GN PHYA OR PHY.
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ALK0243;
RX MEDLINE=94040796; PubMed=8224894;
RA Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A.,
RA Miettinen-Oinonen A., Nevalainen H., Rambosek J.A.;
RT "The cloning and sequencing of the genes encoding phytase (phy) and
RT pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
RT awamori.";
RT Gene 133:55-62(1993).
CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC FROM PHYTATE.
CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
CC D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL: L02421; AAA16898.1; -
DR PIR; JN0889; JN0889.
DR HSSP; P34752; 1IHP.
DR InterPro; IPR000560; -
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 467 3-PHYTASE A.
FT ACT_SITE 82 82 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY).
FT DISULFID 31 40 BY SIMILARITY.
FT DISULFID 71 414 BY SIMILARITY.
FT DISULFID 215 465 BY SIMILARITY.
FT DISULFID 264 282 BY SIMILARITY.
FT DISULFID 436 444 BY SIMILARITY.

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

1

FT DISULFID 31 40
 FT DISULFID 71 414
 FT DISULFID 215 465
 FT DISULFID 264 282
 FT DISULFID 436 444
 FT CARBOHYD 27 27
 FT CARBOHYD 59 59
 FT CARBOHYD 105 105
 FT CARBOHYD 120 120
 FT CARBOHYD 207 207
 FT CARBOHYD 230 230
 FT CARBOHYD 339 339
 FT CARBOHYD 352 352
 FT CARBOHYD 376 376
 FT CARBOHYD 388 388
 SQ SEQUENCE 467 AA; 51086 MW; 88FE8F3584341D6D CRC64;

Query Match 78.5%; Score 1833; DB 1; Length 467;
 Best Local Similarity 77.3%; Pred. No. 1.9e-141;
 Matches 341; Conservative 39; Mismatches 61; Indels 0; Gaps 0;

QY 1 NSHSCDVTGGYQCFEISHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
 Db 27 NQSCDVTGGYQCFSETSHLWQYAPFFSLANESVISPEVAGCRVTFVQVLSRHGARY 86
 QY 61 PTSSASKAYSALIEAIQKNATAFKGYAFKTYNTLGADDLTPGENOMVNSGKIFYRR 120
 Db 87 PTDSKGGKYSALIEEQNNATFDGKYAFKTYNSLGADDLTPGEQELVNSGKIFYRR 146
 QY 121 YKALARKIVPFRASGSDRVIASAEKFIQFQSAKLADPGSOPHOASPVINVIPEGSGY 180
 Db 147 YESLNRIVPFRASSGSDRVIASAGKFIQFQSTKLKDPRAQPGSSKIDVWISEASS 206
 QY 181 NNTLDHGTCTAPDSELGDDVEANFTALPAPAIRARLEADLPGLVLTDEDVYVLMDCPF 240
 Db 207 NNTLDHGTCTVDESLADTVEANFTATVPISQIRLENDLSGVTLTDEVTYVLMDCSF 266
 QY 241 DTVARTSDATELSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 300
 Db 267 DTSTSTVDTKSPFCDLFTHDEWINYDYLQSLKYYGAGNPLGPGQGVGFANELIAR 326
 QY 301 LTHSPVODHTSNHTLDSNPATFPLNATLYADFSDHNTMISIFPAGLYNGTKPLSTTSV 360
 Db 327 LTHSPVDDHTSNHTLDSNPATFPLNSTLYADFSDHNTMISIFPAGLYNGTKPLSTTV 386
 QY 361 ESTEETDGSASWTVPFAARAVEMMQCAEKEPLRVLVNDRVPLHGCAVDKLGCRKR 420
 Db 387 ENITQDGFSSAWTVPFASRLYVEMMQCAEPLRVLVNDRVPLHGCPVDALGRCTR 446
 QY 421 DPFVEGLSPARSGGNWAECEFA 441
 Db 447 DSFVRGLSPARSGGDWAECEFA 467

RESULT 3
 PHYB_EMBL
 ID PHYB_EMBL STANDARD; PRT; 463 AA.
 AC 000093;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
 DE 3-PHOSPHOHYDROLASE B) (3 PHYTASE B) (MYO-INOSITOL HEXAKISPHOSPHATE
 DE PHOSPHOHYDROLASE B).
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=5072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98007872; PubMed=9349716;
 RA Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,

RA van Loon A.P.;
 RT "Cloning of the phytases from Emericella nidulans and the
 RL thermophilic fungus Talaromyces thermophilus.";
 RL Biochim. Biophys. Acta 1353:217-223(1997).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
 CC D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC
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 CC
 CC EMBL; U59803; AAB96871.1; -
 DR InterPro; IPR000560; -
 DR Pfam; PF00328; acid_phosphat; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 463 3-PHYTASE B.
 FT ACT_SITE 80 80 REQUIRED FOR BINDING SUBSTRATE
 FT (BY SIMILARITY).
 FT ACT_SITE 81 81 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 357 357 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 463 AA; 51786 MW; ECC5827D1E1C82A2 CRC64;

Query Match 77.8%; Score 1816.5; DB 1; Length 463;
 Best Local Similarity 76.5%; Pred. No. 4.2e-140;
 Matches 336; Conservative 45; Mismatches 55; Indels 3; Gaps 2;

QY 2 SHSCDVTGGYQCFEISHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 61
 Db 26 NHCNTADGGYQCFPNVSHVWGQYSPFYSIQESAISEDVPHGCEVTFVQVLSRHGARY 85
 QY 62 TSSASKAYSALIEAIQKNATAFKGYAFKTYNTLGADDLTPFGENOMVNSGKIFYRR 121
 Db 86 TESKSKAYSGLIEAIQKNATSFQWQYAFLESYNTLGADDLTFGENOMVDSGAKIFYRR 145
 QY 122 KALARKIVPFRASGSDRVIASAEKFIQFQSAKLADPGSOPHOASPVINVIPEGSGY 181
 Db 146 KNLARKNTFFRASGSDRVIASAEKFIQFQSAKLADPGSOPHOASPVINVIPEGSGY 203
 QY 182 NTLDHGTCTAFEDSELGDDVEANFTALPAPAIRARLEADLPGLVLTDEDVYVLMDCPF 241
 Db 204 NTLDHGTCTVSPENDERADEIEANFTALPAPAIRARLEADLPGLVLTDEDVYVLMDCSF 263
 QY 242 TVARTSDATELSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 301
 Db 264 TWARTAHGTSELSPFCALFTEKEWLYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 323
 QY 302 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMISIFPAGLYNGTKPLSTTSV 361
 Db 324 TQSPVDNTSTNHTLDSNPATFPLDRKLYADFSDHNTMISIFPAGLYNGTKPLSTTSV 383
 QY 362 SIETDGYASWTVPFAARAVEMMQCAEKEPLRVLVNDRVPLHGCAVDKLGCRKR 421
 Db 384 SIQMDGYAASWTVPFARAYFELMQCE-KKEPLRVLVNDRVPLHGCAVDKLGCRKR 442

QY 422 DFVEGLSFARSGNNAECF 440
I:|||||:|||||:|
Db 443 DWVEGLNFARSGNWKTCF 461

RESULT 4
ID PPAB_YEAST STANDARD; PRT; 467 AA.
AC P35842;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 31, Last annotation update)
DE ACID PHOSPHATASE PHO11 PRECURSOR (EC 3.1.3.2) (p56).
GN PHO11 OR YAR071W.

OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=95249563; PubMed=7731988;
RA Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
RA Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
RA Storms R.K.;
RT "The nucleotide sequence of chromosome I from Saccharomyces
cerevisiae";
RL Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen J.Y., Gong Y.I., Ao S.Z.;
RT "The primary structure of acid phosphatase gene PHO11 in S.
cerevisiae and comparison with other gene families";
RL Acta Biochim. Biophys. Sin. 21:437-444(1989).

CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
ALCOHOL + ORTHOPHOSPHATE.
CC -1- INDUCTION: S.CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS
CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.
CC -1- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.

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CC -----
CC EMBL; L28920; AAC09508.1; -;
DR EMBL; L19789; AAA73479.1; -;
DR HSP; P34752; 11HP
DR HSP; S0000094; PHO11.
DR InterPro; IPR000560; -;
DR Pfam; PF00328; acid_phosphat_1; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 17
FT CHAIN 18 467
FT ACT_SITE 75 75
FT ACT_SITE 337 337
FT CARBOHYD 97 97
FT CARBOHYD 162 162
FT CARBOHYD 192 192
FT CARBOHYD 250 250
FT CARBOHYD 315 315
FT CARBOHYD 356 356
FT CARBOHYD 390 390
FT CARBOHYD 439 439
FT CARBOHYD 445 445
FT CARBOHYD 461 461

FT CONFLICT 17 17 A -> L (IN REF. 2).
FT CONFLICT 82 83 VS -> AR (IN REF. 2).
FT CONFLICT 150 150 R -> H (IN REF. 2).
FT CONFLICT 354 354 K -> Q (IN REF. 2).
FT CONFLICT 423 423 D -> G (IN REF. 2).
SQ SEQUENCE 467 AA; 52757 MW; AECDC1C046B326C3 CRC64;

Query Match 16.7%; Score 389; DB 1; Length 467;
Best Local Similarity 26.4%; Pred. No. 4e-24;
Matches 116; Conservative 63; Mismatches 198; Indels 62; Gaps 12;

QY 17 EISHLWGTYSPYSLADESAISPDVDDCRVTFVQVLSRHGARYPTSSASAKYSALEIAI 76
|:|||||:|||||:|
Db 36 EIFPFLGSGPYSPGDYGISRDLPESCEMKQVMVGRHGERYPTVSKAKSIMTTWYKL 95
|:|||||:|||||:|
QY 77 QKNATATKGYAFK-----TNYNLT-----GADDLTPF-GENQMVNSGKIFYR 120
|:|||||:|||||:|
Db 96 SNYTGQFSGALSFLNDYEFIRDTKNLEMETTLANSVNVNLNPTVGTGEMNAKRHARDFLAQ 155
|:|||||:|||||:|
QY 121 YKALARKIVPF-IRASGSDRVIAASAERFIEGFQSAKLADPGSQPHQASPVINVIPEGSG 179
|:|||||:|||||:|
Db 156 YGVWVENOTSAVFTSNRCHDTAQYFDG-----LGDKFNISLQ-----TISEAESAG 205
|:|||||:|||||:|
QY 180 YNNTLDHGTCTAFEDSELGDDVEANFTALFAPATRARLEADLPVLTLDDEVVYLMDCP 239
|:|||||:|||||:|
Db 206 ANTLSAHHSCPAWDD-DVNDLILKKYDTKYLKSLGIAKRLKENKLNLTSSDANTFFAWCA 264
|:|||||:|||||:|
QY 240 PDTVARTSDATLSPFCALFTHDWMIOVDYLSLQKGYGAGNPLGPAQGVGFANELIA 299
|:|||||:|||||:|
Db 265 VEINAR-----GYSDICNIFTKDELVRFSYQDLETTYQTGPGYDVVRSVGANFNASVK 319
|:|||||:|||||:|
QY 300 RLTHSPVDQHTSTNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTS 359
|:|||||:|||||:|
Db 320 LKKESEVDQ-----KVLSETHDTHDILNYLTITIGIIDDKNNLTAEH 361
|:|||||:|||||:|
QY 360 VESIEETGYSASWTPFAARAYVEMMCQAEKPEPLVRLVNDVRVPLHGCADVCLGRCK 419
|:|||||:|||||:|
Db 362 VPFMT-----FHRSSVWVPGARVYTEKFC--SNDYVRYVINDAVVPIETCSTGPGFSCE 417
|:|||||:|||||:|
QY 420 RDDF-----VEGLSFAR 431
|:|||||:|||||:|
Db 418 INDYDYAEKRVAGTDFLK 436
|:|||||:|||||:|

RESULT 5
ID PPAC_YEAST STANDARD; PRT; 467 AA.
AC P38693;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE ACID PHOSPHATASE PHO12 PRECURSOR (EC 3.1.3.2).
GN PHO12 OR YHR215W.

OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favetto A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevisan E., Vaughan K.,
RA Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
VIII";
RL Science 265:2077-2082(1994).

CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN

CC CC ALCOHOL + ORTHOPHOSPHATE.
CC CC -!- INDUCTION: S.CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS
CC CC CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.
CC CC -!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
CC CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC CC
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CC CC
CC CC EMBL; U00029; AAB69729.1; -
CC CC PIR; S48996; S48996.
CC CC HSSP; P34752; 1IHP.
CC CC SGD; S0001258; PHO12.
CC CC InterPro; IPR000360; -
CC CC Pfam; PF00328; acid_phosphat; 1.
CC CC PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
CC CC PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
CC CC Hydrolase; Glycoprotein; Signal; Multigene family.
CC CC SIGNAL 1 17
CC CC BY SIMILARITY.
CC CC CHAIN 18 467
CC CC ACT_SITE 337 75
CC CC NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
CC CC ACT_SITE 337 337
CC CC PROTON DONOR (BY SIMILARITY).
CC CC CARBOHYD 97 97
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 162 162
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 192 192
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 250 250
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 315 315
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 356 356
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 390 390
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 439 439
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 445 445
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 461 461
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC SEQUENCE 467 AA; 52699 MW; BEC606CDF39B845B CRC64;
Query Match 16.7%; Score 389; DB 1; Length 467;
Best Local Similarity 26.4%; Pred. No. 4e-24;
Matches 116; Conservative 63; Mismatches 198; Indels 62; Gaps 12;
QY 17 EISHLWGYSPYFSLADESAISPDVDCRVTFVQVLSRHGARYPTSSAKAYSALIEAI 76
DB 17 EISHLWGYSPYFSLADESAISPDVDCRVTFVQVLSRHGARYPTSSAKAYSALIEAI 76
QY 36 EIFFPLGGGYPYSPGDIYSGISRDLPESCEMKQVMGVRHGERPTYSKAKSMTTWKL 95
DB 36 EIFFPLGGGYPYSPGDIYSGISRDLPESCEMKQVMGVRHGERPTYSKAKSMTTWKL 95
QY 77 QKNATARKGVAFLEK-----TYNYTL-----GADDLTPF-GENQMVNSGKIFYRR 120
DB 77 QKNATARKGVAFLEK-----TYNYTL-----GADDLTPF-GENQMVNSGKIFYRR 120
QY 96 SNYQGFSGALSFNDDEYEFIRDTKNLEMETTLANSVNLNPTGEMNAKRHARDFLAQ 155
DB 96 SNYQGFSGALSFNDDEYEFIRDTKNLEMETTLANSVNLNPTGEMNAKRHARDFLAQ 155
QY 121 YKALARKTVPF-IRASGSDRVIASAEKFIQFQSAKLADPGSQPHQASPVNVLIPGSG 179
DB 121 YKALARKTVPF-IRASGSDRVIASAEKFIQFQSAKLADPGSQPHQASPVNVLIPGSG 179
QY 156 YGVYVENQTSFAVTSNSNRCHDAQYFIDG-----LQDFENISLQ-----TISEAESG 205
DB 156 YGVYVENQTSFAVTSNSNRCHDAQYFIDG-----LQDFENISLQ-----TISEAESG 205
QY 180 YNNYLDHGTCTAFDESELGDDVEANFTALPAIRARLEADLPGLVTLTDEVDVYLMDCP 239
DB 180 YNNYLDHGTCTAFDESELGDDVEANFTALPAIRARLEADLPGLVTLTDEVDVYLMDCP 239
QY 206 ANTLSAHSCPAWDD-DVNDLILKDYTKVLSGIKRLNKENGLNLTSSDANFTFAWCA 264
DB 206 ANTLSAHSCPAWDD-DVNDLILKDYTKVLSGIKRLNKENGLNLTSSDANFTFAWCA 264
QY 240 FDTVARTSDATELSPFCALFTHEWQYDYLQSLGKYYGAGNPLGPAQGVGFANELIA 299
DB 240 FDTVARTSDATELSPFCALFTHEWQYDYLQSLGKYYGAGNPLGPAQGVGFANELIA 299
QY 265 YEINAR-----GYSDICNIFTKDELVSYSQDQDLETYIQTGPGYVVRVSGANLFNASVK 319
DB 265 YEINAR-----GYSDICNIFTKDELVSYSQDQDLETYIQTGPGYVVRVSGANLFNASVK 319
QY 300 RLTHSPVODHTSNHTLDSNPATFPLNATLYADFSDHNTMTISFFALGLYNGTKPLSTTS 359
DB 300 RLTHSPVODHTSNHTLDSNPATFPLNATLYADFSDHNTMTISFFALGLYNGTKPLSTTS 359
QY 320 LLKESEVQDQ-----KWLSTFHTDILNLTITIGIIDDDNNNTAEH 361
DB 320 LLKESEVQDQ-----KWLSTFHTDILNLTITIGIIDDDNNNTAEH 361
QY 360 VESTEEEDGYSASVTVFARAYVEMMQCAEKEPLVRLVLDNRVPLHGCAKDLGRCK 419
DB 360 VESTEEEDGYSASVTVFARAYVEMMQCAEKEPLVRLVLDNRVPLHGCAKDLGRCK 419
QY 362 VPFMENT--PHRSWYVPPQGARVYETKFCQ--SNDTYVRYVINDAVVPIETCSTGPGFSCE 417
DB 362 VPFMENT--PHRSWYVPPQGARVYETKFCQ--SNDTYVRYVINDAVVPIETCSTGPGFSCE 417
QY 420 RDDF-----VEGLSPAR 431
DB 420 RDDF-----VEGLSPAR 431

DB 418 INDFYGYAEKRVAGTDFLK 436
RESULT 6
PPAS_YEAST
ID PPA5_YEAST STANDARD; PRT; 467 AA.
AC P00635;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE REPRESENTABLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (P60).
GN PHO5 OR YBR093C OR YBR0814.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-26.
RA MEDLINE=83168913; PubMed=6300772;
RA Arima K., Oshima T., Kubota I., Nakamura N., Mizunaga T., Toh-E A.;
RT "The nucleotide sequence of the yeast PHO5 gene: a putative precursor
of repressible acid phosphatase contains a signal peptide.";
RL Nucleic Acids Res. 11:1657-1672(1983).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-45.
RA MEDLINE=85037940; PubMed=6093051;
RA Bajwa W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinnen A.;
RT "Structural analysis of the two tandemly repeated acid phosphatase
genes in yeast.";
RL Nucleic Acids Res. 12:7721-7739(1984).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95208357; PubMed=7900426;
RA Mannhaupt G., Stucka R., Ehle S., Vetter I., Feldmann H.;
RT "Analysis of a 70 kb region on the right arm of yeast chromosome II.";
RL Yeast 10:1363-1381(1994).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=87064474; PubMed=3537710;
RA Tait-Kamradt A.G., Turner K.J., Kramer R.A., Elliott Q.D.,
RA Bostian S.J., Thill G.P., Rogers D.T., Bostian K.A.;
RT "Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene
cluster within the acid phosphatase multigene family of Saccharomyces
cerevisiae.";
RL Mol. Cell. Biol. 6:1855-1865(1986).
CC -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O -> AN
CC ALCOHOL + ORTHOPHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- INDUCTION: REPPRESSED BY INORGANIC PHOSPHATE.
CC -!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC
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CC
CC EMBL; V01320; CAA24630.1; -
CC EMBL; X01079; CAA25555.1; -
CC EMBL; X78993; CAA55598.1; -
CC EMBL; Z35962; CAA85046.1; -
CC EMBL; X01080; CAA25556.1; -
CC PIR; S05795; PABYC.
CC PIR; B25241; B25241.
CC HSSP; P34752; 1IHP.
CC SGD; S0000297; PHO5.
CC InterPro; IPR000560; -
CC Pfam; PF00328; acid_phosphat; 1.

[illegible]

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CC -----
CC EMBL; U28658; AAA85503.1; -
CC HSP; P34752; 1HP.
CC InterPro; IPR000560; -
CC Pfam; PF00328; acid_phosphat; 1.
CC PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
CC PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
CC Hydrolyase; Glycoprotein; Signal; Multigene family.
CC SIGNAL 1 22
CC POTENTIAL
CC FT CHAIN 23 468
CC ACT_SITE 84 84
CC ACT_SITE 345 345
CC CARBOHYD 163 163
CC CARBOHYD 196 196
CC CARBOHYD 256 256
CC CARBOHYD 321 321
CC CARBOHYD 360 360
CC CARBOHYD 453 453
CC SEQUENCE 468 AA; 52690 MW; AE5588E27718C2C CRC64;

GN PHYB.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-101; 133-141 AND 376-399.
RX MEDLINE=93371452; PubMed=7916610;
RA Ehrlich K.C., Montalbano B.G., Mullaney E.J., Dischinger H.C. Jr.,
RA Ullah A.H.J.;
RT Identification and cloning of a second phytase gene (phyB) from
RT Aspergillus niger (ficusum).
RL Biochem. Biophys. Res. Commun. 195:53-57(1993).
CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC FROM PHYTATE.
CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
CC D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
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CC -----
CC EMBL; L20567; AAA02934.1; -
CC InterPro; IPR000560; -
CC Pfam; PF00328; acid_phosphat; 1.
CC PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
CC PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
CC Hydrolyase; Glycoprotein; Signal.
CC SIGNAL 1 19
CC CHAIN 20 479
CC ACT_SITE 81 81
CC ACT_SITE 82 82
CC ACT_SITE 337 337
CC CARBOHYD 106 106
CC CARBOHYD 191 191
CC CARBOHYD 227 227
CC CARBOHYD 250 250
CC CARBOHYD 315 315
CC CARBOHYD 425 425
CC CARBOHYD 442 442
CC CARBOHYD 458 458
CC SEQUENCE 479 AA; 52611 MW; 395D4DA2B50DFEC4 CRC64;

Query Match 15.0%; Score 350.5; DB 1; Length 468;
Best Local Similarity 25.5%; Pred. No. 5.3e-21;
Matches 116; Conservative 74; Mismatches 176; Indels 89; Gaps 19;

QY 18 ISHLMGTSPY-----FSLADESAISPDVDDCRVTFVQVLSRRHARGYPTSSASKAY-SALIEAIQKNAT 81
DB 47 LRHL-GSLGPIYINGWGIAESEI-----ESCTIDQAHLLMRHGERYPSTNVGKQLEAL 100
QY 73 IE-AIQKNATAPKGYAFKLTNYTLG-----ADDLTP-----FGENOMVNSGIKRYRYKA 123
DB 101 YOKLLDADVEPTGPLSFFQDYDYFVSDAAWYEQETKGFYSLNTAFDFGTLRLRYDH 160
QY 124 L-----ARKVPIFRASGSDRVIASAEKFIQFQSAKLADPGSQPHOASPVINVIIE- 176
DB 161 LINTSEKKL-SVWAGSQERVVDTAKYFAQGFMSNYTD-----NVEVVALEE 208
QY 177 -GSGYNNTLDHGTCT-----AFESLGDVV-----EANTALFAPAIRARLEADLPGVTL 226
DB 209 EKSOGLNSLTARISCPNYSNHIYKGFDFNDIAERAD-----RLNTLSPGEMI 257
QY 227 TDEDVYVLMDCPFDIVARTSDATELSPCALFTHDEWIQDYDLOSLGKRYGYGAGNPLG 286
DB 258 TADDIPTIALYCGFELNVRGE-----SSFCDLVLSREALLYTAYLRDLGWYVNGNPNLG 312
QY 287 PAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSDHNTMISIFAL 346
DB 313 KTIGYVAN-----ATROLLENTEAD-PRDYPYFSFSDTDLQLQVFTSL 356
QY 347 GLYNGTK-PLUSTSVSIEETDGYASWTVPPFAARYVEMQC--QAEKEPLRVVLNDR 403
DB 357 GLFNVTDLPL-----DQIQFQTSFKSTEIVPMGARILLTERLLCTVEGEKGYVYRTILNDA 411
QY 404 VPLHGCAVDKLGCRKDRDVEGLSFARSGGNWAE 438
DB 412 VFPLSDCSSGPGFSCPLNDYVSRLEALNEDSDFAE 446
RESULT 10
PHYB_ASPNG
ID PHYB_ASPNG STANDARD; PRT; 479 AA.
AC P34756; 1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAKISPHOSPHATE
DE 3-PHOSPHOHYDROLASE B) (3 PHYTASE B) (MYO-INOSITOL HEXAKISPHOSPHATE
DE PHOSPHOHYDROLASE B).

Query Match 14.9%; Score 348.5; DB 1; Length 479;
Best Local Similarity 29.3%; Pred. No. 8e-21;
Matches 119; Conservative 55; Mismatches 169; Indels 63; Gaps 17;
QY 23 CTSPYFSLADESAISPDVDDCRVTFVQVLSRRHARGYPTSSASKAY-SALIEAIQKNAT 81
DB 53 GPYSERSY----GIARDPPGCEVDQVIMVKRGERYPSPSACKSIEEALAKVYSINTT 108
QY 82 AFKGYAFKLTNYTL-----GADDLT-PF-GENOMVNSGIKRYRYKAL--ARKIVPF 131
DB 109 EYKGLAFNDWTYYVVPNECYNAETTSPPYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168
QY 132 TRASGSDRVIASAEKFIQFQSAKLADPGSQPHOASPVINVI--PEGSGYNNTLDHGTCT 190
DB 169 F-SSGVRVIETARKFGEGFFGYN-----YSTNALNIISEVVGADSLTP--TCD 217
QY 191 AFEDSELGDVDEANFTALFAPAIRARLEADLPGVTLTDEDVYVLMDCPFTVARTSDAT 250
DB 218 TDNDQTTCDNLTYYQLPQFKVAA--ARLNSQPNGLMTASDVNLIVMASFELNAR----- 270
QY 251 ELSPFCALFTHDEWIQDYDLOSLGKRYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHT 310
DB 271 PFSNWINAFTQDEWVSFGYVEDLNYYICAGPGDKNMAAVGAVYANASLTLLNQGP----- 325

QY 311 STNHTLSDNATPLNATLYADSHDNTWISIFPAGLY--NGTKPLSTTSVESIETD 368
 DB 326 -----KEAGP-----LFFNFADHTNITPILAAAGLVLPNEDLPL-----DRVAFGNP 367
 QY 369 YSASWTVPFAARAYVEMQCOA-----EKEPLRVLVNDVRVPLHGC 410
 DB 368 YSIGNIVPMGHLTIERLSQATSLSDKGTIVRLVLEAVLPFND 413

RESULT 11
 PHYB_ASAPW STANDARD; PRT; 479 AA.
 AC P34755;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
 GN 3-PHOSPHOHYDROLASE B) (PH 2.5 OPTIMUM ACID PHOSPHATASE).
 OS Aspergillus awamori.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Euriotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=105351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ALK0243;
 RA MEDLINE=94040796; PubMed=8224894;
 RA Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A.,
 RA Miettinen-Oinonen A., Nevalainen H., Rambosek J.A.;
 RT "The cloning and sequencing of the genes encoding phytase (phy) and
 RT pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
 RT awamori.";
 RL Gene 133:55-62(1993).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=99264417; PubMed=10329192;
 RA Kostrewa D., Wyss M., D'Arcy A., van Loon A.P.;
 RT "Crystal structure of Aspergillus niger pH 2.5 acid phosphatase at
 RT 2.4-A resolution.";
 RL J. Mol. Biol. 288:965-974(1999).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
 CC D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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 DR EMBL; L02420; AAA16897.1; -
 DR PIR; JN0890; JN0890.
 DR PDB; 1QFX; 19-APR-00.
 DR InterPro; IPR000560; -
 DR Pfam; PF00328; acid_phosphat; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 479 3-PHYTASE B.
 FT ACT_SITE 82 82 NUCLEOPHILIC ACCEPTOR.
 FT ACT_SITE 337 337 PROTON DONOR.
 FT DISULFID 71 387
 FT DISULFID 128 472
 FT DISULFID 216 441
 FT DISULFID 225 298
 FT DISULFID 413 421

FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .).
 SQ SEQUENCE 479 AA; 52678 MW; 4F8E0F3778CC3B08 CRC64;
 Query Match 14.9%; Score 347.5; DB 1; Length 479;
 Best Local Similarity 29.1%; Pred. No. 9,7e-21;
 Matches 118; Conservative 54; Mismatches 171; Indels 63; Gaps 16;
 QY 23 GYSPYFSLADESAISPDVDDCRVTFVOVLSRHGARIPTSSASK-AYSALTEAIQKNAT 81
 DB 53 GYSERVSY-----GIARDPPTCEVDQVIMVRHGERVPSPSAGKDIEALAKVYSINTT 108
 QY 82 AFKGYAFLKTYNYTL-----GADDLT-PF-GENOMVNSGIKFYRRYKAL--ARKIYPF 131
 DB 109 EYKGDALFLNDWTYYVPNECYNAETSGPYAGLLDAYNHGNDYKARYGHLNGETVVPFF 168
 QY 132 IRASGSDRVIAAEKPIEGFQSAKLADPGSQPHASPVINII-PEGSGYNNNTLDHGTC 190
 DB 169 F-SSGYGRVIETARKFGEGFGYN-----YSTNAALNIISEVANGADSLTP--TCD 217
 QY 191 AFEDSELGDVDEANTALFAPAIRARLEADLPGVTLTDEDVYVLMDCPFDTVARTSAT 250
 DB 218 TDNDQTTCDNLIIYQLPQFKVAA--ARLNSQNPQNMLTASDVYVLMVMAFSEFNAR----- 270
 QY 251 ELSFPFCALFTHDEWIDYDYLQSLGKYGYGAGNPLGPAQGVGFANELLARLTHSPVQDHT 310
 DB 271 PFSNNIAFTQDEWVSFGYVEDLNYCYCAGPCDKNAAVAGAVYANASLTLLNQGPKE--- 327
 QY 311 STNHFLDSNPATFPLNATLYADSHDNTWISIFPAGLY--NGTKPLSTTSVESIETD 368
 DB 328 -----AGSLTFNFAHDTNITPILAAAGLVLPNEDLPL-----DRVAFGNP 367
 QY 369 YSASWTVPFAARAYVEMQCOA-----EKEPLRVLVNDVRVPLHGC 410
 DB 368 YSIGNIVPMGHLTIERLSQATSLSDKGTIVRLVLEAVLPFND 413

RESULT 12
 PPA5_KLULA STANDARD; PRT; 469 AA.
 AC P52289;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
 GN PHO5.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS 2359/152;
 RA Ferminan E.;
 RL Thesis (1995), University of Salamanca, Spain.
 CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
 CC ALCOHOL + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- INDUCTION: REPRESSED BY INORGANIC PHOSPHATE (BY SIMILARITY).
 CC -1- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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 DR EMBL; Z33995; CAA83964.1; -

Db 265 YSECKLFNSVDLNFEEGLDSFSYGMGNSVKWGSIFGCAYANSLSL--RSVENNTQ 322
 QY 312 TNHFLDSNPATFLNATLYADSHDNMTMISIFALGLYNGTKPLSTTSVESIEETDGYSA 371
 Db 323 -----OVFFAFTHDANIIPVETALGFDTDPENDLPTSYOVHSHSKMA 366
 QY 372 SWTVFAARAYVEMMOCAEKLPLVRLVNDVRVPLHGC 410
 Db 367 SEFVPAGNLITELFQCEDSKY-YVRHLNVEVFLPLSDC 404

RESULT 14

PPA2_SCHPO STANDARD; PRT; 463 AA.
 AC Q01682;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 GN PH04 OR SPBC428.03C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-30.
 RX MEDLINE=91064763; PubMed=2249257;
 RA Yang J., Schweingruber M.E.;
 RT The structural gene coding for thiamin-repressible acid phosphatase
 in Schizosaccharomyces pombe.
 RL Curr. Genet. 18:269-272(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M., Rajandream M.A., Barrell B.G., Baker S., Mungall K.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY DEPHOSPHORYLATE THIAMINE PHOSPHATES.
 CC -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
 CC ALCOHOL + ORTHOPHOSPHATE.
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- INDUCTION: REPRESSED BY THIAMINE.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X56939; CAA40258.1; -;
 DR EMBL; AL034382; CAA22278.1; -;
 DR PIR; S14119; S14119.
 DR InterPro; IPR000560; -;
 DR Pfam; PF00328; acid_phosphat; 1.
 DR PROSITE; PS00616; HTS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HTS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Cell wall; Signal.
 FT SIGNAL 1
 FT CHAIN 18
 FT ACT_SITE 19 463
 FT ACT_SITE 69 69
 FT ACT_SITE 340 340
 FT CARBOHYD 98 98
 FT CARBOHYD 104 104
 FT CARBOHYD 186 186
 FT CARBOHYD 221 221
 FT CARBOHYD 251 251
 FT CARBOHYD 328 328
 FT CARBOHYD 433 433
 FT CARBOHYD 439 439
 FT ACT_SITE 69 69
 FT ACT_SITE 340 340
 FT CARBOHYD 98 98
 FT CARBOHYD 104 104
 FT CARBOHYD 186 186
 FT CARBOHYD 221 221
 FT CARBOHYD 251 251
 FT CARBOHYD 328 328
 FT CARBOHYD 433 433
 FT CARBOHYD 439 439

THIAMINE-REPRESSIBLE ACID PHOSPHATASE.
 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 PROTON DONOR (BY SIMILARITY).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 463 AA; 52118 MW; F48EAF8BB6B234A CRC64;

Query Match 11.9%; Score 278.5; DB 1; Length 463;
 Best Local Similarity 25.5%; Pred. No. 3.7e-15;
 Matches 108; Conservative 65; Mismatches 187; Indels 63; Gaps 15;
 QY 20 HLWGTYS----PYFLADESAISPDVDDCRVTFVQVLSRHRGARYPT--SSASKAYS-- 71
 Db 35 HL-GTISVYHEPYF-----NGPTTSFPESCAIKQVHLLQRHGSRNPTGDDTATDVSSAQY 88
 QY 72 -----LIEAIQKNATAFKGYAFLKTYNYTL---GADDLTPFGENQMVNSGIKYYR 120
 Db 89 IDIFONKLLNGSIPVNFSPENPLYFVKHMTFVKAENADQLSSSGRIELFDLGRQVFER 148
 QY 121 YKALARKIVPPIRASGDRVIASAEKFTGQSAKLADPGSQPHQASPVINVIPE--GS 178
 Db 149 YVELFDTDVYDINTAAQQRVVDSAEWFSYMGFGDDMNKTN-----FVLPEDDSA 199
 QY 179 GYNNTLDHGTCTAFEDSELGDD-VEANFTA---LFAPAIRARLEADL-PGVTLLDEDDVY 233
 Db 200 GANSLAWYSCPVVEDNNIDNTTAAHTSWRVFLKPIANLNKYNFDSGYNLTVSVRS 259
 QY 234 LMDMCPDPTVARTSDELSPFALFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGF 293
 Db 260 LYICVVEIALRDN-----SDFCSLFTPSEFLNFEYDSDLDYAYWGGPASEWASTLGAY 314
 QY 294 ANELIARLTHSPVQDHTSTNHTLDSNPATFLNATLADFSDHNTMISIFALGLYNGTK 353
 Db 315 VNNLANL-----RKGVNNSDRK-----VLAFTHDSQIIPVEAALGFFPDIT 358
 QY 354 PLSTTSVESIEETDGYASWTVPPFAARAYVEMMOCAEKLPLVRLVNDVRVPLHGC 413
 Db 359 PEHPLPTDKNIFTYSLKTSFVFPAGNLITELFLC-SDNKYYVRLHVNQVYPLTDCGYG 417
 QY 414 KLG 416
 Db 418 PSG 420

RESULT 15

PPAX_CAEEL STANDARD; PRT; 755 AA.
 AC Q09549; Q17843;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE PUTATIVE ACID PHOSPHATASE F26C11.1 (EC 3.1.3.2).
 GN F26C11.1
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Matthews P., Lloyd C.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
 CC ALCOHOL + ORTHOPHOSPHATE.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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 CC -----

DR EMBL; 247072; CAA87370.1; -;
 DR EMBL; 254342; CAA87370.1; JOINED.

DR EMBL; Z54342; CAA91156.1; -
DR EMBL; Z47072; CAA91156.1; JOINED.
DR WormPep; F26C11.1; CE05732.
DR InterPro; IPR000560; -
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hypothetical protein; Hydrolase.
FT ACT_SITE 356 356 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 399 399 BY SIMILARITY.
FT ACT_SITE 636 636 PROTON DONOR (BY SIMILARITY).
FT DISULFID 702 708 BY SIMILARITY.
SQ SEQUENCE 755 AA; 87783 MW; E7F3050115A235EB CRC64;

Query Match 5.6%; Score 130; DB 1; Length 755;
Best Local Similarity 21.9%; Pred. No. 0.0085;
Matches 90; Conservative 55; Mismatches 130; Indels 136; Gaps 22;

QY 31 LADESAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALEIAIQKNATAFKGYAFL 90
|| | : | | : | | : | | | | | : | | | |
Db 332 LAIEKSFMEV-DNMKEFVQIWRHGR-----SALEGLFPISEKNWTFGG----- 378
QY 91 KYNYTLGADDTLPFGENQMVNSGKIFYRY-----KALARKIVFFIRASGSDRVI 141
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | |
Db 379 -----GLGELTPMGSENNLGTIFRRRYVEDQQLSHRYAAKEI--YIRSTNLNRTI 429
QY 142 ASAEKFIQFSQAKLADPGSQPHQASPVINVIIPGSGYNTLD--HG----- 187
|| | : | | : | | : | | | | | : | | | |
Db 430 ISANSLYG-----MPPPGAW-----NI---OCVDYPNDVWQOQFTFIPVHVDGID 473
QY 188 -----TCTAFED-----SELGDDVEANFTALFAPAIRARLEADLPGLTLDVYVL 234
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 474 QCABAQLCNCRRFQELQEKWAEI-DEKKNATVAMI--ALNRRVAA---FYNVTDQP----- 523
QY 235 MDMCPDPTVARTSDATELSPPC-----ALFTHDEWIOYDYLQSLGKYG-----YG 280
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 524 -----EKNRYTDANK-----CORNWFNDTMYQQLPWYNEDLYNEAQRTYAPFKRFTGN 573
QY 281 AGNP-----LGPACGVGFANELIARLTHSPVODHTSTNHTLD--SNPATFFPLN 326
|| | : | | : | | : | | | | | : | | | |
Db 574 FGNPKFSIVDGDIPQEVSTLQGGPLLNEIFERGREKIRCVADAENCSIDYLPKLF--- 630
QY 327 ATLYADFSDHNTWISTFFALGYNGTKPLSTSVESIEETDGYASWTVPF 377
|| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 631 ---YAYSSHDLVYALLVTLGI-----TDVVKTVDGWPDTSSSLTIEY 670

Search completed: October 16, 2001, 17:57:29
Job time: 567 sec

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	1837	78	6	467	1	JN0889	3-phytase (EC 3.1.1.
2	1833	78.5		467	1	JN0656	3-phytase (EC 3.1.1.
3	1814	77.7		441	1	JN0482	3-phytase (EC 3.1.1.
4	389	16.7		467	2	S53476	acid phosphatase (
5	389	16.7		467	2	S48996	acid phosphatase (
6	381	16.3		467	1	PABYC	acid phosphatase (
7	380	16.3		467	1	PABYCC	acid phosphatase (
8	354	15.2		468	2	S52495	acid phosphatase h
9	350.5	15.0		468	2	JC4285	acid phosphatase h
10	347.5	14.9		479	1	JN0890	acid phosphatase (
11	346.5	14.8		479	1	JN0715	acid phosphatase (
12	297.5	12.7		463	2	T39929	3-phytase (EC 3.1.1.
13	297	12.7		453	1	A25326	thiamin-repressibl
14	278.5	11.9		463	2	SI4119	acid phosphatase (
15	149	6.4		465	2	JB0369	acid phosphatase (
16	145.5	6.2		468	2	A62333	histidine acid pho
17	130	5.6		755	2	T19218	hypothetical prote
18	124.5	5.3		421	2	SI4742	acid phosphatase h
19	119	5.1		449	2	T15933	acid phosphatase (
20	114.5	4.9		423	2	A33395	hypothetical prote
21	112	4.8		721	2	T27570	acid phosphatase (
22	106.5	4.6		380	2	T16883	hypothetical prote
23	104	4.5		354	2	T21241	hypothetical prote
24	103	4.4		1225	2	T16346	hypothetical prote
25	102.5	4.4		423	1	S06167	hypothetical prote
26	101	4.3		452	2	T20556	acid phosphatase (
27	101	4.3		563	2	S33957	hypothetical prote
28	100.5	4.3		730	2	T16455	coat protein gamma
29	98.5	4.2		381	2	JH0152	acid phosphatase (

Db 267 DTISTSTVDTKLSFPDCLTFHDEWHYDLOSLKYYKHGAGNPLGPTGGVGYANELLAR 326
QY 301 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSDHNTMTISFFALGLYNGTKPLSTTSV 360
Db 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTMTISFFALGLYNGTKPLSTTV 386
QY 361 ESTEETDGYASWTVPFAARAYVEMMQCAKEPLVRLVNDVRVPLHGCACVCKLGRCKR 420
Db 387 ENITQTDGFSASWTVPFASRLYVEMMQCAEQEPLVRLVNDVRVPLHGCIDALGRCTR 446
QY 421 DDFVEGLSFARSGGNWAECEFA 441
Db 447 DSFVRGLSFARSGGDWAECSA 467
RESULT 2
JN0656
3-phytase (EC 3.1.3.8) A precursor - Aspergillus niger
N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phya protein
C:Species: Aspergillus niger
C:Date: 03-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999
C:Accession: JN0656; S28456
R:van Hartingsveldt, W.; van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk, M.
A:M.J.J.
Gene 127, 87-94, 1993
A:Title: Cloning, characterization and overexpression of the phytase-encoding gene (phyA)
A:Reference number: JN0656; MUID:93252284
A:Accession: JN0656
A:Molecule type: DNA
A:Residues: 1-467 <VAN>
A:Cross-references: GB:216414; NID:q2392; PIDN:CAA78904.1; PID:g2393
A:Experimental source: strain NRRL3135
A:Note: parts of the sequence, including the amino end of the mature protein, were confi
C:Comment: This enzyme catalyzes the hydrolysis of phytic acid into myo-inositol and ino
C:Genetics:
A:Gene: phya
A:Introns: 15/2
C:Superfamily: yeast acid phosphatase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-467/Product: 3-phytase A #status experimental <WAT>
F:27,59,105,120,207,339,352,376,388/Binding site: carbohydrate (Asn) (covalent) #sta
F:81,361/Active site: Arg, His #status predicted
F:82/Active site: His (phosphohistidine intermediate) #status predicted
Query Match 78.5%; Score 1833; DB 1; Length 467;
Best Local Similarity 77.3%; Pred. No. 1.3e-144;
Matches 341; Conservative 39; Mismatches 61; Indels 0; Gaps 0;
QY 1 NSHSCDVTGQYQCFPEISHLMGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
Db 27 NOSSCDTVDGQYQCFSETSHLMGQYAFESLANESVISPVPACRCRVTFQVLSRHGARY 86
QY 61 PTSSASKAYSALIEIAOKNAFAFKGYAFKTYNTYLGADDLTPFGNQMVNSGKIKYRR 120
Db 87 PTDSKGGKYSALIEIQONATTFDGKYAFKTYNSLGADDLTPFGQELVNSGKIKYOR 146
QY 121 YKALARKIVPFRASGSDRVTAESAKEFEGFQSAKLADPGSQHQAQSPVNIIVEGSGY 180
Db 147 YESLRTNIVPFRIRSSGSRVTAESKFFEGFQSTKLKDPRAQCSQSPKIDVISEASS 206
QY 181 NNTLDHGTCTAFEDSELADGVEANFTALFAPARLEADLPGLVTLDEDDVYVLMDCPF 240
Db 207 NNTLDPGCTCFEDELADTVEANFTATFVPSIRQLENDLSGVTLTDEVTYVLMDCSF 266
QY 241 DTAVTSATLSPFCALFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFANELLAR 300
Db 267 DTISTSTVDTKLSFPDCLTFHDEWHYDLOSLKYYKHGAGNPLGPTGGVGYANELLAR 326
QY 301 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSDHNTMTISFFALGLYNGTKPLSTTSV 360
Db 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTMTISFFALGLYNGTKPLSTTV 386
QY 361 ESTEETDGYASWTVPFAARAYVEMMQCAKEPLVRLVNDVRVPLHGCACVCKLGRCKR 420
Db 387 ENITQTDGFSASWTVPFASRLYVEMMQCAEQEPLVRLVNDVRVPLHGCIDALGRCTR 446
QY 421 DDFVEGLSFARSGGNWAECEFA 441
Db 447 DSFVRGLSFARSGGDWAECSA 467

QY 361 ESTEETDGYASWTVPFAARAYVEMMQCAKEPLVRLVNDVRVPLHGCACVCKLGRCKR 420
Db 387 ENITQTDGFSASWTVPFASRLYVEMMQCAEQEPLVRLVNDVRVPLHGCIDALGRCTR 446
QY 421 DDFVEGLSFARSGGNWAECEFA 441
Db 447 DSFVRGLSFARSGGDWAECEFA 467
RESULT 3
JN0482
3-phytase (EC 3.1.3.8) A - Aspergillus ficum
N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phya protein
C:Species: Aspergillus ficum
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
C:Accession: JN0482; PN0023
R:Ullah, A.H.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 192, 747-753, 1993
A:Title: Aspergillus ficum phytase: Complete primary structure elucidation by chemic
A:Reference number: JN0482; MUID:93249451
A:Accession: JN0482
A:Molecule type: protein
A:Residues: 1-441 <ULL>
A:Note: authors state that the 9 Asn followed by Thr or Ser after an intervening resi
R:Ullah, A.H.J.; Cummins, B.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 178, 45-53, 1991
A:Title: Cyclohexanedione modification of arginine at the active site of Aspergillus
A:Reference number: PN0023; MUID:91298982
A:Accession: PN0023
A:Molecule type: protein
A:Residues: 48-70 <UL2>
C:Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phyt
C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; glycoprotein; phosphohistidine; phosphoprotein; ph
F:4,36,82,97,184,207,316,329,353,365/Binding site: carbohydrate (Asn) (covalent) #sta
F:58,338/Active site: Arg, His #status predicted
F:59/Active site: His (phosphohistidine intermediate) #status predicted
Query Match 77.7%; Score 1814; DB 1; Length 441;
Best Local Similarity 77.2%; Pred. No. 4.6e-143;
Matches 338; Conservative 39; Mismatches 61; Indels 0; Gaps 0;
QY 1 NSHSCDVTGQYQCFPEISHLMGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
Db 4 NOSSCDTVDGQYQCFSETSHLMGQYAFESLANESVISPVPACRCRVTFQVLSRHGARY 63
QY 61 PTSSASKAYSALIEIAOKNAFAFKGYAFKTYNTYLGADDLTPFGNQMVNSGKIKYRR 120
Db 64 PTDSKGGKYSALIEIQONATTFDGKYAFKTYNSLGADDLTPFGQELVNSGKIKYOR 123
QY 121 YKALARKIVPFRASGSDRVTAESAKEFEGFQSAKLADPGSQHQAQSPVNIIVEGSGY 180
Db 124 YESLRTNIVPFRIRSSGSRVTAESKFFEGFQSTKLKDPRAQCSQSPKIDVISEASS 183
QY 181 NNTLDHGTCTAFEDSELADGVEANFTALFAPARLEADLPGLVTLDEDDVYVLMDCPF 240
Db 184 NNTLDPGCTCFEDELADTVEANFTATFVPSIRQLENDLSGVTLTDEVTYVLMDCSF 243
QY 241 DTAVTSATLSPFCALFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFANELLAR 300
Db 244 DTISTSTVDTKLSFPDCLTFHDEWHYDLOSLKYYKHGAGNPLGPTGGVGYANELLAR 303
QY 301 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSDHNTMTISFFALGLYNGTKPLSTTSV 360
Db 304 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTMTISFFALGLYNGTKPLSTTV 363
QY 361 ESTEETDGYASWTVPFAARAYVEMMQCAKEPLVRLVNDVRVPLHGCACVCKLGRCKR 420
Db 364 ENITQTDGFSASWTVPFASRLYVEMMQCAEQEPLVRLVNDVRVPLHGCIDALGRCTR 423
QY 421 DDFVEGLSFARSGGNWAE 438

acid phosphatase (EC 3.1.3.2) repressible, precursor - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: acid phosphatase PHO5; protein YBR0814; protein YBR093c
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 19-Feb-1984 #sequence_revision 30-Sep-1991 #text_change 12-Nov-1999
 C:Accession: S05795; A38792; S48260; S45961; A00777; A38793; S41855; B25241; A25367; A27
 R: Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A. M.; Hinnen, A.
 Nucleic Acids Res. 12, 7721-7739, 1984
 A:Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
 A:Reference number: S05794; MUID: 85037940
 A:Accession: S05795
 A:Molecule type: DNA
 A:Residues: 1-467 <BAJ>
 A:Cross-references: EMBL:X01079; NID:g4162; PIDN:CAA25555.1; PID:g758282
 A:Note: the authors translated the codon TAC for residue 272 as Thr
 A:Accession: A38792
 A:Molecule type: protein
 A:Residues: 18-45 <BAJ2>
 R: Mannhaupt, G.; Stucka, R.; Ehnlé, S.; Vetter, I.; Feldmann, H.
 Yeast 10, 1363-1381, 1994
 A:Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
 A:Reference number: S48255; MUID: 95208357
 A:Accession: S48260
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-467 <MAN>
 A:Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55598.1; PID:g476051
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, April 1994
 R: Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
 submitted to the Protein Sequence Database, August 1994
 A:Reference number: S45927
 A:Accession: S45961
 A:Molecule type: DNA
 A:Residues: 1-467 <FE2>
 A:Cross-references: EMBL:Z35962; NID:g536364; PIDN:CAA85046.1; PID:g536365; GSPDB:GN0000
 R: Arima, K.; Oshima, T.; Kubota, I.; Nakamura, N.; Mizunaga, T.; Toh-e, A.
 Nucleic Acids Res. 11, 1657-1672, 1983
 A:Title: The nucleotide sequence of the yeast PHO5 gene: a putative precursor of repress
 A:Reference number: A00777; MUID: 83168913
 A:Accession: A00777
 A:Molecule type: DNA
 A:Residues: 1-35, 'Y', 37-129, 'G', 131-293, 'Q', 295-445, 'V', 447-461, 'DT', 464-465, 'K', 467 <AR
 A:Cross-references: EMBL:V01320; NID:g4158; PIDN:CAA24630.1; PID:g4159
 A:Accession: A38793
 A:Molecule type: protein
 A:Residues: 18-26, 'X', 28 <ARI2>
 R: Meyhack, B.; Bajwa, W.; Rudolph, H.; Hinnen, A.
 EMBO J. 1, 675-680, 1982
 A:Title: Two yeast acid phosphatase structural genes are the result of a tandem duplicat
 A:Reference number: S41855; MUID: 84236032
 A:Accession: S41855
 A:Molecule type: DNA
 A:Residues: 1-30, 'T', 32-51, 'S', 53-75 <MEV>
 R: Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, C
 Mol. Cell. Biol. 6, 1855-1865, 1986
 A:Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within
 A:Reference number: A93074; MUID: 87064474
 A:Accession: B25241
 A:Molecule type: DNA
 A:Residues: 1-44 <TAI>
 R: Bergman, L.W.
 Mol. Cell. Biol. 6, 2298-2304, 1986
 A:Title: A DNA fragment containing the upstream activator sequence determines nucleosome
 A:Reference number: A25367; MUID: 87064526
 A:Accession: A25367
 A:Molecule type: DNA
 A:Residues: 1-2, 'Y', 4-43, 'T', 45-51 <BER>
 R: Silve, S.; Monod, M.; Hinnen, A.; Hagenauer-Tsapis, R.
 Mol. Cell. Biol. 7, 3306-3314, 1987
 A:Title: The yeast acid phosphatase can enter the secretory pathway without its N-termin
 A:Reference number: A27774; MUID: 88038886
 A:Accession: A27774
 A:Molecule type: DNA

A:Residues: 1-51, 'S', 53-60 <SIL>
 A:Cross-references: GB:M17306

C:Genetics:

A:Gene: SGD:PHO5; MIPS:YBR093c

A:Cross-references: SGD:S0000297; MIPS:YBR093c

A:Map position: 2R

A:Note: YBR093c

C:Superfamily: yeast acid phosphatase

C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydr

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-467/Product: acid phosphatase, repressible #status experimental <MAT>

F:75/Active site: His (phosphohistidine intermediate) #status predicted

F:97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (co

F:337/Active site: His #status predicted

Query Match 16.3%; Score 381; DB 1; Length 467;

Best Local Similarity 25.8%; Pred. No. 9.1e-24;

Matches 113; Conservative 59; Mismatches 194; Indels 72; Gaps 13;

QY 23 GTYSPYFSLADESAISDPDPCRVTFVQLSRHGARYPTSSASKAYSALIEAIQKNATA 82

Db 42 GGAGPYYSFGDYGISRLDPGCEMKQLQWGRHGERYPVSLAKTIKSTWYKLSNVTRO 101

QY 83 PKGYAFLEK-TYNTVLGADD-----LTPF-GENQVNSGIKPYRYKALAR 126

Db 102 FNGSLFLNDDYEFIRDDDDLEMETTFANSDDDVLPYTGEMNAKRHARDFLAQYGYWE 161

QY 127 KIVPF-IRASGSDRVASAEKRFISGFQSAKLADPGSQPHQASPVINVII-----PEGSYG 180

Db 162 NOTSFVFTSNKROHDTAQYFIDGL-----GDQ-----FNITLQIVSEASAGA 206

QY 181 NNTLDHGTCTAFESSELGDDVEANFTALFAPAIRARLEADLPVTLTDEDDVYLMDCPF 240

Db 207 NTLSCNCSAPW-DYDANDDIVNEYDTYLLDDIAKRLNKENKGLNSTDASTLFSWCAF 265

QY 241 DTVARTSDATELSPCALFTHDEWLOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 300

Db 266 EV-----NAKGYSDVCDIFTKDELVHYSYQDLHTYHEGPGYDIKISVGNLNFASVKL 320

QY 301 LTHSPVQDHTSNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 360

Db 321 LKQSEIQDQ-----KWLSTHTDILNLTAGIIDDKNNLTAEV 362

QY 361 ESIEETDGYASWTVFFAARAYVEMMOCAKEPLRVLVNDVRVPLHGCAVDKLGCKR 420

Db 363 PFMGNT--FHRSWYVPGQARVYTEKFQC--SNDTVRYVINDAVVPIETCTGPGFGSCEI 418

QY 421 DDF-----VGLSFA 431

Db 419 NDFDYAEKRVAGTDFLK 436

RESULT 7

PAYCC

acid phosphatase (EC 3.1.3.2) precursor, constitutive - yeast (*Saccharomyces cerevisi*

N:Alternate names: acid phosphatase PHO3; protein YBR0813; protein YBR092c

C:Species: *Saccharomyces cerevisiae*

C:Date: 30-Sep-1991 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999

C:Accession: S48259; S45960; S05794; A25241; S44674

R: Mannhaupt, G.; Stucka, R.; Ehnlé, S.; Vetter, I.; Feldmann, H.

Yeast 10, 1363-1381, 1994

A:Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.

A:Reference number: S48255; MUID: 95208357

A:Accession: S48259

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-467 <MAN>

A:Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g476050

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994

R: Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.

submitted to the Protein Sequence Database, August 1994

A:Reference number: S45927

A:Accession: S45960
A:Molecule type: DNA
A:Residues: 1-467 <PE2>
A:Cross-references: EMBL:Z35961; NID:g536362; PIDN:CAA85045.1; PID:g536363; GSPDB:GN0000
R:Bayja, W.; Meynack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A:Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A:Reference number: S05794; MUID:85037940
A:Accession: S05794
A:Molecule type: DNA
A:Residues: 1-218, 'MKT', 222-467 <BAU1>
A:Cross-references: EMBL:X01080; NID:g4148; PIDN:CAA25557.1; PID:g758281
A:Note: the authors translated the codon AAT for residue 134 as Asp and TAC for residue
R:Tait-Kanrad, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G.
Mol. Cell. Biol. 6, 1855-1865, 1986
A:Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within
A:Reference number: A93074; MUID:87064474
A:Accession: A25241
A:Molecule type: DNA
A:Residues: 1-44 <TAI>
C:Genetics:
A:Gene: SGD:PHO3; MIPS:YBR092C
A:Cross-references: SGD:S0000296; MIPS:YBR092C
A:Map position: 2R
C:Superfamily: yeast acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-467/Product: acid phosphatase, constitutive #status predicted <MAT>
F:75/Active site: His (phosphohistidine intermediate) #status predicted
F:97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (covalent)
F:337/Active site: His #status predicted

Query Match 16.3%; Score 380; DB 1; Length 467;
Best Local Similarity 26.3%; Pred. No. 1.1e-23;
Matches 114; Conservative 61; Mismatches 196; Indels 62; Gaps 11;
QY 23 GTYSPYSLADESAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATA 82
Db 42 GGAGPYFSPGYSRDLPEGCKMLQMLARHGERYPTYSKATINKTWYKLSNYTRQ 101
QY 83 FKGYAFLLK-TYNYTLGADD-----LTPF-GENOMVNSGIKRYRYKALAR 126
Db 102 FNGSLFLNDYEFFIRDDDDLEMTTFANSNDVNLNPTGEMDAKRHAREFLAQYGYMFE 161
QY 127 KIVPF-IRASGSDRVIASAEKFIQFQSAKLADPGSQPHQASPVINVIPEGSGVNTLD 185
Db 162 NOTSPPIFAASSERVHDTAQVFDGL-----GDQFNISLQTVSEAMSAGA---NTLS 210
QY 186 HGTCTAFEDSELGDDVEANFTALFAPARLEADLPGLVTLTDEVVYLMDCPPFTVAR 245
Db 211 AGNACPGWDEANDDILDKYDTTLDLDAKRLNKENKGLNLSKDNATLFAWCAYELNAR 270
QY 246 TSDATLSPFCALFTHDEWIDYQLQSLGKYGYGAGNPLGPAQGVGFANELIARLTHSP 305
Db 271 -----GYSDVCDIFTEDELRYSGQDILVSFYQDGVDMTRSGANLFLNATLKLKQSE 325
QY 306 VQDHTSTNHTLDSNPATPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEE 365
Db 326 TQD-----LKVLSFTHTDILNLTTLTAGIIDDKNLTAEVYVPPGN 367
QY 366 TDGYSASWTVPFAARAYVEMMOCAEPLRVLVNDRVPLVPLHGCVAIDKGRKRDFF-- 423
Db 368 T--FHKSIVYVQGARVTEKEFQC---SNDTVYRVYVINDAVVPIETCSTGPGFSCEINDFYD 423
QY 424 -----VEGLSFAR 431
Db 424 YAEKRVAGTDFLK 436

RESULT 8

S52495

acid phosphatase homolog YDL024c - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein D2815
C:Species: Saccharomyces cerevisiae
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C:Accession: S52495; S67356
R:Andre, B.; Vissers, S.; Urrestarazu, L.
submitted to the EMBL Data Library, February 1995
A:Description: The sequence of a 42 kb segment located on the left arm of chromosome
A:Reference number: S52492
A:Accession: S52495
A:Molecule type: DNA
A:Residues: 1-468 <ANI>
A:Cross-references: EMBL:Z48432; NID:g683669; PIDN:CAA88335.1; PID:g683673
R:Urrestarazu, L.A.; Andre, B.; Vissers, S.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67535
A:Accession: S67556
A:Molecule type: DNA
A:Residues: 1-468 <URR>
A:Cross-references: EMBL:Z74072; NID:g1430996; PIDN:CAA98583.1; PID:g1430997; MIPS:YD
A:Experimental source: strain S288C
C:Genetics:
A:Map position: 4L
C:Superfamily: yeast acid phosphatase

Query Match 15.2%; Score 354; DB 2; Length 468;
Best Local Similarity 25.9%; Pred. No. 1.6e-21;
Matches 114; Conservative 63; Mismatches 183; Indels 80; Gaps 14;
QY 23 GTYSPYSLADESAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATA 82
Db 43 GGSAPYFSPFANYGIPDTDPEGCRLTQVMIGRHGERYPTRSEAKDIFEVWYKISNYTK 102
QY 83 FKGYAFLLK-TYNYTL-----GADDLTFP-GENOMVNSGIKRYRYKALAR 126
Db 103 YEGSLFLNNGYEFFIDLESLEMETTLQNSIDVNLNPTGEMNAKRHAREFLAKYKGLME 162
QY 127 KIVPF-IRASGSDRVIASAEKFIQFQSAKLADPGSQPHQASPVINVIPEGSG 179
Db 163 NCTNFIPTTNSKRIYTAQVFAEALGDGFGNISLQTLSENSS-----SG 206
QY 180 YNNTLDHGTCTAFEDSELGDDVEANFTALFAPARLEADLPGLVTLTDEVVYLMDCMP 239
Db 207 ANLIAKSSCPNM-NSNANDILMSYSDYLENISDRLENKGLNLSRDKDAALFSWCA 265
QY 240 FDTVARTSDATELSPFCALFTHDEWIDYQLQSLGKYGYGAGNPLGPAQGVGFAN---E 296
Db 266 FEL-----NAKGYSNICDIFSAELIHYSETDITSFYQNGPGYKLLKISIGANLFPATVK 320
QY 297 LIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADFSHDNTMISIFFALGLYNGTKPLS 356
Db 321 LIQSAH-----LDQKVLSTHTDILNLTTLTAGLIDDTNLT 359
QY 357 TTSVESIEETDGYASWTVPFAARAYVEMMOCAEPLRVLVNDRVPLVPLHGCVAIDKLG 416
Db 360 TNHVPRDHS--YHRSWYIQQGARVTEKEFQC---SNDTVYRVYVINDAVVPIESCSPGPF 415
QY 417 RCKRDDFE-----GLSF 429
Db 416 SCEEGTFYEVAKDRLRGVSF 435

RESULT 9

JC4285

acid phosphatase (EC 3.1.3.2) precursor - yeast (Pichia pastoris)

N:Alternate names: orthophosphoric monoester phosphohydrolase (acid optimum); Pho

C:Species: Pichia pastoris

C:Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 29-Oct-1999

C:Accession: JC4285

R:Payne, W.E.; Gannon, P.M.; Kaiser, C.A.

Gene 163, 19-26, 1995

A:Title: An inducible acid phosphatase from the yeast Pichia pastoris: Characterizati

C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-479/Product: 3-phytase #status predicted <MAT>
F;81,337/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 14.9%; Score 347.5; DB 1; Length 479;
Best Local Similarity 29.1%; Pred. No. 5.8e-21;
Matches 118; Conservative 54; Mismatches 171; Indels 63; Gaps 16;

QY 23 GTVSPYFLADESAISPDVDDCRVTFVQVLSRHGARYPTTSASK-AYSALIDAIKKNAT 81
DB 53 GPYSERYSY---GIARDPPTSCVEVDQVINVKRGERYPSPSACKDIEALAKVYSINTT 108

QY 82 AFKGYAFLKTYNYTL-----GADLT--PF-GENOMVNSGIKIFYRYKAL--ARKIVPF 131
DB 109 EYKGLAFLNDWTYVNPCEYNAETTSQPYAGLLDYNHNDYKARYGHLWNGETVVPF 168

QY 132 IRASGSDRVIASAEKTEGFSQAKLADPGSOPHOASPVINVII-PEGSGYNNLTDHGCTC 190
DB 169 F-SSGGRVIEIETARKFGEFGYN-----YSTNAALNLISESEVMGADSLTP--TCD 217

QY 191 AFDESELGDDVEANFTALFAPAIRARLEADLPVTLDEDDVYILMDMCPDPTVARTSDAT 250
DB 218 TDNDOTCCDNLTYQLPOPKVAA--ARLNSQNPQGNLTASDVYINLVMWASFELNAR----- 270

QY 251 ELSFPCALFTHEIDYQVLOSGLKYYGAGNPLGPAOGVGFANELIARLTHSPVODHT 310
DB 271 PFSWNINAFQDEWVSFGYVEDLNYCYCAGPGDKNMAAGVAVANASITLLNOGPKF--- 327

QY 311 STNHTLDSNPATFPLNATLYADFSHNTMISIFFALGLY--NGTKPLSTTSVSEIETDG 368
DB 328 -----AGSLFENFAHNTITPILAAAGLVLPNEDLPL-----DRVAFGNP 367

QY 369 YSASWTVPFAARAYVEMMQCOA-----EKEPLRVLVNDRVVPLHCC 410
DB 368 YSIGNIVPMGGHLTIERLSQATLSDEGTYYRVLVNEAVLPFNDC 413

RESULT 11
JN0715
3-phytase (EC 3.1.3.8) B precursor - Aspergillus ficuum
N:Alternate names: pH 2.5-Optimum acid phosphatase
C:Species: Aspergillus ficuum
C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
C:Accession: JN0715; PNO594; PNO460
R:Ehrlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J
Biochem. Biophys. Res. Commun. 195, 53-57, 1993
A:Title: Identification and cloning of a second phytase gene (phyB) from Aspergillus
A:Reference number: JN0715; MUID:93371452
A:Accession: JN0715
A:Molecule type: DNA
A:Residues: 1-479 <EHR>
A:Cross-references: GB:L20567
A:Accession: PNO594
A:Molecule type: protein
A:Residues: 20-101;133-146;376-399 <EH2>
R:Ullah, A.H.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 192, 754-759, 1993
A:Title: Identification of active-site residues in Aspergillus ficuum extracellular p
A:Reference number: PNO460; MUID:93249452
A:Accession: PNO460
A:Molecule type: protein
A:Residues: 65-66,68-93 <ULL>
C:Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.3.2),
C:Genetics:
A:Gene: phyB
A:Introns: 261/1; 300/2; 335/2
C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph

A:Reference number: JC4285; MUID:96001238
A:Accession: JC4285
A:Molecule type: DNA
A:Residues: 1-468 <PAV>
A:Cross-references: GB:U286658; NID:g881955; PIDN:AAA85503.1; PID:g881956
A:Experimental source: GS115
C:Genetics:
A:Gene: pho1
C:Superfamily: yeast acid phosphatase
C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydroly
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-468/Product: acid phosphatase #status predicted <MAT>
F;84/Active site: His (phosphohistidine intermediate) #status predicted
F;163,196,256,321,360,453/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;345/Active site: His #status predicted

Query Match 15.0%; Score 350.5; DB 2; Length 468;
Best Local Similarity 25.5%; Pred. No. 3.2e-21;
Matches 116; Conservative 74; Mismatches 176; Indels 89; Gaps 19;

QY 18 ISHLWCTSPY-----FSLADESAISPDVDDCRVTFVQVLSRHGARYPTTSASKAYSAL 72
DB 47 LRHL-CGLGPGYICNGWGAESIEI-----ESCTIDQAHLLMRHGERYPSTNVGKQLEAL 100

QY 73 IE-AIQKNATAFKGYAFLKTYNYTLG-----ADLTLP---FGENOMVNSGIKIFYRYKA 123
DB 101 YOKLLDADVEVPTGPLSFQDYDYFVSDAAWYEQETTKGYSGLNTAFDFTGLRERYDH 160

QY 124 L-----ARKIVPFIRASGSDRVIASAEKTEGFSQAKLADPGSOPHOASPVINVIIPE- 176
DB 161 LIWTSBEGKAL--SVWAGSGRQVVDVAKFAQGFMSKNYTD-----MVEVVAALEE 208

QY 177 --GSGYNNLTDHGCTCT-----AFDESELGDDV---PANTTALFAPAIRARLEADLPVTL 226
DB 209 EKSGGLNSLTARISCPNYSNHYKGDGFPNDIAERAD-----RLNLTSPGFNI 257

QY 227 TDEDVYILMDMCPDPTVARTSDATLSFPCALFTHEIDYQVLOSGLKYYGAGNPLG 286
DB 258 TADDIPTIALYCGFELNVGCE-----SSFCVDLSRALLYATVLRDLGWYVNGVNGNPLG 312

QY 287 PAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHNTMISIFFAL 346
DB 313 KTIGYVYAN-----ATROLLENTEAD--PRDYPLYFSFSHDTDLLOVFTSL 356

QY 347 GLYNGTK-PLSTTSVSEIETDGYASWTVPFAARAYVEMMQC--QAEKEPLRVLVNDR 403
DB 357 GLFNVTDLPL-----DQIQFQTSFKSTEIVPMGARLLTERLLCTVEGEKYYVVRTIINDA 411

QY 404 VVPLHGCADVCKLGRCKRDDFVEGLSFARSGGNWAE 438
DB 412 VFPLSDSGSGFGFSCPLNDYVSRLEALNEDSDFAE 446

RESULT 10
JN0890
acid phosphatase (EC 3.1.3.2) precursor - Aspergillus awamori
C:Species: Aspergillus awamori
C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999
C:Accession: JN0890
R:Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; N
Gene 133, 55-62, 1993
A:Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-opti
A:Reference number: JN0889; MUID:94040796
A:Accession: JN0890
A:Molecule type: DNA
A:Residues: 1-479 <PID>
A:Cross-references: GB:I02420; NID:g166481; PIDN:AAA16897.1; PID:g166482
A:Experimental source: strain ALK0243
C:Comment: The highly similar enzyme from A. ficuum has been shown to have 3-phytase (EC
C:Genetics:
A:Gene: aph
A:Introns: 261/1; 300/2; 335/2

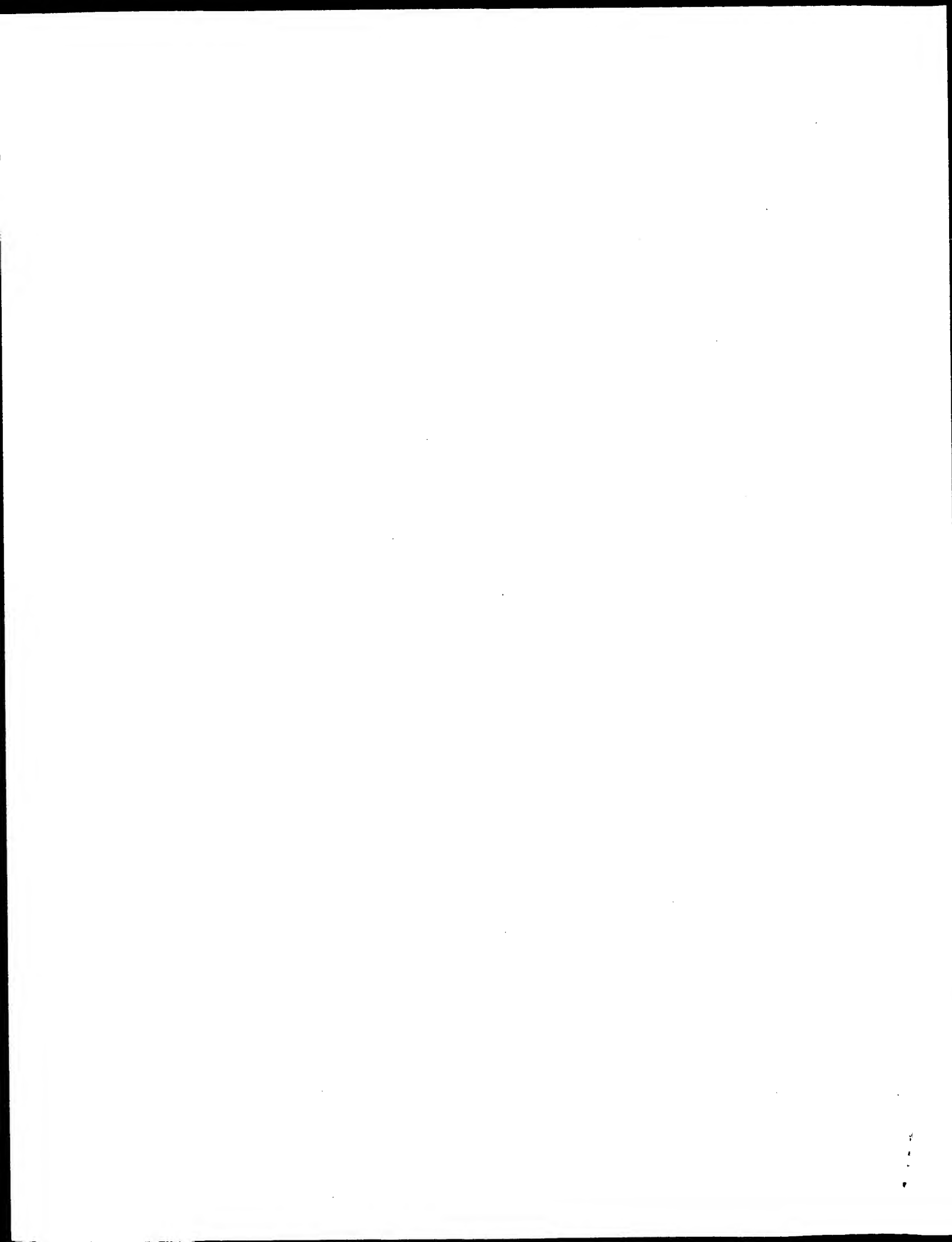
Db 210 SDADFTTTPALEAMRVNMPPIRQRLNPFYFNYNLTNDIILNLYGICSYETALO-----D 264
 QY 252 LSPFCALFTHDWMIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTS 311
 Db 265 YSEFKLENSVDLFNFEYEGDLFSFYGMGNSVKWGSIFGGAYANSLNSL--RSVENNTQ 322
 QY 312 TNHTLDSNPATPLNATLYADFSDHNTMISIFPALGLYNGTKPLSTTSVESIETDGYSA 371
 Db 323 -----QVFEAFTHDANIPVETALGFFTDNTPENPLPTSQVSHSMKA 366
 QY 372 SWTVFAARAYVEMMQCAEKEPLRVLVNDRVVPLHGC 410
 Db 367 SEFVPFAGNLITELFCEDSKY-YVRHLNVEEVFLSDC 404
 RESULT 14
 S14119
 C:Species: Schizosaccharomyces pombe
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 10-Dec-1999
 C:Accession: S14119; T40455
 R:Yang, J.; Schweingruber, M.E.
 Curr. Genet. 18, 269-272, 1990
 A:Title: The structural gene coding for thiamin-repressible acid phosphatase in Schizosaccharomyces pombe
 A:Reference number: S14119; MUID:91064763
 A:Accession: S14119
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-463 <YAN>
 A:Cross-references: GB:X56939; NID:g5006; PIDN:CAA40258.1; PID:g5007
 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
 submitted to the EMBL Data Library, November 1998
 A:Reference number: T40455
 A:Accession: T40455
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-463 <LYN>
 A:Cross-references: EMBL:AL034382; PIDN:CAA22278.1; GSPDB:GN00067; SPDB:SPBC428.03c
 A:Experimental source: strain 972h-; cosmid c428
 C:Genetics:
 A:Gene: SPBC428.03c
 A:Map position: 2
 C:Superfamily: yeast acid phosphatase
 C:Keywords: phosphoric monoester hydrolase

Query Match 11.9%; Score 278.5; DB 2; Length 463;
 Best Local Similarity 25.5%; Pred. No. 3e-15;
 Matches 108; Conservative 65; Mismatches 187; Indels 63; Gaps 15;
 QY 20 HLWGTYS----PYFLADESAISPDVDDCRVTFVQVLSRHGARYPT--SSASKAYSA-- 71
 Db 35 HL-GTISVYHEPYF-----NGPTTSPESCAIKQVHLRHGSRNFTGDDTADVSSAQ 88
 QY 72 -----LIEATQKNATAFKGYAFKTYNYRL---GADDLTPFGENQMVNSGKIFYRR 120
 Db 89 IDIFQNLKLSIPVNPSPENPLFYVKKHTPVVKAENADQLSSGRIELFDLGRQVFER 148
 QY 121 YKALARKIVPFRASGSDRVASAEKFIQFQSAKLADPGSQPHQASPVINVIPE--GS 178
 Db 149 YYELFDTDVYDINTAAQEVVDSAEWFSYGMFGDDMKNKTN-----FTVLPEDDSA 199
 QY 179 GYNTLHDGCTAFEDSELGDD--VEANFTA---LFAPAIRARLEADL--PGVTUTDDEVY 233
 Db 200 GANSLAMYSCPVYEDNIDENITEAHTSWRNVLKPIANRLKYFDSGYNLTVSDVRS 259
 QY 234 LMDMCPDFTVARTSDATLSPFCALFTHDWMIOYDYLQSLGKYGYGAGNPLGPAQGVGF 293
 Db 260 LYICVVEIALRDN-----SDFCSLFTPSEFLNFEYDSDLDYAYWGGPASEWASTLGGAY 314
 QY 294 ANELIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADFSDHNTMISIFPALGLYNGTK 353

Db 315 VNNLANNL-----RKGVNNASDRK-----VFLAFTHDSQIIPVEAALGFPPDIT 358
 QY 354 PISETTSVESIETDGYSAWTVFAARAYVEMMQCAEKEPLRVLVNDRVVPLHGCAYD 413
 Db 359 PEHPLPTDKNIFTYSLKTSFVFPAGNLITELFLC--SDNKYYVRHLVNOQVYPLTDCGYG 417
 QY 414 KLG 416
 Db 418 PSG 420
 RESULT 15
 JE0369
 histidine acid phosphatase (EC 3.1.3.-) - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
 C:Accession: JE0369
 R:Mullaney, E.J.; Ullah, A.H.J.
 Biochem. Biophys. Res. Commun. 251, 252-255, 1998
 A:Title: Identification of a histidine acid phosphatase (phyA)-like gene in Arabidopsis
 A:Reference number: JE0369; MUID:99009256
 A:Accession: JE0369
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-465 <MUL>
 C:Superfamily: yeast acid phosphatase
 C:Keywords: phosphoric monoester hydrolase

Query Match 6.4%; Score 149; DB 2; Length 465;
 Best Local Similarity 22.3%; Pred. No. 0.00018;
 Matches 101; Conservative 63; Mismatches 199; Indels 90; Gaps 22;
 QY 9 DGGYQCPEISHLWGTYSVPYFLAD--ESAI-SPDVDDCRVTFVQVLSRHGARYPTSSA 65
 Db 16 DGGF----DVRHLLSTVTRYSTSKDVTQNLIEGSNVSECTPIHLNLVARHGRSTRPTKKR 71
 QY 66 SKAYSAL---TEATQKNATAPK-----GKYAFKTYNYTLGADDLTPFGENQMVN 112
 Db 72 LREMESLAGRFKELVRDAEARKLPDKIPGWLQWK--SPWEGKVKGELIROGEDELYQ 129
 QY 113 SGIKFYRYKALARK---IVPFTRASGSDRVASAEKFTIEGFSAKLADPGSQPHQAS 168
 Db 130 LGIRVRERFPFLFEEDYHPDVTTIRATQIPRASASAVAFGNGLESEK-----GNL----- 179
 QY 169 VINVIPEGSGYNTLHDGCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTD 228
 Db 180 -----GPGNRFAF-----AVTSENRASTDKLRFEC--CQNKYSYRKAKEPAVDK 224
 QY 229 EDVYVLMDC---PFDTVARTSDATLSPFCALFTHDWMIOYDYLQSLGKYGYGAGNPL 285
 Db 225 EPVLNKITASVAKRYDLKFTTKODISSLWFLCKQVALLW-----TDDLEVFLKGYGNSL 279
 QY 286 GPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADFSDHNTMISIFFA 345
 Db 280 NYKMGV-----PLLEDVLSMEEAIKAREKLP--PGSYE--KARL--REHAETIVPPFC 330
 QY 346 -LGLYNGTKPLSTTSVESIE-----ETDGYSAWTVFAARAYVEMMQCAE 392
 Db 331 LIGLF-----LDGSEFKIOKEKPLELPQPPKTRDFRGSTMAPFGGNNILVLYSCPAES 385
 QY 393 EP--LVRVLNDRVVPLHGCAYDKLGRCKRDF 423
 Db 386 SPKYFQVQLNHEHPVAVPGC--DGKDFCPLDEF 416

Search completed: October 16, 2001, 17:52:55
 Job time: 20214 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 16, 2001, 17:50:59 ; Search time 88.89 Seconds
(without alignments)
102.153 Million cell updates/sec

Title: US-09-488-265-29_COPY_27_467

Perfect score: 2336
Sequence: 1 NSHSCDVTGQYCFPEISH.....DFVEGLSFARSGNNAECFA 441

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2282	97.7	441	4	US-09-121-425-1
2	2144	91.8	467	4	US-09-121-425-2
3	1837	78.6	467	1	US-07-923-724-8
4	1837	78.6	467	2	US-08-609-426A-8
5	1837	78.6	467	2	US-08-374-652C-2
6	1833	78.5	467	1	US-08-151-574-32
7	1833	78.5	467	1	US-08-146-424-20
8	1833	78.5	467	1	US-08-693-709-2
9	1833	78.5	467	2	US-08-419-448-32
10	1833	78.5	467	2	US-08-819-825-3
11	1833	78.5	467	4	US-09-163-642-3
12	1818	77.8	443	4	US-09-155-855-1
13	1818	77.8	443	4	US-09-155-855-3
14	1813	77.6	443	4	US-09-155-855-2
15	1332	57.0	475	2	US-08-819-825-2
16	1332	57.0	475	4	US-09-163-642-2
17	802.5	34.2	443	3	US-08-993-359-30
18	798.5	34.2	439	3	US-08-993-359-24
19	798.5	34.2	439	3	US-09-221-654-2
20	798.5	34.2	439	3	US-08-989-358A-2
21	795.5	34.1	453	3	US-08-993-359-22
22	781	33.4	442	3	US-08-993-359-28
23	778	33.3	442	3	US-08-993-359-26
24	358.5	15.3	446	1	US-07-627-539G-2
25	358.5	15.3	468	1	US-07-627-539G-2
26	347.5	14.9	479	1	US-07-923-724-2
27	347.5	14.9	479	2	US-08-609-426A-2

28	347.5	14.9	479	2	US-08-374-652C-4	Sequence 4, Appli
29	170.5	7.3	449	3	US-08-680-506-7	Sequence 7, Appli
30	148.5	6.4	92	3	US-08-993-359-32	Sequence 32, Appli
31	122	5.2	113	1	US-08-241-853-8	Sequence 8, Appli
32	122	5.2	113	2	US-08-850-917-8	Sequence 8, Appli
33	119	5.1	24	2	US-08-374-652C-32	Sequence 32, Appli
34	118	5.1	318	3	US-08-680-506-3	Sequence 3, Appli
35	111	4.8	113	1	US-08-241-853-10	Sequence 10, Appli
36	111	4.8	113	2	US-08-850-917-10	Sequence 10, Appli
37	96.5	4.1	386	1	US-08-738-213-1	Sequence 1, Appli
38	96.5	4.1	386	2	US-08-692-787-48	Sequence 1, Appli
39	96.5	4.1	386	4	US-09-097-199-48	Sequence 48, Appli
40	96.5	4.1	515	2	US-09-146-283-2	Sequence 2, Appli
41	96.5	4.1	515	3	US-08-579-823A-2	Sequence 2, Appli
42	96.5	4.1	515	4	US-09-344-195-2	Sequence 2, Appli
43	94	4.0	1732	2	US-08-570-311-10	Sequence 10, Appli
44	94	4.0	1732	2	US-08-353-485-10	Sequence 10, Appli
45	93.5	4.0	20	1	US-07-923-724-43	Sequence 43, Appli

ALIGNMENTS

RESULT 1
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-1

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				Gaps	0
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Db	1	NSHSCDVTGQYCFPEISHLWCTYSPYFSLADESAISDPDPCDRCVTFVQLSRHGARY	60		
Qy	61	PTSSKRAYSALIEAIOKNATAFKGYAFUKTYNYTLGADDLTPFGENOMVNSGKFKFYRR	120		
Db	61	PTSSKRAYSALIEAIOKNATAFKGYAFUKTYNYTLGADDLTPFGENOMVNSGKFKFYRR	120		
Qy	121	YKALARKIVPFIRASGSDRVIAASAERFIEGFSQAKLADPGSOPHOASPVINVIIEGSGY	180		
Db	121	YKALARKIVPFIRASGSDRVIAASAERFIEGFSQAKLADPGSOPHOASPVINVIIEGSGY	180		
Qy	181	NNTLDHGCTCTAFDESELGDDEVEANFTALFAPARLEADLPFGVTLTDEDVYVLMDCPF	240		
Db	181	NNTLDHGCTCTAFDESELGDDEVEANFTALFAPARLEADLPFGVTLTDEDVYVLMDCPF	240		
Qy	241	DTVARTSDATELSPFCALTFHDEWIOYLSIGKYGYGAGNPLGPAQGVGFANELIAR	300		
Db	241	ETVARTSDATELSPFCALTFHDEWIOYLSIGKYGYGAGNPLGPAQGVGFANELIAR	300		
Qy	301	LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSDHNTWISIFFALGLYNGTKPLSTTSV	360		
Db	301	LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSDHNTWISIFFALGLYNGTKPLSTTSV	360		

Db 301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNSMISIFFALGLYNGTAPLSTTSV 360
QY 361 ESTEETDGYASWTFVFAARAYEMMQCAEKEPLRVLVNDVRVPLHGCADVKGCRKR 420
Db 361 ESTEETDGYASWTFVFAARAYEMMQCAEKEPLRVLVNDVRVPLHGCADVKGCRKR 420
QY 421 DDFVEGLSFARSGGNWAECEFA 441
Db 421 DDFVEGLSFARSGGNWAECEFA 441
RESULT 2
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-2
Query Match 91.8%; Score 2144; DB 4; Length 467;
Best Local Similarity 89.2%; Pred. No. 4.8e-220;
Matches 411; Conservative 3; Mismatches 7; Indels 40; Gaps 2;
QY 1 NSHSCDVTGGYQCFPEISHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
Db 27 NSHSCDVTGGYQCFPEISHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 86
QY 61 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNTLTGADDLTPFGENQMVNSGKIFYRR 120
Db 87 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNTLTGADDLTPFGENQMVNSGKIFYRR 126
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Db 127 YKALARKIVPFIIRASGSDRVITASAEKFIIEGFSQAKLADPGSQPHQASPVIDILIEATOKNA 186
QY 172 -----VIIPEGSGYNTLHDGCTCTAFEDSELGDDVEANFTALFAPAIRARLEAD 220
Db 187 TAFKGYAFLAVIIPEGSGYNTLHDGCTCTAFEDSELGDDVEANFTALFAPAIRARLEAD 246
QY 221 LPGAIVLTDVYVLMDCPPTVARTSDATLSLPCALFTDHWIOYDYLQSLGKYYGYG 280
Db 247 LPGAIVLTDVYVLMDCPPTVARTSDATLSLPCALFTDHWIOYDYLQSLGKYYGYG 306
QY 281 AGNPLGPAQGVGFANELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMI 340
Db 307 AGNPLGPAQGVGFANELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMI 366
QY 341 SIFFALGLYNGTAPLSTTSVSEIETDGYASWTFVFAARAYEMMQCAEKEPLRVLV 400
Db 367 SIFFALGLYNGTAPLSTTSVSEIETDGYASWTFVFAARAYEMMQCAEKEPLRVLV 426
QY 401 NDRVVLPHGCAVDKLGCRKRDFFVEGLSFARSGGNWAECEFA 441
Db 427 NDRVVLPHGCAVDKLGCRKRDFFVEGLSFARSGGNWAECEFA 467

RESULT 3

US-07-923-724-8
; Sequence 8, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,724
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0240004
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-923-724-8
Query Match 78.6%; Score 1837; DB 1; Length 467;
Best Local Similarity 77.3%; Pred. No. 2.7e-187;
Matches 341; Conservative 39; Mismatches 61; Indels 0; Gaps 0;
QY 1 NSHSCDVTGGYQCFPEISHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
Db 27 NOSTCDVTGGYQCFSETSHLWQYAPFSLANESAISSPDVPAGCRVTFVQVLSRHGARY 86
QY 61 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNTLTGADDLTPFGENQMVNSGKIFYRR 120
Db 87 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNTLTGADDLTPFGELVNSGKIFYRR 146
QY 121 YKALARKIVPFIIRASGSDRVITASAEKFIIEGFSQAKLADPGSQPHQASPVINIIPEGSGY 180
Db 147 YESLTRNLPIIRSSGSSRVIASGEKFIIEGFSQAKLADPGSQPHQASPVINIIPEGSGY 206

QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVTLTDEDDVYLMDCPF 240
 Db 207 NNTLDPGCTVFEDSELADIVANFTATFAPSIRQRLNLSGVTLTDTETVYLMDCSF 266
 QY 241 DTARTSDATLSPFCALFTHDEMIQDYLSLGLKYYGYGAGNPLGPAQGVGFANELIAR 300
 Db 267 DTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLKYYGHGAGNPLGPTQGVGFANELIAR 326
 QY 301 LTHSPVODHTSTNHTLDSNPATPLNATLYADFSHNTMISIFALGLYNGTKPLSTTSV 360
 Db 327 LTHSPVODHTSSNHTLDSNPATPLNATLYADFSHNTMISIFALGLYNGTKPLSTTSV 386
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 Db 387 ENITQTDGFSASNTVPPFASRLYVEMMQCAEQEPLRVLVNDRVPLHGCACVDKLGRCKR 446
 QY 421 DDFVEGLSFARSGGNWAECSA 441
 Db 447 DDFVEGLSFARSGGNWAECSA 467

RESULT 4

US-08-609-426A-8

; Sequence 8, Application US/08609426A

; Patent No. 5830733

; GENERAL INFORMATION:

; APPLICANT: Nevalainen, Helena K.M.

; APPLICANT: Paloheimo, Marja T.

; APPLICANT: Miettinen-Oinonen, Arja S.K.

; APPLICANT: Torkkeli, Tuula K.

; APPLICANT: Cantrell, Michael

; APPLICANT: Piddington, Christopher S.

; APPLICANT: Rambosek, John A.

; APPLICANT: Turunen, Marja K.

; APPLICANT: Fagerstr m, Richard B.

; APPLICANT: Houston, Christine S.

; TITLE OF INVENTION: Production of Phytase Degrading Enzymes

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/609,426A

; FILING DATE: 01-MAR-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/923,724

; FILING DATE: 31-JUL-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/496,155

; FILING DATE: 19-MAR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/044,077

; FILING DATE: 29-APR-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: UK 8610600

; FILING DATE: 30-APR-1986

; ATTORNEY/AGENT INFORMATION:

; NAME: Reed, Grant E.

; REGISTRATION NUMBER: P-41,264

; REFERENCE/DOCKET NUMBER: 1050.0080001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 467 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-609-426A-8

Query Match

Best Local Similarity 78.6%; Score 1837; DB 2; Length 467;

Matches 341; Conservative 39; Mismatches 61; Indels 0; Gaps 0;

QY 1 NNSHCDTVDGGYQCPEISHLWGTVPYFESLADESATSPDPPDCRVTFVVOVLSRHGARY 60
 Db 27 NOSTCDTVDGGYQCPEISHLWGTVPYFESLADESATSPDPPAGCRVTFVVOVLSRHGARY 86
 QY 61 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLGGADLTFFGQELVNSGKIKFYQR 120
 Db 87 PTESKGGKYSALIEEIQONVTFDGYAFLKTYNTLGGADLTFFGQELVNSGKIKFYQR 146
 QY 121 YKALARKIVPFRASGSDRVIAAEKFLGQSAKLADPGSQHPQASPVINVIIPESGY 180
 Db 147 YESLTRNLIPIRSGSSRVIASGEKFLGQSTKLKDPRAQPGQSSPKIDVISEASS 206
 QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVTLTDEDDVYLMDCPF 240
 Db 207 NNTLDPGCTVFEDSELADIVANFTATFAPSIRQRLNLSGVTLTDTETVYLMDCSF 266
 QY 241 DTARTSDATLSPFCALFTHDEMIQDYLSLGLKYYGYGAGNPLGPAQGVGFANELIAR 300
 Db 267 DTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLKYYGHGAGNPLGPTQGVGFANELIAR 326
 QY 301 LTHSPVODHTSTNHTLDSNPATPLNATLYADFSHNTMISIFALGLYNGTKPLSTTSV 360
 Db 327 LTHSPVODHTSSNHTLDSNPATPLNATLYADFSHNTMISIFALGLYNGTKPLSTTSV 386
 QY 361 ESIEETDGYASNTVPPFAARAYVEMMQCAEQEPLRVLVNDRVPLHGCACVDKLGRCKR 420
 Db 387 ENITQTDGFSASNTVPPFASRLYVEMMQCAEQEPLRVLVNDRVPLHGCACVDKLGRCKR 446
 QY 421 DDFVEGLSFARSGGNWAECSA 441
 Db 447 DDFVEGLSFARSGGNWAECSA 467

RESULT 5

US-08-374-652C-2

; Sequence 2, Application US/08374652C

; Patent No. 5834286

; GENERAL INFORMATION:

; APPLICANT: NEVALAINEN, HELENA K.M.

; APPLICANT: PALOHEIMO, MARJA T.

; APPLICANT: FAGERSTROM, RICHARD B.

; APPLICANT: MIETTINEN-OINONEN, ARJA S.

; APPLICANT: TURUNEN, MARJA K.

; APPLICANT: RAMBOSEK, JOHN A.

; APPLICANT: PIDDINGTON, CHRISTOPHER S.

; APPLICANT: HOUSTON, CHRISTINE S.

; APPLICANT: CANTRELL, MICHAEL A.

; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,

; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/374,652C
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07058
; FILING DATE: 27-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/925,401
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E. 41,264
; REGISTRATION NUMBER: 1050.071001
; REFERENCE/DOCKET NUMBER: 1050.071001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-374-652C-2

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Query Match 78.6%; Score 1837; DB 2; Length 467;
 Best Local Similarity 77.3%; Pred. No. 2.7e-187;
 Matches 341; Conservative 39; Mismatches 61; Indels 0; Gaps 0;

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QY 1 NSHSCDVTGGYQCFPEISHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
DB 27 NQSTCDVTGGYQCFSETSHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 86
QY 61 PTSSAKAYSALIEAOKNATAFKGYAFKTYNTLGADDTLPGFENQMVNSGKIFKYYR 120
DB 87 PTESKGGKYSALIEEQNNVTTFDGYAFKTYNTSLGADDTLPGFENQMVNSGKIFKYYR 146
QY 121 YKALARKIVPFIASGRDVIASAEKFTFEGFSQAKLADPGSQPHQASPVINVIPEGSY 180
DB 147 YESLTRNIVPFIASGRDVIASAEKFTFEGFSQAKLADPGSQPHQASPVINVIPEGSY 206
QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALPAPARLAEADLPGLTLDDEVVYLMDCPF 240
DB 207 NNTLDHGTCTAFEDSELGDDVEANFTALPAPARLAEADLPGLTLDDEVVYLMDCSF 266
QY 241 DTVARTSDATSELPFCALFTHDEWIQYDYLOSGLKYYGYGAGNPLGPAQGVGFANELIAR 300
DB 267 DTISTSTVDTKLSFPCDLFTHDEWIYDYLOSGLKYYGYGAGNPLGPAQGVGFANELIAR 326
QY 301 LTHSPVQDHTSNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 360
DB 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 386
QY 361 ESIEETGYSASVTTPFAARAYVEMMQCAEKEPPLVRLVNDVRVPLHGCADVCKLGRCKR 420
DB 387 ENIQTDGFSASVTTPFAARAYVEMMQCAEKEPPLVRLVNDVRVPLHGCADVCKLGRCKR 446
QY 421 DDFVGLSFAFGSGNWAECFA 441
DB 447 DSFVRGLSFAFGSGNWAECFA 467

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RESULT 6
 US-08-151-574-32
 ; Sequence 32, Application US/08151574

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; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-151-574-32

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Query Match 78.5%; Score 1833; DB 1; Length 467;
 Best Local Similarity 77.3%; Pred. No. 7.2e-187;
 Matches 341; Conservative 39; Mismatches 61; Indels 0; Gaps 0;

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QY 1 NSHSCDVTGGYQCFPEISHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
DB 27 NQSSCDVTGGYQCFSETSHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 86
QY 61 PTSSAKAYSALIEAOKNATAFKGYAFKTYNTLGADDTLPGFENQMVNSGKIFKYYR 120
DB 87 PTDSKGGKYSALIEEQNNVTTFDGYAFKTYNTSLGADDTLPGFENQMVNSGKIFKYYR 146
QY 121 YKALARKIVPFIASGRDVIASAEKFTFEGFSQAKLADPGSQPHQASPVINVIPEGSY 180
DB 147 YESLTRNIVPFIASGRDVIASAEKFTFEGFSQAKLADPGSQPHQASPVINVIPEGSY 206
QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALPAPARLAEADLPGLTLDDEVVYLMDCPF 240
DB 207 NNTLDHGTCTAFEDSELGDDVEANFTALPAPARLAEADLPGLTLDDEVVYLMDCSF 266
QY 241 DTVARTSDATSELPFCALFTHDEWIQYDYLOSGLKYYGYGAGNPLGPAQGVGFANELIAR 300
DB 267 DTISTSTVDTKLSFPCDLFTHDEWIYDYLOSGLKYYGYGAGNPLGPAQGVGFANELIAR 326
QY 301 LTHSPVQDHTSNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 360
DB 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 386

```

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QY 361 ESIEETDGYASATVPFAARAYVEMMQCAEKEPLRVLVNDRVPLHGCAYDKLGRCKR 420
|:| :|||:|:|||||:| :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|
Db 387 ENITDTGDSASATVPFASRLYVEMMQCAEQEPLRVLVNDRVPLHGCVPDALGRCTR 446
QY 421 DDFEGLSFARSGGNWAECA 441
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 447 DSFVGLSFARSGGDWAECA 467
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
US-08-146-424-20
; Sequence 20, Application US/08146424
; Patent No. 5593963
; GENERAL INFORMATION:
; APPLICANT: VAN OIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,424
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: 44615-20011.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-146-424-20

Query Match 78.5%; Score 1833; DB 1; Length 467;
Best Local Similarity 77.3%; Pred. No. 7.2e-187;
Matches 341; Conservative 39; Mismatches 61; Indels 0; Gaps

QY 1 NSHSCDVTGGYQCFPEISHLWGYTPYFSLADESAISPDVPDCRVTFQVFLSRHGARY 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 27 NOSSDVTDDGQYQCFSETSHLWGYAPFFSLANESVISPVPAGACRVTFQVFLSRHGARY 86
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 PTSSASKAYSALIEAIOKNATFAKGYAEFLKTYNTILGADDLTPFGENQMVNSGIKFYRR 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 87 PTDSKGKYSALIEIQNATTFDGGKFAFLKTYNSLGADDLTPFGEQELVNSGINKFYQR 146
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 YKALARKIVPTIRASGDRVTSAAEKIEGFSQAKLADPGSQPHQASPVINVTIPEGSGY 180
|:| :|||:|:|||||:| :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|
Db 147 YESLTRNIVPTIRSSGSRVTSAGKKEIEGFSQTKLKDPRACQCSGPKDIVVISEASS 206
|:| :|||:|:|||||:| :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|
QY 181 NNTLDHGCTCTAFEDSELDGDDVEANFTALFAPATRALEARLEADLPGLVTLTDEDVYVLMDCPF 240
|:| :|||:|:|||||:| :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|

```

US-08-693-709-2

Query Match 78.5%; Score 1833; DB 1; Length 467;
Best Local Similarity 77.3%; Pred. No. 7.2e-187;
Matches 341; Conservative 39; Mismatches 61; Indels 0; Gaps 0;

QY 1 NNSHCDTVDGGYQCPEISHLMGTYSFYSLADESAISPDVDCRVTFVQVLSRHGARY 60
DB 27 NOSSCDTVDGGYQCPEISHLMGTYSFYSLADESAISPDVDCRVTFVQVLSRHGARY 86
QY 61 PTSSASKAYSALIEAIQKNATAFKGYAFKTYNTLGGADLTTPGEGELVNSGKIFYRR 120
DB 87 PTDSKGGKYSALIEIQONATTFDGKYAFKTYNTLGGADLTTPGEGELVNSGKIFYRR 146
QY 121 YKALARKIVPFIIRASGSDRVIAAEKFTIEGFSQAKLADPGSQPHQASPVINVIPEGSY 180
DB 147 YESLTRNIVPFIIRSSGSSRVIAAGKFFIEGFQSTKLDPRAQPGQSPKIDVISEASS 206
QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALPAPARLEADLPGVTLTDEVDVYLMDCPF 240
DB 207 NNTLDPGTCTVFESELDATVEANFTATFVPSIRORLNDLSGVTLTDEVTYLMDCSF 266
QY 241 DTVARTSDATELSPCALFTHDEWTOYDYLQSLGKYGYGAGNPLGPAQGVGFANELLAR 300
DB 267 DTSTSTVDTKLSPFCDLFTHDEWINYDYLQSLKYYGHGAGNPLGPTQGVGFANELLAR 326
QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 360
DB 327 LTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLSTTV 386
QY 361 ESTEETDGYASWTVPFAARAYVEMMOCQAEPLRVLVNDRVPLHGCVDKLGRCR 420
DB 387 ENITQDTGSSAWTVPFASRLYVEMMOCQAEPLRVLVNDRVPLHGCVDALGRCTR 446
QY 421 DDFVEGLSFARSGGNWAECEFA 441
DB 447 DSFVRGLSFARSGGDWAECEFA 467

RESULT 9

US-08-419-448-32
; Sequence 32, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorkom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Sellen
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,448
; FILING DATE: 10-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.10

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-887-1500

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-419-448-32

Query Match 78.5%; Score 1833; DB 2; Length 467;

Best Local Similarity 77.3%; Pred. No. 7.2e-187;

Matches 341; Conservative 39; Mismatches 61; Indels 0; Gaps 0;

QY 1 NNSHCDTVDGGYQCPEISHLMGTYSFYSLADESAISPDVDCRVTFVQVLSRHGARY 60
DB 27 NOSSCDTVDGGYQCPEISHLMGTYSFYSLADESAISPDVDCRVTFVQVLSRHGARY 86
QY 61 PTSSASKAYSALIEAIQKNATAFKGYAFKTYNTLGGADLTTPGEGELVNSGKIFYRR 120
DB 87 PTDSKGGKYSALIEIQONATTFDGKYAFKTYNTLGGADLTTPGEGELVNSGKIFYRR 146
QY 121 YKALARKIVPFIIRASGSDRVIAAEKFTIEGFSQAKLADPGSQPHQASPVINVIPEGSY 180
DB 147 YESLTRNIVPFIIRSSGSSRVIAAGKFFIEGFQSTKLDPRAQPGQSPKIDVISEASS 206
QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALPAPARLEADLPGVTLTDEVDVYLMDCPF 240
DB 207 NNTLDPGTCTVFESELDATVEANFTATFVPSIRORLNDLSGVTLTDEVTYLMDCSF 266
QY 241 DTVARTSDATELSPCALFTHDEWTOYDYLQSLGKYGYGAGNPLGPAQGVGFANELLAR 300
DB 267 DTSTSTVDTKLSPFCDLFTHDEWINYDYLQSLKYYGHGAGNPLGPTQGVGFANELLAR 326
QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 360
DB 327 LTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTKPLSTTV 386
QY 361 ESTEETDGYASWTVPFAARAYVEMMOCQAEPLRVLVNDRVPLHGCVDKLGRCR 420
DB 387 ENITQDTGSSAWTVPFASRLYVEMMOCQAEPLRVLVNDRVPLHGCVDALGRCTR 446
QY 421 DDFVEGLSFARSGGNWAECEFA 441
DB 447 DSFVRGLSFARSGGDWAECEFA 467

RESULT 10

US-08-819-825-3

; Sequence 3, Application US/08819825

; Patent No. 5866118

; GENERAL INFORMATION:

; APPLICANT: Berka, Randy M.

; APPLICANT: Ray, Michael W.

; APPLICANT: Klotz, Alan V.

; TITLE OF INVENTION: Polypeptides Having Phytase Activity

; TITLE OF INVENTION: And Nucleic Acids Encoding Same

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.

; STREET: 405 Lexington Avenue, Suite 5400

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

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RESULT 11
US-09-163-642-3
; Sequence 3, Application US/09163642
; Patent No. 6221644
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 6221644o No. 6221644disk of No. 6221644th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York

```

RESULT 12
US-09-155-855-1
; Sequence 1, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa

us-09-488-265-29_copy_27_467.ra1

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; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-155-853-3

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Query Match 77.88; Score 1818; DB 4; Length 467;

QY	1	NSHSCDTVDGGYQCFPEISHLWCTGYSPFSLADESAISDPDPPDCRVTFVQVLSRHGARY	60
	-	: : : : :	
Db	27	NQSTCTVDGGYQCFSETSHLWQYAPPFSLANKSAISDPDPAGCHVTFQAQVLSRHGARY	86

Query Match 77.8%; Score 1818; DB 4; Length 443;
Best Local Similarity 75.7%; Pred. No. 2.6e-185;
Matches 334; Conservative 46; Mismatches 61; Indels 0; Gaps

[illegible]

Db 267 DTISTSTVDTKLSPCDLFHEEWINYDYLQSLNKYYHGAGNPLGPTQGVGYANELIAR 326

Db 327 LTHSPVHDTSSNHTLDSNPATFPLNSTLYAFSDHNGIISILFALGLYNGTKPLSSTTA 386

[illegible]

DB 447 DSVKGLSFARSGGDWCEFA 467

RESULT 14
US-09-155-855-2
; Sequence 2, Application US/09155855
; Patent No. 613902

; GENERAL INFORMATION:
 ; APPLICANT: KONDO, Hidemasa
 ; APPLICANT: ANAZAWA, Hideharu
 ; APPLICANT: KANEKO, Svinichi

; APPLICANT: NAGASHIMA, Tadashi
 ; APPLICANT: TANGE, Tatsuya
 ; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
 ; FILE REFERENCE: 81356/124

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; CURRENT APPLICATION NUMBER: US/09/133,833
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04

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; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 2
; LENGTH: 443
; TYPE: prt
; ORGANISM: Aspergillus niger

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FEATURE:
OTHER INFORMATION: Xaa at positions 2 & 3 may be any amino acid or unknown
US-09-155-855-2

Query Match 77.6%; Score 1813; DB 4; Length 443;
Best Local Similarity 76.0%; Pred. No. 9e-185;
Matches 333; Conservative 46; Mismatches 59; Indels 0; Gaps 0;

QY 4 SCDVDDGGYQCFPEISHLWGTYSPIYSLADESAISPDVDDCRVTFVQVLSRHGARYPTPS 63
DB 6 TCDVDDGGYQCFSETSLWQYAPFFSLANKSAISPDVAGCHVTFQAQVLSRHGARYPTD 65

QY 64 SASKAYSALIEATQKNATAFKGYAFLKTYNTILGADDLTPFGENOMVNSGIKFYRYKA 123
DB 66 SKGKYSALIEEQNATTEGKYAFLKTYNTISLGADDLTPFGELVNSGVKFYRYES 125

QY 124 LARKIVPFIASGSDRVIASAEKFIQFQSAKLADPGSQPHQASPVINVIPEGSGYNNNT 183
DB 126 LTRNIVPFISSGSRVSIASGNKFIQFQSTKLKDPRAQPGQSSPKIDVVISEASTSNT 185

QY 184 LDHGTCTAFDESDGDDVEANFTALFAPALRLEADLPQVTLTDEDVYVLMDCPFDTV 243
DB 186 LDPGCTVFEDELADIEANFTATVPSTLORLENDLSGVSLTDEVTYVLMDCSFDTI 245

QY 244 ARTSDATELSPFCALFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFANELIARLTH 303
DB 246 STSTVDTKLSPFCDLFTHEWINVDYVLSLKYGHGAGNPLGPGQGVYANELLARLTH 305

QY 304 SPVODHTSNHTLDSNPATFPLNATLYADFSDHNTMISIFALGLYNGTKPLSTTSVESI 363
DB 306 SPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTMISIFALGLYNGTKPLSTSTAEI 365

QY 364 EETDGYASWTVPFAARAYVENMQCAEKEPLRVVLNDRVPLVHGCVDKLGCRKRD 423
DB 366 TOTDGFSSAWTVPFAARAYVENMQCSEGEPLRVVLNDRVPLVHGCVDALGCRTRDSF 425

QY 424 VEGLSFARSGGNWAECEFA 441
DB 426 VKGLSFARSGGNWAECEFA 443

RESULT 15
US-08-819-825-2
Sequence 2, Application US/08819825
Patent No. 5866118

GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.

TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5866118 of No. 5866118th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758.200-US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-819-825-2

Query Match 57.0%; Score 1332; DB 2; Length 475;
Best Local Similarity 59.3%; Pred. No. 2e-133;
Matches 262; Conservative 57; Mismatches 101; Indels 22; Gaps 7;

QY 17 EISHLWGTYSPIYSLADESAISPDVDDCRVTFVQVLSRHGARYPTPSASKAYSALIEAI 76
DB 38 DIARHWGQYSPFFSLAEYSEISPAVPGRCRVFQVLSRHGARYPTAHKSEVYAEELLQRI 97

QY 77 QKNATAFKGYAFLKTYNTILGADDLTPFGENOMVNSGIKFYRYKALARKIVPFIASG 136
DB 98 QDTATEFKGDFALFEDYAYHGLADNLTRFEGEQMMESGRQFYHRYEQAREIVPFIASG 157

QY 137 SDRVIASAEKFIQFQSAKLADPGSQPHQASPVINVIPEGSGYNNNTLDHGTCTAFEDSE 196
DB 158 SARVIASAEKFIQFQSAKLADPGSQPHQASPVINVIPEGSGYNNNTLDHGTCTAFEDSE 215

QY 197 LGDDVE-ANFTALFAPALRLEADLPQVTLTDEDVYVLMDCPFDTVARTSDAT---E 251
DB 216 APDTQPAEFQVFGPRLVKITKHMFGVNLTDVDFLMDLCPFDITVG--SDPVLEFPQ 273

QY 252 LSPFCALFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFANELIARLT-HSPVODHT 310
DB 274 LSPFCHLFTADDMAYDYIYTLDKYSHGGGSAFSGPGRGVGFVNELIARLTGNLTPVKDHT 333

QY 311 STNHTLDSNPATFPLNATLYADFSDHNTMISIFALGLYNGTKPLSTTSVE--SIEETDG 368
DB 334 TVNHTLDDNPETFPFLDAVLADFSDHNTMTGIFSAMGLYNGTKPLSTSKTQPPTGAADG 393

QY 369 YSASWTVPFAARAYVENMQC-----QAEKEPLRVVLNDRVPLVHGCVDKLGRC 418
DB 394 YASWTVPFAARAYVELLRCTETETSSSEEEGEDEPFVRVLNDRVPLVHGCVRDRWGR 453

QY 419 KRDFVEGLSFARSGGNWAECEFA 440
DB 454 RDEWIKGLTFARQGGHWDRCF 475

Search completed: October 16, 2001, 17:51:00
Job time: 20369 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 16, 2001, 17:49:19 ; Search time 124.2 Seconds
(without alignments)
215.259 Million cell updates/sec

Title: US-09-488-265-29_COPY_27_467
Perfect score: 2336

Sequence: 1 NSHSCDVTGQYQCFPEISH.....DFVEGLSFARSGNWAECFA 441

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8:	/SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9:	/SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10:	/SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
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14:	/SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15:	/SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16:	/SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17:	/SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
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20:	/SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
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22:	/SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2336	100.0	467	20 AAY43169	Consensus phytase-
2	2336	100.0	467	21 AAB20526	Consensus phytase
3	2336	100.0	467	21 AAY69568	Mutant phytase-1,
4	2317	99.2	467	21 AAB20532	Consensus phytase
5	2312	99.0	467	21 AAB20531	Consensus phytase
6	2288	97.9	467	20 AAW93382	Fungal consensus p
7	2282	97.7	441	21 AAB20514	Consensus phytase
8	2282	97.7	467	20 AAY39906	Ascomycete consens
9	2282	97.7	467	20 AAW93380	Fungal phytase pro
10	2282	97.7	467	20 AAW93381	Fungal consensus p
11	2282	97.7	467	21 AAB20515	Consensus phytase

12	2282	97.7	467	21 AAY69558	Phytase-1, a conse
13	2281	97.6	467	20 AAW93383	Fungal consensus p
14	2279	97.6	467	20 AAW93384	Fungal consensus p
15	2273	97.3	467	20 AAW93385	Fungal consensus p
16	2236	95.7	467	21 AAB20527	Consensus phytase-
17	2236	95.7	467	21 AAB20527	Consensus phytase-
18	2236	95.7	467	21 AAB20527	Consensus phytase-
19	2234	95.6	467	21 AAB20534	Mutant phytase-10,
20	2229	95.4	467	21 AAB20533	Consensus phytase
21	2216	94.9	441	21 AAB20523	Consensus phytase
22	2216	94.9	441	21 AAB20523	Consensus phytase
23	2216	94.9	467	21 AAB20523	Consensus phytase
24	2164	92.6	467	20 AAY69566	Consensus phytase
25	2164	92.6	467	20 AAY69572	Phytase-10, a cons
26	2161	92.5	467	21 AAY69571	Consensus phytase-
27	2134	91.4	431	21 AAB20529	Phytase-7, a deriv
28	2134	91.4	431	21 AAB20535	Consensus phytase
29	2089	89.4	467	21 AAY69557	Consensus phytase
30	2089	89.4	467	21 AAB20530	Initial consensus
31	2044	87.5	437	21 AAY69572	Consensus phytase
32	2044	87.5	437	21 AAY69567	Consphy12, a deriv
33	1956.5	83.8	424	21 AAY69567	Consensus phytase
34	1956.5	83.8	424	21 AAB20536	Phytase-11, a cons
35	1911.5	81.8	467	21 AAY69565	Consensus phytase
36	1891.5	81.0	467	21 AAY69574	Initial consensus
37	1891.5	81.0	467	20 AAY43171	Mutant Aspergillus
38	1891.5	81.0	467	21 AAB20528	A. fumigatus phyta
39	1857.5	79.5	440	21 AAY69570	Aspergillus fumiga
40	1857.5	79.5	440	21 AAY69549	Mutant Aspergillus
41	1857.5	79.5	465	19 AAW84356	Aspergillus fumiga
42	1854.5	79.4	440	20 AAY39905	Aspergillus fumiga
43	1854.5	79.4	440	21 AAB20507	A. fumigatus phyta
44	1849.5	79.2	440	21 AAY69550	Aspergillus fumiga
45	1849.5	79.2	440	21 AAB20508	Aspergillus fumiga
			440	21 AAY69551	Aspergillus fumiga

ALIGNMENTS

RESULT 1

AAV43169

ID AAV43169 standard; Protein; 467 AA.

AC AAV43169;

DT 06-JAN-2000 (first entry)

DE Consensus phytase-1-thermo(8)-Q50T-K9IA protein sequence.

KW Phytase; animal feed preparation; thermostable phytase; transgenic plant;

KW Consensus sequence.

OS Synthetic.

PN WO9948380-A1.

PD 30-SEP-1999.

PF 22-MAR-1999; 99WO-DK00154.

PR 23-MAR-1998; 98DK-0000407.

PR 19-JUN-1998; 98DK-0000806.

PR 18-SEP-1998; 98DK-0001176.

PR 22-JAN-1999; 99DK-0000091.

PR 22-JAN-1999; 99DK-0000093.

PA (NOVO) NOVO-NORDISK AS.

PI Petersen S;

PR WPI; 1999-591030/50.

DR N-PSDB; AAZ31520.

XX

- preparing animal feed using a thermostable phytase -

Example 3: Fig 9; 71pp; English.

This sequence represents the consensus phytase-1 thermo(8)-Q50T-K91A. The invention relates to a process for preparing animal feed by agglomerating feed ingredients with a thermostable phytase, which is added before or during agglomeration. These plants are useful in the preparation of transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytase allows animal feed to be produced more efficiently, in addition to improved phytase-expressing transgenic plants. These plants provide a feed ingredient and a feed additive (phytase) simultaneously.

sequence 467 AA:

Query Match	100.0%;	Score 2336;	DB 20;	Length 467;
Best Local Similarity	100.0%;	Pred. No. 4.2e-231;		
Matches 441:	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

1	NSHSCDVT	DGGY	QCPEP	SHLWGY	SPYFSLADE	SAISPDPD	CDRCVTF	QVQLSRHG	ARY	60	
27	nshscdvt	dggycf	qcpelshl	wgtyspyl	safsladesa	ispdpddcr	vtfvqlsrng	ary	86		
61	PTSSASKAY	SALIEALQ	NAFAFG	KGYAF	LKTYNTY	TGADDLTP	FGENOMV	SGIKFYRR	120		
87	ptssaskay	salielalq	naftafg	kyaflyk	tyntylga	dltpfgen	omvsgikfy	rr	146		
121	YKALARKI	VPFIRAS	GSORVIR	ASA	EKFTEG	FQS	AKLADPG	SQPHAS	PVINIIP	180	
147	ykalar	ki	v	p	f	r	a	s	g	s	206
181	NNTLDHGT	CTAFED	SELG	DDVEAN	TALFAP	AIRARLE	ADLPV	GTLTDE	DVYLMDC	240	
207	nntldhgt	ctafed	selg	ddvean	tal	f	a	p	a	i	266
241	DTVARTSD	ATELS	SPFCAL	FTHDEW	TOYDYL	OSL	GKYYCY	GAGNP	LPAGCVG	300	
267	dtvartsd	atelsp	fcalt	hde	wydy	l	o	s	l	g	326
301	LTHSPVDH	STNHT	LDSNP	ATFLNAT	LADFS	HND	TMTSIF	FALG	LYNGT	360	
327	lthspv	d	h	s	t	n	t	l	d	s	386
361	ESTIETD	GY	SAS	TVTPFA	ARAY	VEM	COAKE	PELIVR	VYLVN	420	
387	estietd	gy	s	a	s	t	v	p	f	a	446

RESULT 2
AAB20526
ID AAB20526 standard. Protein: 467 AA.

AA AAB20526;

05-DEC-2000 (first entry)

consensus phytaase 1 thermo 8 a50t. k91a protein seo id no:29.

XX phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW temperature stability; pH profile; temperature profile; reaction rate;
KW specific activity; substrate specificity; substrate cleavage pattern;
KW substrate binding; position specificity; phytate degradation rate;
KW food; feed; phytate; manure.

XX Synthetic.

XX
7000043E02-81

PN # WO200043503-A1.

XX PD XX PF XX PR PR XX PA XX PI XX DR DR XX PT PT XX PS XX CC CC CC CC CC CC CC CC CC CC CC CC CC CC

27-JUL-2000.

21-TAN-2000: 2000WO-DK00025

[illegible]

21-SEP-1999; 99DK-0001340.

(NOVO) NOVO NORDISK AS.

100

N-PSDB: AAA73233.

Several observations with

pH stability and substrate

Introduction

Claim 3; Fig 1a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate and level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present invention.

sequence 467 AA:

```

Query Match      100.0%; Score 2336; DB 21; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.2e-231;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

[illegible]

RESULT 3
 AAY69568
 ID AAY69568 standard; protein; 467 AA.
 XX AAY69568;
 XX
 DT 19-APR-2000 (first entry)
 XX
 DE Mutant phytase-1, phytase-1-thermo[8]-Q50T-K91A.
 XX
 KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
 KW thermostable; animal feed; monogastric animal; phytate phosphorus;
 KW phosphate availability; consensus; mutant; mutein.
 XX
 OS Aspergillus terreus 9A1.
 OS Aspergillus terreus cbs16.46.
 OS Aspergillus niger var. awamori.
 OS Aspergillus niger T213.
 OS Aspergillus fumigatus str. NRRL3135.
 OS Aspergillus fumigatus ATCC13073.
 OS Aspergillus fumigatus ATCC32722.
 OS Aspergillus fumigatus ATCC58128.
 OS Aspergillus fumigatus ATCC26906.
 OS Aspergillus fumigatus ATCC32239.
 OS Emericella nidulans.
 OS Talaromyces thermophilus ATCC20186.
 OS Myceliophthora thermophila.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..26
 FT /note= "Phytase signal peptide from Aspergillus terreus
 FT Protein 27..467
 FT /note= "Mature phytase-1-thermo[8]-Q50T-K91A"
 FT
 PN EP969089-A1.
 XX
 PD 05-JAN-2000.
 XX
 PF 23-JUN-1999; 99EP-0111949.
 XX
 PR 29-JUN-1998; 98EP-0111960.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Brugger R, Lehmann M, Wyss M;
 DR WPI; 2000-099429/09.
 XX N-PSDB; AA259715.
 XX
 PT New stabilized enzyme formulation, useful for feed compositions for
 FT monogastric animals.
 XX
 PS Example 5; Fig 19; 101pp; English.
 XX
 CC The invention relates to a novel stabilised dry or liquid enzyme
 CC formulation, comprising phytase (myo-inositol hexakisphosphate
 CC phosphohydrolase) and one or more stabilising agents including
 CC xylitol or ribitol; polyethylene glycols with a molecular weight of 600
 CC to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
 CC glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
 CC The stabilised phytase formulation is used in a method for preparing a
 CC feed composition for monogastric animals (e.g., pigs, poultry) and
 CC provides a monogastric animal with its dietary requirements of
 CC phosphorus. Although a large amount of phosphate is present in animal
 CC feed in the form of phytate phosphorus, monogastric animals are unable
 CC to utilise this form of phosphate, resulting in the addition of extra
 CC phosphate to the feed of such animals. Phytase enhances the nutritional
 CC value of plant material without the need for adding additional phosphate
 CC to the feed. The level of phosphate pollution in the environment is

CC reduced by adding phytase to animal feed, as the animal can make use of
 CC the inorganic phosphate liberated from phytate phosphorus using the
 CC enzyme. The phytase formulation of the invention has an improved
 CC thermostability and can therefore remain stable during long-term storage
 CC and can withstand feed processing methods such as extrusion, expansion
 CC and pelleting. The present sequence represents a mutant phytase-1
 CC consensus sequence, phytase-1-thermo[8]-Q50T-K91A, which has a
 CC temperature optimum and melting point 7 degrees Celsius higher than that
 CC of phytase-1 (AAY69558).
 XX
 SQ Sequence 467 AA;

Query Match 100.0%; Score 2336; DB 21; Length 467;
 Best Local Similarity 100.0%; Pred. No. 4.2e-231;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NSHSCDVTGCGYQCPETSHLWGTYSPTFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 27 nshscdvtvggycfpeishlwgtyspyfsiadesaispdvddcrvtfvqvlshrghary 86
 QY 61 PTSSASKAYSALIEAIQKNATAFKGYAFLKTYNYTLGADDLTFPGENQWVNSGKIFRR 120
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 87 ptssaskaysalieaiqnatafkgyaflktyntlgaddltpfgenqwmvnsqikfrr 146
 QY 121 YKALARKIVPFIIRASGSDRVIASAEKFTGFSQSAKLADPGSQPHQASPVINVIPEGSY 180
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 147 ykalkarkivpfiirassgsdrviaseekftgfsqakladpgsqphqaspviniipegsy 206
 QY 181 NNTLDHGTCATFEDSELGDDVEANFTALFAPAIRARLEADLPVTLTDEDVYLMDCPF 240
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 207 nntldhgctafedseigddveanftalfapairarleadlpvltltdedvylmdmcpf 266
 QY 241 DTVARTSDATESLSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 300
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 267 dtvartsdateslspfcalfthdewiodylqslgkygygagnpplgpagvgvgfaneliar 326
 QY 301 LTHSPVDQHTSTNITLDSNPATPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 360
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 327 lthspvqdhtstnhtldsnpatplnatlyadfsdntmisiffalglyngtkplsttsv 386
 QY 361 ESIEETDGYASATVPFAARAYVEMMOCQAEKPELVRLVNDVRVPLHGCAYDKLGRCKR 420
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 387 esieetdgyasatvtpfaarayvemmqcqaekpevlrvlvndrvrvplhgcavdklgrckr 446
 QY 421 DDFVEGLSFARSGGNWAECPA 441
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 447 ddfveglsfarsggnwaecca 467

RESULT 4
 AAB20532
 ID AAB20532 standard; Protein; 467 AA.
 XX
 AC AAB20532;
 XX
 DT 05-DEC-2000 (first entry)
 XX
 DE Consensus phytase 3 thermo 11 Q50T K91A protein SEQ ID NO:93.
 XX
 KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.
 XX
 OS Synthetic.
 XX
 PN WO200043503-A1.
 XX
 PD 27-JUL-2000.
 XX
 PF 21-JAN-2000; 2000WO-DK000025.

XX	22-JAN-1999;	99DK-0000092.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
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ID	AAB20531 standard; Protein; 467 AA.		
XX			
AC	AAB20531;		
XX			
DT	05-DEC-2000 (first entry)		
XX			
DE	Consensus phytase 3 thermo 11 Q50T protein SEQ ID NO:91.		
XX			
KW	Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.		
XX			
OS	Synthetic.		
XX			
PN	WO200043503-A1.		
XX			
PD	27-JUL-2000.		
XX			
PF	21-JAN-2000; 2000WO-DK00025.		
XX			
PR	22-JAN-1999; 99DK-0000092.		
PR	21-SEP-1999; 99DK-0001340.		
XX			
PA	(NOVO) NOVO NORDISK AS.		
XX			
PI	Lehmann M;		
XX			
DR	WPI: 2000-491161/43.		
DR	N-PSDB; AAA73290.		
XX			
PT	Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -		
PT			
PS	Disclosure; Fig 22a-c; 240pp; English.		
XX			
CC	The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of substrate binding, position specificity, reaction rate, phytate degradation rate, release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate.		
CC	The present sequence represents a phytase sequence from the present invention.		
XX			
SQ	Sequence 467 AA;		
Query Match 99.0%; Score 2312; DB 21; Length 467;			
Best Local Similarity 99.1%; Pred. No. 1.2e-228;			
Matches 437; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
QY	1	NSHSCDVTGGYQCFPEISHLWCTSPYFSLADESAISPDPDCCRVTTFVQVLSRHGARY 60	
Db	27	nshscdtvddygcfeishlwtyfsladesaispdpkdcrtvtfvqlsrhgary 86	
QY	61	PTSASKAYSALTEAOKNATFKGYAFKTYNYTLGADDLTPFGENOMVNSGKIFYYR 120	
Db	87	ptsasakaysalteaoknatafkgyafktyntylgaddltpfgendmnsngikfyrr 146	
QY	121	YKALARKIVPFIASGSDRVIASAEKFIQFQSAKLADPGSQPHQASPVINVIPEGSGY 180	
Db	147	ykalarxivpfirasgsdrviasaekfiqfqsakladpgsqphqaspvinvipegsgy 206	
QY	181	NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGLVTLTDEDVYVLMDCPF 240	

Db 207 nntldhgtctafedstlsgddveanftalfapairarleadlpgvltldeedvvyimdmcpf 266
 QY 241 DTVARTSDATLSPFCALFTHDWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 300
 Db 267 dtvartsdaceispcalfthdewidylqslgkygygagnglpagvgvfanelliar 326
 QY 301 LTHSPVDHTSTNHTLDSNPATFPPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 360
 Db 327 lthspvqdhstnhtldsnpatfpinatlyadfnshdnmisisiffalglyngtkplsttsv 386
 QY 361 ESTEETDGYASWTVPFAARAYVEMMQCAEKEPLRVLVNDRVVPLHGCADVGLGRCKR 420
 Db 387 esleetdgyaswtvpfaarayvemmqcaekplrvlvndrvvplhgcaadvklgrckr 446
 QY 421 DDFVEGLSFARSGGNWAECA 441
 Db 447 ddfveglsfarsggnwaecca 467

RESULT 6
 AAW93382
 ID AAW93382 standard; Protein; 467 AA.
 AC AAW93382;
 XX
 DT 11-JUN-1999 (first entry)
 XX
 DE Fungal consensus phytase protein mutant Q50T.
 XX
 KW Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food;
 KW feed additive; variant; muten; feed; pharmaceutical.
 XX
 OS Fungi.
 XX Synthetic.
 XX
 PN EP897985-A2.
 XX
 PD 24-FEB-1999.
 XX
 PF 15-JUL-1998; 98EP-0113176.
 XX
 PR 24-JUL-1997; 97EP-0112688.
 XX
 PA (HOFF) HOFFMANN LA ROCHE AG F.
 XX
 PI Lehmann M;
 XX
 DR WPI; 1999-134647/12.
 XX
 PT Preparation of a consensus protein, especially a phytase - using
 PT programs to compare evolutionary similarity of sequences
 XX
 PS Claim 9; Page -: 30pp; English.
 XX
 CC This invention describes a novel process for the preparation of a
 CC consensus protein. The specific example given in the specification is
 CC that of a fungal phytase (myo-inositol hexakisphosphate) which
 CC hydrolyses phytase to valuable feed additives, with a fully defined amino
 CC acid sequence given in the specification, or variant or muten. The
 CC method is useful for improving protein properties by altering their
 CC sequence. The consensus protein and muten are useful in food, feed or
 CC pharmaceutical compositions. This sequence is a mutant phytase protein of
 CC the invention which does not appear in the specification but has been
 CC created from the protein represented in AAW93380.
 XX
 SQ Sequence 467 AA;

Query Match 97.9%; Score 2288; DB 20; Length 467;
 Best Local Similarity 98.0%; Pred. No. 3.6e-226;
 Matches 432; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 NNSHCDTVDGGYQCPEISHLWGTYSVPYFLADESAISPDPDDCRVTFVQLSRHGARY 60

Db 27 nshscdtvdggycqfeishlwtyspyfsladesaispdpddcrvtfvqlsrhgary 86
 QY 61 PTTSSAKAYSALIEALQKNATAFKGYAFLKTYNTYTLGADDLTPFGENQMVNSGKIFYRR 120
 Db 87 pttsskaysalieleaigknatafkgyafktyntylgaddltpfgenqmvnsgikfyrr 146
 QY 121 YKALARKIYVFFIRASGSDRVIAAEKFIETGFSQAKLADPGSQHQASPVINVIPESSGY 180
 Db 147 ykalarkiypffirasgsdrviaaeekfieltgfsakladpgsqhqaspvilvipessgy 206
 QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVLTDEEDVYIMDMCPF 240
 Db 207 nntldhgtctafedselgddveanftalfapairarleadlpgvltdeedvvyimdmcpf 266
 QY 241 DTVARTSDATLSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 300
 Db 267 etvartsdatelspcalfthdewrtydylqslgkygygagnglpagvgvfanelliar 326
 QY 301 LTHSPVDHTSTNHTLDSNPATFPPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 360
 Db 327 ltrspvqdhstnhtldsnpatfpinatlyadfnshdnmisisiffalglyngtaplstsv 386
 QY 361 ESIEETDGYASWTVPFAARAYVEMMQCAEKEPLRVLVNDRVVPLHGCADVGLGRCKR 420
 Db 387 esieetdgyaswtvpfagarayvemmqcaekplrvlvndrvvplhgcaadvklgrckr 446
 QY 421 DDFVEGLSFARSGGNWAECA 441
 Db 447 ddfveglsfarsggnwaecca 467

RESULT 7
 AAB20514
 ID AAB20514 standard; Protein; 441 AA.
 XX
 AC AAB20514;
 XX
 DT 05-DEC-2000 (first entry)
 XX
 DE Consensus phytase SEQ ID NO:14.
 XX
 KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.
 XX
 OS Synthetic.
 XX
 PN WC2000043503-A1.
 XX
 PD 27-JUL-2000.
 XX
 PF 21-JAN-2000; 2000WO-DK000025.
 XX
 PR 22-JAN-1999; 99PK-00000092.
 XX
 PR 21-SEP-1999; 99PK-0001340.
 XX
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Lehmann M;
 XX
 DR WPI; 2000-491161/43.
 XX
 PT Novel phytases with improved properties such as temperature stability,
 PT pH stability and substrate specificity, for use in pharmaceuticals and
 PT compound foods and feeds -
 XX
 PS Example 9; Fig 1a-d; 240pp; English.
 XX
 CC The present invention describes improved phytases, preferably with
 CC increased thermostability, and methods for producing them. The methods

CC can be used for producing phytases with improved properties e.g.
 CC temperature stability, pH stability, pH profile, temperature profile,
 CC specific activity, substrate specificity, substrate cleavage pattern,
 CC substrate binding, position specificity, the velocity and level of
 CC release of phosphate from corn, reaction rate, phytase degradation rate,
 CC and end level of released phosphate. The phytases can be used to produce
 CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.
 CC The present sequence represents a phytase sequence from the present
 CC invention.

XX Sequence 441 AA;

Query Match 97.7%; Score 2282; DB 21; Length 441;
 Best Local Similarity 97.7%; Pred. No. 1.3e-225;
 Matches 431; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 NNSCDTVDGGYQCPEISHLWGTSPYFSLADESAISPDVDDCRVTFVQLSRHGARY 60
 DB 1 nshscdtvddggycpeishlwgtspysfsladesaispdvddcrvtfvqlsrhgary 60
 QY 61 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLGADDLTPGQNMVNSGKIFYYR 120
 DB 61 ptssaskaysalieleaioknatafkgyaflktyntlgaddltpgengmvsngikfyrr 120
 QY 121 YKALARKIVPFIRASGSDRVIASAEKFIQSGAKLADPGSQPHQASPVINVIPEGSGY 180
 DB 121 ykalarakiyvpfirasgsdrviaseakfiqsgakladpgsqphqaspvdiviiepgsgy 180
 QY 181 NNTLDHGTCTAFEDSELGDVEANFTALFAPALRARLEADLPGLTDDVYLLMDMCPF 240
 DB 181 nntldhgtctafedselgdveanfalfapalarleadlpgltdedvvyllmdmcpf 240
 QY 241 DTVARTSDATLSPFCALFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFANELLAR 300
 DB 241 dtvartsdatslspfcalfthdewiqdylylqslgkygygagnplgpaggvgfaneliar 300
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 360
 DB 301 ltrspvqdhstnhtldsnpatfplnatlyadfshdntmisiffalglngtkplsttsv 360
 QY 361 ESTEETDGYASWTVPFAARAYVEMMQCAEKEPLRVLVNDRVPLHGCVAVDKLGRCR 420
 DB 361 esietdgyaswtvpfagarayvemmqqcaekeplrvlvndrvvplhgcavdklgrckr 420
 QY 421 DDFVEGLSFARSGGNWAECEFA 441
 DB 421 ddfveglsfarsggnwaecefa 441

RESULT 8
 AAY39906
 ID AAY39906 standard; Protein: 467 AA.

XX AC AAY39906;

XX DT 07-DEC-1999 (first entry)

XX DE Ascomycete consensus phytase protein sequence.

XX KW phytase; variant; enzyme; phosphorus liberation; phytase substrate;
 KW phytate level reduction; animal manure; food preparation;
 KW soy processing; inositol manufacture.

XX OS Synthetic.

XX PN WO9949022-A1.

XX PD 30-SEP-1999.

XX PF 22-MAR-1999; 99WO-DK00153.

XX PR 23-MAR-1998; 98DK-0000407.
 PR 19-JUN-1998; 98DK-0000806.
 PR 18-SEP-1998; 98DK-0001176.
 PR 22-JAN-1999; 99DK-0000091.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX SV Svendsen A;
 XX WI 1999-580444/49.
 DR N-PSDB; AA27423.
 XX PT New variant phytase enzymes, used for liberating phosphorus from a
 PT phytase substrate, for reducing phytate levels in animal manure and in
 PT feed and food preparations -
 PS Claim 26; Fig 9a-d; 14lpp; English.
 XX CC This sequence represents the ascomycets consensus phytase sequence.
 CC The invention relates to variant phytase enzymes with specific amino acid
 CC substitutions for improved properties. The phytase variants can be used
 CC for liberating phosphorus from a phytase substrate. They can be used for
 CC reducing phytate levels in animal manure. They can be used in feed or
 CC food preparations. The phytase DNA can also be used to produce transgenic
 CC plants which can be used in feeds or foods. The phytase variants can also
 CC be used in soy processing and in the manufacture of inositol or
 CC derivatives. The phytase variants can have altered activities such as pH
 CC stability, temperature stability, pH profile, temperature profile,
 CC specific activity (in particular in relation to pH and temperature),
 CC substrate specificity, substrate cleavage pattern, substrate binding,
 CC position specificity, the velocity and level of release of phosphate
 CC from corn, reaction rate, phytase degradation rate and end level of
 CC released phosphate reached.
 XX SQ Sequence 467 AA;

Query Match 97.7%; Score 2282; DB 20; Length 467;
 Best Local Similarity 97.7%; Pred. No. 1.5e-225;
 Matches 431; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 NNSCDTVDGGYQCPEISHLWGTSPYFSLADESAISPDVDDCRVTFVQLSRHGARY 60
 DB 27 nshscdtvddggycpeishlwgtspysfsladesaispdvddcrvtfvqlsrhgary 86
 QY 61 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLGADDLTPGQNMVNSGKIFYYR 120
 DB 87 ptssaskaysalieleaioknatafkgyaflktyntlgaddltpgengmvsngikfyrr 146
 QY 121 YKALARKIVPFIRASGSDRVIASAEKFIQSGAKLADPGSQPHQASPVINVIPEGSGY 180
 DB 147 ykalarakiyvpfirasgsdrviaseakfiqsgakladpgsqphqaspvdiviiepgsgy 206
 QY 181 NNTLDHGTCTAFEDSELGDVEANFTALFAPALRARLEADLPGLTDDVYLLMDMCPF 240
 DB 207 nntldhgtctafedselgdveanfalfapalarleadlpgltdedvvyllmdmcpf 266
 QY 241 DTVARTSDATLSPFCALFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFANELLAR 300
 DB 267 dtvartsdatslspfcalfthdewiqdylylqslgkygygagnplgpaggvgfaneliar 326
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 360
 DB 327 ltrspvqdhstnhtldsnpatfplnatlyadfshdntmisiffalglngtkplsttsv 386
 QY 361 ESTEETDGYASWTVPFAARAYVEMMQCAEKEPLRVLVNDRVPLHGCVAVDKLGRCR 420
 DB 387 esietdgyaswtvpfagarayvemmqqcaekeplrvlvndrvvplhgcavdklgrckr 446
 QY 421 DDFVEGLSFARSGGNWAECEFA 441
 DB 447 ddfveglsfarsggnwaecefa 467

DB 87 psskskaysalialqknatafkgyafiktyntlgaddltfpgenqmvnsigkfyrr 146
QY 121 YKALARKIYVPIFRASGSDRVIASAEKFIQFOSAKLADPGSQPHOASPVINVIIEGSGY 180
DB 147 YKALARKIYVPIFRASGSDRVIASAEKFIQFOSAKLADPGSQPHOASPVINVIIEGSGY 206
QY 181 NNTLDHCTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVTLTDEDVYVLMDCMCP 240
DB 207 nntldhgtctafedsgddveanftalfapairarleadlpvgtltddedvylmdmcpf 266
QY 241 DTVARTSDATLSPFCALTHDEWIQDYLOSGLKYYGYGAGNPLGPAQGVGFANELLAR 300
DB 267 etvartsdatselpfcalthdewrtdylosglkyygygagnpigpaqgvvfanelliar 326
QY 301 LTHSPVQDHTSTNHTLDSNPATPLNATLYADFSDHNTMISIFALGLYNGTKPLSTTSV 360
DB 327 ltrspvqdhstnthtldsnpatplnatlyadfsdnsmisiffalglnglaplsttsv 386
QY 361 ESTEETDGYASWTVPFAARAYVEMMQCAKEPILRVLVNDRVPLHGCADVKGRCR 420
DB 387 esieetdgyaswtvpfagarayvemmqqcqekeplrvlvndrvvplhgcavdkgkr 446
QY 421 DDFVEGLSFARSGGNWAECEFA 441
DB 447 ddfveglsfarsggnwaecfa 467
RESULT 11
AAB20515
ID AAB20515 standard; Protein; 467 AA.
AC AAB20515;
XX
XX
DT 05-DEC-2000 (first entry)
XX
XX
DE Consensus phytase SEQ ID NO:16.
XX
XX
KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW temperature stability; pH profile; temperature profile; reaction rate;
KW specific activity; substrate specificity; substrate cleavage pattern;
KW substrate binding; position specificity; phytate degradation rate;
KW food; feed; phytate; manure.
XX
XX
OS Synthetic.
XX
XX
FN WO200043503-A1.
XX
XX
PD 27-JUL-2000.
XX
XX
PF 21-JAN-2000; 2000WO-DK00025.
XX
XX
PR 22-JAN-1999; 99DK-0000092.
PR 21-SEP-1999; 99DK-0001340.
XX
XX
PA (NOVO) NOVO NORDISK AS.
XX
XX
XX Lehmann M;
XX
XX
DR WPI; 2000-491161/43.
DR N-PSDB; AAA73231.
XX
XX
PT Novel phytases with improved properties such as temperature stability,
PT pH stability and substrate specificity, for use in pharmaceuticals and
PT compound foods and feeds -
XX
XX
PS Example 9; Fig 2a-c; 240pp; English.
XX
XX
CC The present invention describes improved phytases, preferably with
CC increased thermostability, and methods for producing them. The methods
CC can be used for producing phytases with improved properties e.g.
CC temperature stability, pH stability, pH profile, temperature profile,
CC specific activity, substrate specificity, substrate cleavage pattern,

CC substrate binding, position specificity, the velocity and level of
CC release of phosphate from corn, reaction rate, phytate degradation rate,
CC and end level of released phosphate. The phytases can be used to produce
CC pharmaceutical compositions or compound food or feeds. The feed can be
CC used to reduce levels of phytate in animal manure, by converting it
CC into lower inositol phosphates and/or inositol and inorganic phosphate.
CC The present sequence represents a phytase sequence from the present
CC invention.
XX
SQ Sequence 467 AA;
Query Match 97.7%; Score 2282; DB 21; Length 467;
Best Local Similarity 97.7%; Pred. No. 1.5e-225;
Matches 431; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 NSHSCDVTGQYQCFPELISHLWGTYSYFSLADESAISPDVDPDCRVTFEQVLSRHGARY 60
DB 27 nshscdvtggyqcfpeishlwggysyfsledesaisspdvddcrvtfvqvlsrhgary 86
QY 61 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNTYTLGADDLTFFGENQMVNSIGKIFYRR 120
DB 87 ptsskskaysalialqknatafkgyafiktyntylgaddltfpgenqmvnsigkifyrr 146
QY 121 YKALARKIYVPIFRASGSDRVIASAEKFIQFOSAKLADPGSQPHOASPVINVIIEGSGY 180
DB 147 YKALARKIYVPIFRASGSDRVIASAEKFIQFOSAKLADPGSQPHOASPVINVIIEGSGY 206
QY 181 NNTLDHCTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPVTLTDEDVYVLMDCMCP 240
DB 207 nntldhgtctafedsgddveanftalfapairarleadlpvgtltddedvylmdmcpf 266
QY 241 DTVARTSDATLSPFCALTHDEWIQDYLOSGLKYYGYGAGNPLGPAQGVGFANELLAR 300
DB 267 etvartsdatselpfcalthdewrtdylosglkyygygagnpigpaqgvvfanelliar 326
QY 301 LTHSPVQDHTSTNHTLDSNPATPLNATLYADFSDHNTMISIFALGLYNGTKPLSTTSV 360
DB 327 ltrspvqdhstnthtldsnpatplnatlyadfsdnsmisiffalglnglaplsttsv 386
QY 361 ESTEETDGYASWTVPFAARAYVEMMQCAKEPILRVLVNDRVPLHGCADVKGRCR 420
DB 387 esieetdgyaswtvpfagarayvemmqqcqekeplrvlvndrvvplhgcavdkgkr 446
QY 421 DDFVEGLSFARSGGNWAECEFA 441
DB 447 ddfveglsfarsggnwaecfa 467
RESULT 12
AAY69558
ID AAY69558 standard; protein; 467 AA.
XX
XX
AC AAY69558;
XX
XX
DT 19-APR-2000 (first entry)
XX
XX
DE Phytase-1, a consensus phytase.
XX
XX
KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
KW thermostable; animal feed; monogastric animal; phytate phosphorus;
KW phosphate availability; consensus; phytase-1.
XX
XX
OS Aspergillus terreus 9A1.
OS Aspergillus terreus cbs16.46.
OS Aspergillus niger var. awamori.
OS Aspergillus niger T213.
OS Aspergillus niger str. NRRL3135.
OS Aspergillus fumigatus ATCC13073.
OS Aspergillus fumigatus ATCC32722.
OS Aspergillus fumigatus ATCC58128.
OS Aspergillus fumigatus ATCC26906.
OS Aspergillus fumigatus ATCC32239.

OS Emericella nidulans.
OS Talaromyces thermophilus ATCC20186.
OS Myceliophthora thermophila.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..26
FT /note= "Phytase signal peptide from Aspergillus terreus
FT cbs16.46"
FT Protein 27..467
FT /note= "Mature phytase-1 consensus"
XX
PN EP963089-A1.
XX
PD 05-JAN-2000.
XX
PF 23-JUN-1999; 99EP-0111949.
XX
PR 29-JUN-1998; 98EP-0111960.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PI Brugger R, Lehmann M, Wyss M;
DR WPI; 2000-099429/09.
DR N-PSDB; AA259637.
XX
PT New stabilized enzyme formulation, useful for feed compositions for
PT monogastric animals -
PS
PS Example 3; Fig 14; 101pp; English.
XX
CC The invention relates to a novel stabilised dry or liquid enzyme
CC formulation, comprising phytase (myo-inositol hexakisphosphate
CC phosphohydrolase) and one or more stabilising agents including
CC xylitol or ribitol; polyethylene glycols with a molecular weight of 600
CC to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
CC glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
CC The stabilised phytase formulation is used in a method for preparing a
CC feed composition for monogastric animals (e.g., pigs, poultry) and
CC provides a monogastric animal with its dietary requirements of
CC phosphorus. Although a large amount of phosphate is present in animal
CC feed in the form of phytate phosphorus, monogastric animals are unable
CC to utilise this form of phosphate, resulting in the addition of extra
CC phosphate to the feed of such animals. Phytase enhances the nutritional
CC value of plant material without the need for adding additional phosphate
CC to the feed. The level of phosphate pollution in the environment is
CC reduced by adding phytase to animal feed, as the animal can make use of
CC the inorganic phosphate liberated from phytate phosphorus using the
CC enzyme. The phytase formulation of the invention has an improved
CC thermostability and can therefore remain stable during long-term storage
CC and can withstand feed processing methods such as extrusion, expansion
CC and pelleting. The present sequence represents a consensus sequence,
CC designated phytase-1, which was derived from the mature phytase
CC sequences from a variety of fungi (AA69544-Y69556), and additionally
CC contains the Aspergillus terreus cbs16.46 signal peptide at the
CC N-terminus.
XX
SQ Sequence 467 AA;

Query Match 97.7%; Score 2282; DB 21; Length 467;
Best Local Similarity 97.7%; Pred. No. 1.5e-225;
Matches 431; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Qy 1 NSHSDTVGQYQCFPEISHLWGTYSYFSLADESATSPOVDPDRCYTFQVLSRHGARY 60
Db 27 nshscdtvgyqcfpeishlwgyqsyfsladesatspvdpcrcvtfqvlsrigrary 86
Qy 61 PTSSASKAYSALIAIOKNATAFGKGYAFUKTYNTYTLGADDLTPFGENQMVNSGKIFYRR 120
Db 87 ptsskaysalialiaidqknatafkgkyafiktyntylgaddltptfgenvnsgikfyrr 146

QY 121 YKALARKIVPFIRASGSDRVIASAEKFIQFQSAKLADPGSQPHQASPVINWIIPEGSGY 180
Db 147 Ykalarkivpfirasgsdrviasaekfiegfsakladpgsqphdaspvldvipegsgy 206
QY 181 NNTLHGCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDDVYVLMDCMPF 240
Db 207 nntldhgtctafedseelgdvveanftalfapairarleadlpvgvltddedvvyldmcmcf 266
QY 241 DTVARTSDATELSPFCALFTHDEWIOYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 300
Db 267 etvartsdatselspfcalfthdewiqdyqlsglkyygygagnpilgpaqgvgfaneliar 326
QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWISIFFALGILYNGTKPLSTTSV 360
Db 327 ltrspvqdhstnhtldsnpatfplnatlyadfsndmsisiffalgyngtaptstsv 386
QY 361 ESIEETDGYASWTVPFAARAYVEMMOCQAEKEPLVRVLVNDRVVPLHGCACVADKLGRCKR 420
Db 387 esieetdgysaswtvpfagarayvemmqcackeplrvvlvndrvvplhgcavdklgrckr 446
QY 421 DDFVEGLSFARSGGNWAECPA 441
Db 447 ddfveglsfarsggnwaecca 467
RESULT 13
AAW93383
ID AAW93383 standard; Protein; 467 AA.
XX
AC AAW93383;
XX
DT 11-JUN-1999 (first entry)
XX
DE Fungal consensus phytase protein mutant Q50G.
XX
KW Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food;
KW feed additive; variant; mutein; feed; pharmaceutical.
XX
OS Fungi.
OS Synthetic.
XX
PN EP897985-A2.
XX
PD 24-FEB-1999.
XX
PF 15-JUL-1998; 98EP-0113176.
XX
PR 24-JUL-1997; 97EP-0112688.
XX
PA (HOFF) HOFFMANN LA ROCHE AG F.
XX
PI Lehmann M;
XX
DR WPI; 1999-134647/12.
XX
PT Preparation of a consensus protein, especially a phytase - using
PT programs to compare evolutionary similarity of sequences
XX
PS Claim 9; Page -; 30pp; English.
XX
CC This invention describes a novel process for the preparation of a
CC consensus protein. The specific example given in the specification is
CC that of a fungal phytase (myo-inositol hexakisphosphate) which
CC hydrolyses phytase to valuable feed additives, with a fully defined amino
CC acid sequence given in the specification, or variant or mutein. The
CC method is useful for improving protein properties by altering their
CC sequence. The consensus protein and mutein are useful in food, feed or
CC pharmaceutical compositions. This sequence is a mutant phytase protein of
CC the invention which does not appear in the specification but has been
CC created from the protein represented in AAW93380.
XX
SQ Sequence 467 AA;

CC This invention describes a novel process for the preparation of a
 CC consensus protein. The specific example given in the specification is
 CC that of a fungal phytase (myo-inositol hexakisphosphate) which
 CC hydrolyses phytase to valuable feed additives, with a fully defined amino
 CC acid sequence given in the specification, or variant or mutagen. The
 CC method is useful for improving protein properties by altering their
 CC sequence. The consensus protein and mutagen are useful in food, feed or
 CC pharmaceutical compositions. This sequence is a mutant phytase protein of
 CC the invention which does not appear in the specification but has been
 CC created from the protein represented in AAW93380.
 XX
 SQ Sequence 467 AA;

Query Match 97.6%; Score 2279; DB 20; Length 467;
 Best Local Similarity 97.7%; Pred. No. 3e-225;
 Matches 431; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 NSHSCDTVDGGYQCPEISHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
 DB 27 nshscdtvdggyqcpeishlwgtnspyfslesdesaispdvddcrvtfvqvsrhgary 86
 QY 61 PTSSASKAYSALIEAOKNATAFKGYAFKTYNTLGADDLTPFGENQMVNSGKIKFYRR 120
 DB 87 ptssaskaysalieaoknatafkgyafktyntlgaddltfpfgenqmvnsgikfyrr 146
 QY 121 YKALARKIVPFIRASGSDRVIASAEKTEGFQSAKLADPGSQPHQASPVINVIPEGSGY 180
 DB 147 ykalarlivpfiragsdrviasaekfiegfsakladpgsqphqaspvdivipegsgy 206
 QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVYVLMDCPF 240
 DB 207 nntldhgtctafedselgddveanftalfapairarleadlpgvltddedvvyvldmcpf 266
 QY 241 DTVARTSDATSELSFPCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 300
 DB 267 etvartsdatselspfcalfthdewioydlqslgkygygagnplgpaqgvgfaneliar 326
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 360
 DB 327 ltrspvqdhstnhtldsnpatfplnatlyadfsdhntmisiffalglyngtaplstsv 386
 QY 361 ESIEETDGYASWTVPFAARAYVEMMQCAKEPLRVLVNDRVPLHGCVAVDKLGRCR 420
 DB 387 esieetdgyaswtvpfagarayvemmqcqeplrvrlvndrvvplhgcavdklgrckr 446
 QY 421 DDFVEGLSFARSGGNWAECEFA 441
 DB 447 ddfveglsfarsggnwaecefa 467

RESULT 15
 AAW93385
 ID AAW93385 standard; Protein; 467 AA.
 XX
 AC AAW93385;
 XX
 DT 11-JUN-1999 (first entry)
 XX
 DE Fungal consensus phytase protein mutant Q50L-Y51N.
 XX
 KW Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food;
 KW feed additive; variant; mutagen; feed; pharmaceutical.
 OS Fungi.
 OS Synthetic.
 XX
 PN EP897985-A2.
 XX
 PD 24-FEB-1999.
 XX
 PF 15-JUL-1998; 98EP-0113176.
 XX

Query Match 97.6%; Score 2281; DB 20; Length 467;
 Best Local Similarity 97.7%; Pred. No. 1.9e-225;
 Matches 431; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 NSHSCDTVDGGYQCPEISHLWGTSPYFSLADESAISPDVDDCRVTFVQVLSRHGARY 60
 DB 27 nshscdtvdggyqcpeishlwgtnspyfslesdesaispdvddcrvtfvqvsrhgary 86
 QY 61 PTSSASKAYSALIEAOKNATAFKGYAFKTYNTLGADDLTPFGENQMVNSGKIKFYRR 120
 DB 87 ptssaskaysalieaoknatafkgyafktyntlgaddltfpfgenqmvnsgikfyrr 146
 QY 121 YKALARKIVPFIRASGSDRVIASAEKTEGFQSAKLADPGSQPHQASPVINVIPEGSGY 180
 DB 147 ykalarlivpfiragsdrviasaekfiegfsakladpgsqphqaspvdivipegsgy 206
 QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVYVLMDCPF 240
 DB 207 nntldhgtctafedselgddveanftalfapairarleadlpgvltddedvvyvldmcpf 266
 QY 241 DTVARTSDATSELSFPCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 300
 DB 267 etvartsdatselspfcalfthdewioydlqslgkygygagnplgpaqgvgfaneliar 326
 QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSV 360
 DB 327 ltrspvqdhstnhtldsnpatfplnatlyadfsdhntmisiffalglyngtaplstsv 386
 QY 361 ESIEETDGYASWTVPFAARAYVEMMQCAKEPLRVLVNDRVPLHGCVAVDKLGRCR 420
 DB 387 esieetdgyaswtvpfagarayvemmqcqeplrvrlvndrvvplhgcavdklgrckr 446
 QY 421 DDFVEGLSFARSGGNWAECEFA 441
 DB 447 ddfveglsfarsggnwaecefa 467

RESULT 14
 AAW93384
 ID AAW93384 standard; Protein; 467 AA.
 XX
 AC AAW93384;
 XX
 DT 11-JUN-1999 (first entry)
 XX
 DE Fungal consensus phytase protein mutant Q50T-Y51N.
 XX
 KW Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food;
 KW feed additive; variant; mutagen; feed; pharmaceutical.
 OS Fungi.
 OS Synthetic.
 XX
 PN EP897985-A2.
 XX
 PD 24-FEB-1999.
 XX
 PF 15-JUL-1998; 98EP-0113176.
 XX
 PR 24-JUL-1997; 97EP-0112688.
 XX
 PA (HOFF) HOFFMANN LA ROCHE AG F.
 XX
 PI Lehmann M;
 XX
 DR WPI; 1999-134647/12.
 XX
 PT Preparation of a consensus protein, especially a phytase - using
 PT programs to compare evolutionary similarity of sequences
 XX
 PS Claim 9; Page -; 30pp; English.
 XX

```

PR 24-JUL-1997; 97EP-0112688.
XX
XX PA (HOFF ) HOFFMANN LA ROCHE AG F.
XX PI Lehmann M;
XX DR WPI; 1999-134647/12.
XX
PT Preparation of a consensus protein, especially a phytase - using
XX programs to compare evolutionary similarity of sequences
XX
PS Claim 9; Page -: 30pp; English.
XX
CC This invention describes a novel process for the preparation of a
CC consensus protein. The specific example given in the specification is
CC that of a fungal phytase (myo-inositol hexakisphosphate) which
CC hydrolyses phytase to valuable feed additives, with a fully defined amino
CC acid sequence given in the specification, or variant or mutagen. The
CC method is useful for improving protein properties by altering their
CC sequence. The consensus protein and mutagen are useful in food, feed or
CC pharmaceutical compositions. This sequence is a mutant phytase protein of
CC the invention which does not appear in the specification but has been
CC created from the protein represented in AAW93380.
XX
SQ Sequence 467 AA;

```

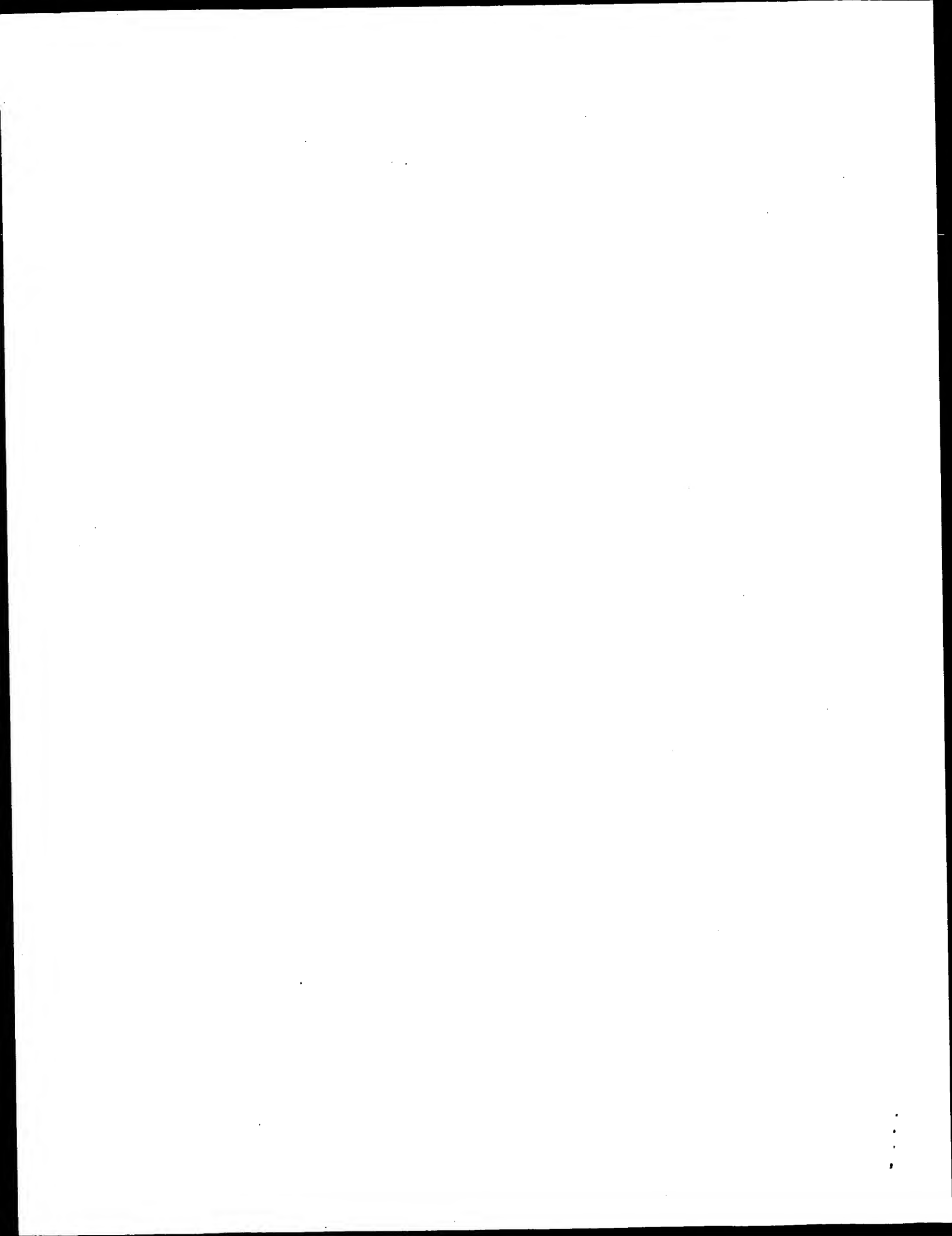
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Db |||||
QY 87 pttsskaysalteaoknatafkayalktynylgaddltpfgenqmvnsgikfyr 146
Db |||||
QY 121 YKALARKIVPFIIRASGDRVIRASAEKFTFEGFSQAKLADPGSQPHQASPVINVIPEGSY 180
Db |||||
QY 147 ykalarxivpfirasgsdrviasaeekftiegfsakladpgsqphqaspvdivipegsgy 206
QY 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRLEADLPVTLTDEDDVYIMDMCPF 240
Db |||||
QY 207 nntldhgtctafedselgddveanftalfapairleadlpvltcdedvvyldmcpf 266
QY 241 DTVARTSDATELSPFCALFTHDEWTDYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 300
Db |||||
QY 267 etvartsdatelspfcalfthdewrtydyqslgkygygagnplgpqgvgfaneliar 326
QY 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMISIFFALCLYNGTKPLSTTSV 360
Db |||||
QY 327 ltrspvqdhstnhtldsnpatfplnatlyadfsdhntmisiffalglyngtaplsttsv 386
QY 361 ESIEETDGYASWTVPFAARAYVEMMQCAEKEPLVRVLVNDVRVPLHGCADVKGKRCRR 420
Db |||||
QY 387 esieetdgyaswtvpfgarayvemmqcaekeplvrvlvndrvvplhgcavdklgrckr 446
QY 421 DDFVEGLSFARSGONWAECEFA 441
Db |||||
QY 447 ddfveglsfarsggnwaecefa 467

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Search completed: October 16, 2001, 17:49:21
Job time: 20970 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 17:47:29 ; Search time 7358.5 Seconds
(without alignments)
1703.402 Million cell updates/sec

Title: US-09-488-265-28_COPY_79_1404
Perfect score: 1326
Sequence: 1 aattcactcttgacac.....gggtgaatttcgcttaa 1326

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Thu Oct 18 11:34:44 2001

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Db 51 GCGATGCCGACAGTATGGGTGCTTCACACGCTGAGCAAGTTCCTTGAGAGCT 1

RESULT 2
LOCUS   AQ255459      837 bp      DNA      GSS      23-OCT-1998
DEFINITION   mgxb0014M15r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
              clone mgxb0014M15r, DNA sequence.
ACCESSION   AQ255459
VERSION     AQ255459.1  GI:3779774
KEYWORDS    GSS.
SOURCE      Magnaporthe grisea.
ORGANISM    Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
REFERENCE   1 (bases 1 to 837)
AUTHORS     Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
            Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE       A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
            Genome
JOURNAL     Unpublished (1998)
COMMENT     Contact: Dean RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson University, Clemson, SC 29634
            Tel: 864 656 5737
            Fax: 864 656 4293
            Email: rdean@clemson.edu
            Seq primer: GGAACAGCTATGACCATG
            Class: BAC ends
            High quality sequence start: 60
            High quality sequence stop: 277.
            Location/Qualifiers
            1..837
               /organism="Magnaporthe grisea"
               /strain="70-15"
               /db_xref="taxon:148305"
               /clone="mgxb0014M15r"
               /clone_lib="CUGI Rice Blast BAC Library"
               /tissue_type="Protoplasts"
               /lab_host="E. coli DH10B"
               /note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
               Rice blast is one of the most devastating fungal diseases
               of rice world wide. It is a filamentous ascomycete with
               a haploid genome (n=7) of approximately 40 Mbp. Rice
               blast is an important model fungal pathogen for studying
               numerous aspects of the fungal-host interaction. In
               order to facilitate genome wide analysis, a BAC library
               containing 9216 clones with an average insert size of 130
               kbp was constructed. This library represents greater
               than 25X genome coverage. High density colony filters
               are available upon request."
               248 a 154 c 188 g 243 t 4 others

BASE COUNT  248 a 154 c 188 g 243 t 4 others
ORIGIN
Query Match      9.2%; Score 122.4; DB 226; Length 837;
Best Local Similarity 55.7%; Pred. No. 5.7e-25;
Matches 234; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

QY 632 cagctattagacgtagattggaagctgactgcccagtggttactttgactgacgaagacg 691
Db 113 CCGGTCTTATACAGCATAGCGTGGGATTTTCAAGTGTGGGTAAACCGGTCAAGACG 172
QY 692 ttgtttacttgagacatgttcattcgacactgctgctagaactcttgacgctactg 751
Db 173 TTGTAATCTTATGGACTGTGCACCATGGAAACACGCGCACTTTGAAAAAATGGCC 232
QY 752 aattgtctccattctgtctgttttctactcacgacgaatgatccatcactgacttgc 811
Db 233 AACTTTACCGCTTTTGCAATCTGTTTACGGAAGCAGATTTGGGTAAAAATATGTTACTTGT 292
QY 812 aaagcttgggtaagtactacgttactgctggttaacccattgggtccagctcaagtg 871

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Db 293 CCAGGCTGCAAAAATGGTACAGATACGAAACGGTAATCTTTGGGCCCAACTATGGCG 352
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Db 353 TGGGATGGGTAAACGAACTTATTCACGATTAAACCCGAAAGCCAGTCCCAAGATCAAAACCA 412
QY 932 ctactaaccaacttgactgacttaaccagctactttcccatggaacgactactttgtacg 991
Db 413 TGTCCAATACGACACTTCACATGAACCGCGGAAACCTTACCTCTACAAAGGCAAAATGTTATG 472
QY 992 ctgactttctctcaagacacactatgatctatcttattttctgtgttgggtttgtacaacg 1051
Db 473 CTGATTTTATCCATACGACGATATATAGGATTTAGCGCGCTTTGGGCTATTTAAACG 532

RESULT 3
LOCUS   AJ274007      581 bp      mRNA      EST      29-DEC-1999
DEFINITION   AJ274007 Metarhizium anisopliae ARSEF 2575 Metarhizium anisopliae
              cDNA clone Ma#1628, mRNA sequence.
ACCESSION   AJ274007
VERSION     AJ274007.1  GI:6433380
KEYWORDS    EST.
SOURCE      Metarhizium anisopliae.
ORGANISM    Metarhizium anisopliae
            Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Metarhizium.
REFERENCE   1 (bases 1 to 581)
AUTHORS     Screen, S.E., Mathur, P. and St. Leger, R.J.
TITLE       EST analysis of the insect pathogenic fungus Metarhizium anisopliae
JOURNAL     Unpublished (1999)
COMMENT     Contact: Screen SE
            Entomology
            University of Maryland
            4112 Plant Sciences Building, College Park, MD 20742, USA.

FEATURES             source
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                        /db_xref="taxon:5530"
                        /clone="Ma#1628"
                        /clone_lib="Metarhizium anisopliae ARSEF 2575"
                        /note="Vector: Unizap; Metarhizium anisopliae was grown on
                        insect cuticle for 24 hours. A cDNA library was
                        constructed in the unidirectional Lambda vector, Unizap"
BASE COUNT  138 a 153 c 146 g 144 t
ORIGIN
Query Match      8.1%; Score 107.4; DB 104; Length 581;
Best Local Similarity 57.5%; Pred. No. 1.3e-20;
Matches 233; Conservative 0; Mismatches 166; Indels 6; Gaps 2;

QY 64 tgggttacctactctccatactctcttggcagacgaatctgctattctctccagcgtt 123
Db 163 TGGGCCCATGACTCGCGGTACTTCTC---AGCACACAAGGATCTATTAAAGCTGCATC 219
QY 124 ccagacgactgtagagttacttttctcaagttttcttagacacggtgctgataccca 183
Db 220 CCGTCGGGATCGGAGGTCACCTTTCCTTCAATCTTCTCGCATGGGTCCGCGCAACCG 279
QY 184 acttctctcgctcaaggcttactctgcttggattgaagctattccaaagaacgctact 243
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QY 244 gctttcaagggttaagtacgcttttttgaagacttacaactcttggttggtgacgac 303
Db 340 GACTATGGGAAGGGCTTCGAGTTTCTCAAGATTAACAAGTACTTAGTCTCTGACGAC 399
QY 304 ttgactccattcggtgaaacccaaatggttaacctctggtatttaagtctcacagaatac 363
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QY 364 aaggcttgggttagaaa---gatgttccattcattagagcttctggttctgacagatt 420
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Db 460 CAGAGTTAGCGGAGGATTGACCCATCCCTTTGTCGAGCCCTCGGGCTCTGAAGAGTC 519
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QY 421 attgcttctgctgaaaaagttcattgaaggtttccaattctgctaa 465
    || || || || || || || || || || || || || || || || || || || || ||
Db 520 GTCATGTGACGGCAAGATTTTGTTCATGGCTTCTACAAAGCCCAAG 564
    || || || || || || || || || || || || || || || || || || || || ||

RESULT 4
LOCUS AQ163004 753 bp DNA GSS 09-SEP-1998
DEFINITION mgxb0021D19r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0021D19r, DNA sequence.
ACCESSION AQ163004
VERSION AQ163004.1 GI:3559405
KEYWORDS GSS.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 753)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 448.
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/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/Note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
BASE COUNT 208 a 180 c 156 g 206 t 3 others
ORIGIN

Query Match 6.1%; Score 80.8; DB 225; Length 753;
Best Local Similarity 48.8%; Pred. No. 1e-12;
Matches 274; Conservative 0; Mismatches 280; Indels 7; Gaps 2;

QY 12 ttgtgacactgttgacgtgttaccacattttccacagaaattctcactgttggtgtac 71
    || || || || || || || || || || || || || || || || || || || || ||
Db 189 TTTTGTATGCGCCAGCGCGGTTTCAATTAAAGCAGCAATCACTCAATTTGGGCCA 248
    || || || || || || || || || || || || || || || || || || || || ||
QY 72 ctactctccacttctcttcttgacagacgaatctgtatttctccagagttccagac-- 129
    || || || || || || || || || || || || || || || || || || || || ||
Db 249 GTATGCACCAATTTTCTGTCACCGTCAGCACCATCGGATTATGATCTCTGCTACCTT 308
    || || || || || || || || || || || || || || || || || || || || ||

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QY 130 ----gactgtagagttacttctgctcaagtttctgtctagacacggtgctagatacccaac 185
    || || || || || || || || || || || || || || || || || || || || ||
Db 309 GCCAGGTTAGCAATACGTTTGCCCAAGTCTTCAGAGGCACGCGGCTCGATACCCAAC 368
    || || || || || || || || || || || || || || || || || || || || ||
QY 186 ttcttgcgtctaaagccttactctgctgttggattgaagctatttcaaaagaacgctactgc 245
    || || || || || || || || || || || || || || || || || || || || ||
Db 369 CGCTCAAAACCGGCGGAAATCTCGAACAGATTACCGGACTCCAAACCTCAGTACCGG 428
    || || || || || || || || || || || || || || || || || || || || ||
QY 246 ttcaaggglaagtaagccttcttgaagagcttacaactacacttcttgggtgctgaagactt 305
    || || || || || || || || || || || || || || || || || || || || ||
Db 429 TAGTGGCGTATTGAATTAACATTAATAAACTACAAATACAATCTCGGAGTCGAGGAATN 488
    || || || || || || || || || || || || || || || || || || || || ||
QY 306 gactccactcgttggaacacccaatggttaactctgttatttaagttctacagaagatacaa 365
    || || || || || || || || || || || || || || || || || || || || ||
Db 489 GAATGATTTCGGCGCTCGGCAACACAGAACTCCGGGTATTNATTTTCCAAAGATACCA 548
    || || || || || || || || || || || || || || || || || || || || ||
QY 366 ggcttggctagaagaattgttccattcattagagcttctggttctgacagagttattgc 425
    || || || || || || || || || || || || || || || || || || || || ||
Db 549 AATCTGGCCAGAGGAACGAACCAATTTATTCGCTATGATGACAAANAACGCGTGTGGA 608
    || || || || || || || || || || || || || || || || || || || || ||
QY 426 ttctgtgaaaagttcattgaaggtttccaatctgctaaagttggctgaccaggttctca 485
    || || || || || || || || || || || || || || || || || || || || ||
Db 609 TAGCGCAGAACTCTGGGCTAGGGGTTT-CATCGAGCTTCTATAACAGATAAAGCCGGGC 667
    || || || || || || || || || || || || || || || || || || || || ||
QY 486 accacaccagcttctccagttatttaacgctgattcattccagaagatccggtttacaacaa 545
    || || || || || || || || || || || || || || || || || || || || ||
Db 668 TAGACCAGAAACCTTTCCCTCACAAAGCTGTGGCGCTTCTCACCAGCATGGTTTATAA 727
    || || || || || || || || || || || || || || || || || || || || ||
QY 546 cacttggaccagcgttacttg 566
    || || || || || || || || || || || || || || || || || || || || ||
Db 728 TACCTTTGACAAATAAGCTTG 748
    || || || || || || || || || || || || || || || || || || || || ||

RESULT 5
LOCUS AQ162040/6 699 bp DNA GSS 09-SEP-1998
DEFINITION mgxb0010F06r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0010F06r, DNA sequence.
ACCESSION AQ162040
VERSION AQ162040.1 GI:3558441
KEYWORDS GSS.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 699)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 285.
Location/Qualifiers
1. .699
/organism="Magnaporthe grisea"
/strain="70-15"
/db.xref="taxon:148305"
/clone="mgxb0010F06r"
/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/Note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
BASE COUNT 208 a 180 c 156 g 206 t 3 others
ORIGIN

Query Match 6.1%; Score 80.8; DB 225; Length 753;
Best Local Similarity 48.8%; Pred. No. 1e-12;
Matches 274; Conservative 0; Mismatches 280; Indels 7; Gaps 2;

QY 12 ttgtgacactgttgacgtgttaccacattttccacagaaattctcactgttggtgtac 71
    || || || || || || || || || || || || || || || || || || || || ||
Db 189 TTTTGTATGCGCCAGCGCGGTTTCAATTAAAGCAGCAATCACTCAATTTGGGCCA 248
    || || || || || || || || || || || || || || || || || || || || ||
QY 72 ctactctccacttctcttcttgacagacgaatctgtatttctccagagttccagac-- 129
    || || || || || || || || || || || || || || || || || || || || ||
Db 249 GTATGCACCAATTTTCTGTCACCGTCAGCACCATCGGATTATGATCTCTGCTACCTT 308
    || || || || || || || || || || || || || || || || || || || || ||

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1. .699
/organism="Magnaporthe grisea"
/strain="70-15"
/db.xref="taxon:148305"
/clone="mgxb0010F06r"
/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/Note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with

a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

Query Match	6.0%	Score 79.8;	DB 225;	Length 699;
Best Local Similarity	59.5%;	Pred. No. 2e-12;		
Matches 135;	Conservative	0;	Mismatches 92;	Indels 0; Gaps 0;
Qy	1100	acggttactctgtcttgcaactctccattcgctgctagagcttacgttgaaatgatgc	1159	
Db	651	ACGGGTTCCTCCTCAGTTGGCGGTACCGTTCGCACGGAGAATGTTGTGAAAAATGA	592	
Qy	1160	aatgtcaagctgaaaggaaccattggttagagtttggttaacagacagagttgttccat	1219	
Db	591	CTTGGCGCAGGCGCAGAACGAGAGCTTGTGAGAAATCCTGGTCAACGACAGGTTGACGCCGC	532	
Qy	1220	tgaacggttgctgttgacaagttaggttagatgtaagagagacacacttcggtgaagtt	1279	
Db	531	TGCAGAACTGGCATGCCGCACAGTATGGTTCCTTGCACGTGACCAAGTTCGTTGAGAGCT	472	
Qy	1280	tgtctttcgctagatctggtgtaactgggctgaatttttcgcttaa	1326	
Db	471	TAAAGCTTTGCCAGAGGTTGGAGTGCCTGGGATCAATGTTTTGTCTGA	425	

RESULT 6	810 bp	DNA	GSS	09-SEP-1998
SEQ161556/c				
LOCUS	mgxb0008k02r	CUGI Rice Blast BAC Library	Magnaporthe grisea genomic	
DEFINITION	clone mgxb0008k02r,	DNA sequence.		
ACCESSION	A0161556			
VERSION	A0161556.1	GI:3557957		
KEYWORDS	GSS.			
SOURCE	Magnaporthe grisea.			
ORGANISM	Magnaporthe grisea			
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
AUTHORS	Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.			
	1 (bases 1 to 810)			
	Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,			
	Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.			
TITLE	A BAC End Sequencing Framework to Sequence the Magnaporthe grisea			
	Genome			
JOURNAL	Unpublished (1998)			
COMMENT	Contact: Dean RA			
	Clemson University Genomics Institute			
	Clemson University			
	100 Jordan Hall, Clemson University, Clemson, SC 29634			
	Tel: 864 656 5737			
	Fax: 864 656 4293			
	Email: rdean@clemson.edu			
	Seq primer: GGAACACAGCTATGACCATG			
	Class: BAC ends			
	High quality sequence stop: 321.			

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FEATURES
source
1. .810
Location/Qualifiers
/organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0008K02r"
/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with

```

a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important fungal pathogen for studying numerous aspects of the fungal-host interaction. In facilitating genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

BASE COUNT	196 a	219 c	188 g	207 t	
Query Match	5.6%	Score 74;	DB 225;	Length 810;	
Best Local Similarity	58.0%;	Pred. No. 1.1e-10;			0;
Matches 131;	Conservative	0; Mismatches 95;	Indels	0; Gaps	
QY	1101	cggttaactctgtcttctggaactgttcacatcgtcgtctagagctttagcttgaaatgatgca	1160		
Db	650	CGGGTTCFCGCCAGCTGGGGGGTACCGTTCGCAGCGCAGATCTTTGTGAAAAAATGAC	591		
QY	1161	atgtcaagctgaaagaaacccattgggttagagttttggttaacgacagagttgttccatt	1220		
Db	590	TTGCCAGGGCAGAACGAGGAGCTTGTGAGATCTCTGGTCAACGACAGGGTGACGCCGCT	531		
QY	1221	gaocggttgctgctgttgacaagttgggtatagataagagacgactctgttgaaggttt	1280		
Db	530	GCAGAACTTGCATGCCACAGTAGTGGGTCTCTTGCACTGTGACCAAGTCGTTGAGAGCTT	471		
QY	1281	gtcttgcctagatctggtgtgaactgggctgaatttttcgttaa	1326		
Db	470	AGCGCTTCGGAGCTGGAGCTCCCTGGGATCAATGTTTGTCTGA	425		

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RESULT 7
AQ361495/c
LOCUS
DEFINITION
        669 bp      DNA
        GSS
        O3-FEB-1999
        BAC Library Magnaporthe grisea genomic
        clone mgxb0004K10r, DNA sequence.
ACCESSION
        AQ361495
VERSION
        1
KEYWORDS
        GI:4211334
SOURCE
        Magnaporthe grisea.
        Magnaporthe grisea
        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
        Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
        1 (bases 1 to 693)
REFERENCE
        Yu, Y., Zhu, H., Boyd, C.A., Caudette, B., Gayle, A., Kingsbury, R.,
        Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
        A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
        Genome
        Unpublished (1998)
        Contact: Dean RA
        Clemson University Genomics Institute
        Clemson University
        100 Jordan Hall, Clemson University, Clemson, SC 29634
        Tel: 864 656 5737
        Fax: 864 656 4293
        Email: rdean@clemson.edu
        Seq primer: GGAACAGCTATGACCATG
        Class: BAC ends
        high quality sequence stop: 465.

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FEATURES
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Location/Qualifiers
1. .669
/organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
/clone_lib="mgxb0004K10r"
/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII; Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with

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QY 423 tgcttctgctgaagaagttcattgaaggttc 453
| | | | | | | | | | | | | | | | | | | | |
Db 692 TGATGCGCAGAACCTTGGGCTTAGGGTTTC 722

RESULT 9
AQ020816 481 bp DNA GSS 20-APR-1999
LOCUS
DEFINITION
  RPc111-48J14.TK RPc11-11 Homo sapiens genomic clone RPc11-48J14,
  DNA sequence.
ACCESSION
  AQ020816
VERSION
  AQ020816.1 GI:3613607
KEYWORDS
  GSS.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 481)
REFERENCE
  Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
  Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
  Use of human BAC End Sequences for Sequence-Ready Map Building
  Unpublished (1998)
  Other GSSs: RPc111-48J14.TJ
  Contact: Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: mdadams@tigr.org
  Clones are derived from the human BAC library RPc11-11. For BAC
  library availability, please contact pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
  Research Genetics (info@resgen.com). BAC end search page:
  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
  Class: BAC ends.

FEATURES
  source
  Location/Qualifiers
  1..481
  /organism="Homo sapiens"
  /db_xref="GDB:751827"
  /db_xref="taxon:9606"
  /clone="RPc11-48J14"
  /clone_lib="RPc11-11"
  /sex="Male"
  /cell_type="Lymphocytes"
  /note="Vector: pBac3.6; Site_1: EcoRI; Site_2: EcoRI;
  RPc111 Human Male BAC Library"
  BASE COUNT 150 a 99 c 81 g 151 t
  ORIGIN

Query Match 3.3%; Score 43.4; DB 225; Length 481;
Best Local Similarity 45.8%; Pred. No. 0.097;
Matches 149; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 888 attatgctagattgactcactccagttcaagaccacactctactaacacacttt 947
| | | | | | | | | | | | | | | | | | | | |
Db 58 ATTATTATTTGCTTGAATTTCTCGAGAGTACCTGATTTCTGCTCCATCCCACTCT 117
| | | | | | | | | | | | | | | | | | | | |

QY 948 ggaacttaacccagctactttcccattgaacgctactttgacgtgactctctcaca 1007
| | | | | | | | | | | | | | | | | | | | |
Db 118 ATACACCTCCCTCCACTTTTCCAAATGAAGTGAATCTAGCCACTTACTCAATTCCTCC 177
| | | | | | | | | | | | | | | | | | | | |

QY 1008 caacactatgatattcttctcgtttgttggtttgtatacaacggtaccagcaattgtc 1067
| | | | | | | | | | | | | | | | | | | | |
Db 178 AGATAAGAAGCTCCTAAGATGGTCCACCCCGCTTTTAAACACCACTATCAGAAAGTTCG 237
| | | | | | | | | | | | | | | | | | | | |

QY 1068 tactactctgttgtaactattgaagaactgaacggttactctctcttcttggaactgttc 1127
| | | | | | | | | | | | | | | | | | | | |
Db 238 TTATATTACACTGAAGCCTCTCGAAAATGAGGATGATGATAAAGTTCAAGATGTACTTTTAC 297
| | | | | | | | | | | | | | | | | | | | |

QY 1128 attcgtctgtagacttactgctgaaatgatgcaatgctcaagctgaagaagcaaccttggt 1187
| | | | | | | | | | | | | | | | | | | | |

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Db 298 CTGGTACCTTTTGTATCACTTGGCTAAGAACTAGTCAGACGTTTGAACAAACAAAGTA 357
| | | | | | | | | | | | | | | | | | | | |
QY 1188 tagagttttggttaacgacagagatt 1212
| | | | | | | | | | | | | | | | | | | | |
Db 358 AAGGTATTCTTTTAGTAAAGATTT 382
| | | | | | | | | | | | | | | | | | | | |

RESULT 10
AV129427 231 bp mRNA EST 01-JUL-1999
LOCUS
DEFINITION
  AV129427 Mus musculus C57BL/6J 11-day embryo Mus musculus CDNA
  clone 2700068B02, mRNA sequence.
ACCESSION
  AV129427
VERSION
  AV129427.1 GI:5315662
KEYWORDS
  EST.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 231)
REFERENCE
  Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
  Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
  ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
  Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
  Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
  ,Y., Suzuki,H., Tateo,M., Tomaru,Y., Tomimaga,N.,
  Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
  Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  RIKEN Mouse ESTs
  Unpublished (1999)
  Contact: Chie Owa
  Genome Science Laboratory
  RIKEN
  3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
  Tel: 81-298-36-9145
  Fax: 81-298-36-9098
  Email: genome-res@rtc.riken.go.jp
  Thermostabilization and thermoactivation of thermolabile enzymes by
  trehalose and its application for the synthesis of full length cDNA
  (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
  Transcriptional sequencing: A method for DNA sequencing using RNA
  polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
  Please visit our web site (http://genome.rtc.riken.go.jp) for
  further details.
FEATURES
  Location/Qualifiers
  1..231
  /organism="Mus musculus"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="2700068B02"
  /clone_lib="Mus musculus C57BL/6J 11-day embryo"
  /sex="mixed"
  /dev_stage="11-day embryo"
  BASE COUNT 59 a 51 c 66 g 55 t
  ORIGIN

Query Match 3.1%; Score 41.2; DB 25; Length 231;
Best Local Similarity 52.3%; Pred. No. 0.34;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1076 ctgttgaaactattgaagaactgacgggttactcttcttgactgttccattcgtcg 1135
| | | | | | | | | | | | | | | | | | | | |
Db 40 CAGCTGGACCCGATCCAGCACTGAAGCTGTGCCCTGGTGGTGTCTGTTCATCCACTG 99
| | | | | | | | | | | | | | | | | | | | |

QY 1136 ctagagcttacgttgaatgatgcaatgccaagctgaagaagcaaccattggttagattt 1195
| | | | | | | | | | | | | | | | | | | | |
Db 100 CCGCCGCCCGCTGAGGAGAGAAAGTGGAGGCAAGAAAGAGTGTCCGAGGAGTCTG 159
| | | | | | | | | | | | | | | | | | | | |

QY 1196 tggtttaacgacagagttgttccattgcacgggttgctgtgttgacaagttggata 1249
| | | | | | | | | | | | | | | | | | | | |
Db 160 AAGATGACATGGGCTTCGGTCTCTTTTGTACTAAACACTGCTTTTGAAGTTGGCTA 213
| | | | | | | | | | | | | | | | | | | | |

```


us-09-488-265-28_copy_79_1404.rst

Thu Oct 18 11:34:44 2001

GenCore version 4.5
Copyright (C) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 12:04:44 ; Search time 220.1 Seconds
(without alignments)
1140.511 Million cell updates/sec

Title: US-09-488-265-28_COPY_79_1404

Perfect score: 1326

Sequence: 1 aattctcaactctgtgacac.....gggctgaatttctcgcttaa 1326

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCNTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1282.8	96.7	1426	3	US-09-121-425-3
2	621.2	46.8	1404	1	US-08-151-574-33
3	621.2	46.8	1404	1	US-08-146-424-19
4	621.2	46.8	1404	1	US-08-693-709-1
5	621.2	46.8	1404	2	US-08-419-448-33
6	621.2	46.8	6756	2	US-08-151-574-31
7	621.2	46.8	6756	2	US-08-419-448-31
8	617.8	46.6	2363	1	US-07-923-724-7
9	617.8	46.6	2363	2	US-08-609-426A-7
10	617.8	46.6	2379	2	US-08-374-652C-1
11	609.8	46.0	1332	3	US-09-155-855-4
12	609.8	46.0	1515	3	US-09-155-855-5
13	333.2	25.1	2200	2	US-08-819-825-1
14	333.2	25.1	2200	4	US-09-163-642-1
15	122.8	9.3	1320	3	US-09-221-654-1
16	122.8	9.3	1320	3	US-08-989-358A-1
17	112.8	8.3	1593	3	US-08-993-359-23
18	112.8	8.3	1593	3	US-08-993-359-21
19	95.6	7.2	1522	3	US-08-993-359-25
20	88	6.6	1642	3	US-08-993-359-27
21	83.4	6.3	1536	3	US-08-993-359-29
22	45.6	3.4	7218	1	US-08-232-463-14
23	45.2	3.4	99	2	US-08-151-574-12
24	45.2	3.4	99	2	US-08-419-448-12
25	42.4	3.2	1631	2	US-08-498-263-5
26	42.4	3.2	1631	2	US-08-977-060-5
27	42.4	3.2	1631	3	US-09-014-583-2

28	33.2	2.5	1309	6	5221624-4	Patent No. 5221624
29	32.6	2.5	585	3	US-08-882-501-28	Sequence 28, Appl
c 30	32.6	2.5	1167	1	US-08-261-110A-3	Sequence 3, Appl
c 31	32.6	2.5	1404	1	US-08-261-110A-1	Sequence 1, Appl
32	32.4	2.4	66	2	US-08-151-574-11	Sequence 11, Appl
33	32.4	2.4	66	2	US-08-419-448-11	Sequence 11, Appl
34	32.4	2.4	2126	4	US-08-235-836C-75	Sequence 75, Appl
35	32	2.4	32	3	US-09-121-425-13	Sequence 13, Appl
c 36	32	2.4	32	3	US-09-121-425-14	Sequence 14, Appl
c 37	31.8	2.4	1193	2	US-08-747-788-1	Sequence 1, Appl
c 38	31.8	2.4	2406	1	US-07-689-008-4	Sequence 4, Appl
c 39	31.8	2.4	9540	1	US-07-689-008-1	Sequence 1, Appl
c 40	31.6	2.4	1803	3	US-08-657-868B-2	Sequence 2, Appl
c 41	31.6	2.4	1829	3	US-08-657-868B-1	Sequence 1, Appl
c 42	31.2	2.4	412	1	US-08-084-718-74	Sequence 74, Appl
43	31.2	2.4	412	1	US-08-443-976-74	Sequence 74, Appl
44	31.2	2.4	412	1	US-08-443-977-74	Sequence 74, Appl
45	31.2	2.4	720	3	US-09-479-309-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-121-425-3

; Sequence 3, Application US/09121425

; Patent No. 6153418

; GENERAL INFORMATION:

; APPLICANT: Lehmann, Martin

; TITLE OF INVENTION: Consensus Phytases

; FILE REFERENCE: Consensus Phytases 13239

; CURRENT APPLICATION NUMBER: US/09/121,425

; CURRENT FILING DATE: 1998-07-23

; EARLIER APPLICATION NUMBER: EPO 97112688.3

; EARLIER FILING DATE: 1997-07-24

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 3

; LENGTH: 1426

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:consensus

; OTHER INFORMATION: sequence

US-09-121-425-3

Query Match 96.7%; Score 1282.8; DB 3; Length 1426;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1299; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY	1	aattctcaactctgtgacacactgttgacggtgtgtaccgaatgtttccagaaaatttctcac	60
DB	90	aattctcaactctgtgacacactgttgacggtgtgtaccgaatgtttccagaaaatttctcac	149
QY	61	ttgtgggtgtacactctctcaccactctctttgtgcagacgaatctgctatttctccagac	120
DB	150	ttgtgggtgtacactctctcaccactctctttgtgcagacgaatctgctatttctccagac	209
QY	121	gttcacagacgactgtagagttactctgttcgaattttgtctagacacggtgtctagatac	180
DB	210	gttcacagacgactgtagagttactctgttcgaattttgtctagacacggtgtctagatac	269
QY	181	ccaactctctgtcgtcctaaagcttactctgttcgaattttgtctagacacggtgtctagat	240
DB	270	ccaactctctgtcgtcctaaagcttactctgttcgaattttgtctagacacggtgtctagat	329
QY	241	actgctttcaagggtgaagtacgcttcttgaagacttcaactacactttgggtgctgac	300
DB	330	actgctttcaagggtgaagtacgcttcttgaagacttcaactacactttgggtgctgac	389
QY	301	gacttgactccattcggtgaaacacaaatggttaactctggtatttaagttctacagaaga	360

QY 252 gggtaagtaagcttcttgaagacttaacactacacttgggtgtgacgacttgactcc 311
Db 330 CGGAAATATGCTTCTGGAAGACATACAACTACAGCTTGGGTGCAGATGACCTGACTCC 389
QY 312 attgggtgaacacacaaatggttaactctgtgtattaaagttctacagaagaacaggttt 371
Db 390 CTTGGGAGAACAGAGTAGTCAACTCCGGCATCAAGTTCTACAGCGGTAGCAATCGCT 449
QY 372 ggttagaagatgttccattcattagagcttctgtttctgtttctgacagagtattgtcttc 431
Db 450 CACAAGGAACATCGTTCATTCATCGATCCTCTGGCTCCAGCCGCTGATCGCTCCGG 509
QY 432 tgaagagttcattgaaggtttccaaactgtcgttaagttggtgacccagattctcaaccaca 491
Db 510 CAAGAAATTCATCGAGGGTTCAGAGCACCAGCTGAAGATCTCTGTCGCCAGCCGG 569
QY 492 ccaagcttccagattattaaagtgatcattccagaagatccggttacaacacacttt 551
Db 570 CCATCGTCGCCACAGATCGAGCTGCTCATTTCCGAGGCCAGCTCATCCAACACACTCT 629
QY 552 ggaacacggtactgttactgtcttctgaagactctgaattaggtgaagctgacttgccaggtgt 671
Db 630 CGACCCAGGACCTGCACCTGTCTTCAAGACAGCGAATGGCCGATACCGTCGAAGCCAA 689
QY 612 cttcactgtttgttctcagctatttagagctagattgagctgacttgccaggtgt 749
Db 690 TTTACCGCCAGCTGCTGCTCCCTCCATTCGTCACGCTGAGAACGACCTGTCCGGTGT 731
QY 672 tacttgactgacgagagctgtttactgttactgtatggaacatgtgtccatcgacactgtcgc 791
Db 750 GACTCTCAGACACAGAAAGTGACCTACCTCATGGACATGTGTCTTCGACCATCCTC 809
QY 732 tagaactctgacgctactgttctccattctgtcttctgttcttactcagacagaaatg 791
Db 810 CACCAGCACCGTCGACACCAAGCTGTCCCTCTCTGTGACTGTTCACCATGACCAATG 869
QY 792 gatccaataacactacttgcaaaacttgggttaagtaactacggttaacggtgctgtaaccc 851
Db 870 GATCAACTACGACTACCTCCAGTCCCTTGAAGAAAGTATTAGGGCATGCTGCAGGTAACCC 929
QY 852 attgggtccagctcaaggtgtgtgtctgctacgaaatgactgactgactgactcactc 911
Db 930 GCTCGGCCCGACCCAGGCGCTGCTGCTAGCTAGGAGCTCATGCCCGCTGTGACCCACTC 989
QY 912 tccagttcaagacacacttctactaaccacactttggactctaaacccagctacttccc 971
Db 990 GCCTGTCCAGCATGACACCAAGCTTCCAAACACACTTTGGACTCGAGCCCGCTACCTTCC 1049
QY 972 attgaagctactttgacgctacttctcagacacacactatgatctatttttt 1031
Db 1050 GCTCAACTCTACTCTTACGCGGACTTTTCGATGACAAAGGCAATCATCTCCATTCTCT 1109
QY 1032 cgtttgtgggtttgataacggttaccagcattgtctactacttctgttgatctatga 1091
Db 1110 TGCTTTTAGTCTGTACACCGCACTAAGCGCTATCTACCAGCAGCTCGGAGAAATATCAC 1169
QY 1092 agaaactgacggttactctctcttctgactgttccactcgtgtgtagacttaagttga 1151
Db 1170 CCAGACAGATGGATCTCTGCTGTGGACGGTTCGGTTGCTGCGGTTGTAGCTCGA 1229
QY 1152 aatgatgcaatgtcaagctgaaaggaacattggttagatttttggtaacagacagagt 1211
Db 1230 GATGATGCACTGTACGCGGAGCAGAGCGCTGTGCTGCTGTGCTGTGCTGTGCTGTGCT 1289
QY 1212 ttttcaattgacaggtttgtctgtttgacaagttgggttagatgaagagacgacttcgt 1271
Db 1290 TGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1349
QY 1272 tgaaggtttgtctcgttagatctgtgtgttaactgggctgaatgttcgctta 1325
Db 1350 GAGGGGTTGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1403

RESULT 3
US-08-146-424-19
Sequence 19, Application US/08146424
Patent No. 5593963
GENERAL INFORMATION:
APPLICANT: VAN OIJEN, ALBERT J. J.
APPLICANT: RIETVELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: PEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,424
FILING DATE: 02-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KENNEDY, BILL
REGISTRATION NUMBER: 33,407
REFERENCE/DOCKET NUMBER: 44615-20011.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1401
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 70
US-08-146-424-19

Query Match 46.8%; Score 621.2; DB 1; Length 1404;
Best Local Similarity 67.0%; Pred. No. 5.7e-178;
Matches 881; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

QY 12 ttgtgacactgttgacggtgtttaccatgtttccagaaatttctcactgtgtgggtac 71
Db 90 TTGCGATGCGGTCTGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATCTTTGGGTCA 149
QY 72 ctactctccatacttcttggcagacgaactctgtctatttctccagacgttccagaca 131
Db 150 ATAGGACCGTCTTCTCTCTCTGCAACGAATCGGTCTATCTCCCTGAGGTGCCCGCG 209
QY 132 ctgtagagtacttttctgaagtttcttagacacggtgtgtagatcccaactttctc 191
Db 210 ATGAGAGTCACTTTTCCTCAGGTCTCTCCCGTATCGAGCGGTATCGACCGACTC 269
QY 192 tgcgtctaaggttactctgtttgttattgaagctattcaaaagacgctactgtttcaa 251
Db 270 CAAAGGCAAGAAATATCTCGCTCTCATTTGAGAGATCCAGCAGAACGACCACTTTGA 329
QY 252 gggtaagtaagcttcttgaagacttaacactacacttgggtgtgacttgactcc 311

Thu Oct 18 11:34:44 2001

DB 330 CGGAAATATGCTTCCCTGACACATACACATACAGCTTGGGTGCAGATGACCTGACTCC 389
QY 312 attcgtgtaaaacaaatggttaactctgttattatgaattctacagaagatatacaggcttt 371
DB 390 CTTGCGAGAACAGGAGCTAGTCAACTCGCGCATCAAGTTCTACCAAGCGGTAGCAATCGCT 449
QY 372 gactagaagaattgttccattatgactcttctgttctgttctgtacagagatttattgctctgc 431
DB 450 CACAAGAACATCGTTCCATTATTCGATCTCTGGCTCCAGCCGGTGATCGCTCCGG 509
QY 432 tgaagatttcattgaaggtttccaatctgtctgaattggtgctgacccaggtttctcaaccaca 491
DB 510 CAAGAATTCATCGAGGGTTCAGAGCACCAGCTGAAGGATCTCGTGGCCAGCCGG 569
QY 492 ccaagcttccagttattaaagtgatcattccagaagatcgggttacaacaaacacttt 551
DB 570 CCAATCGTCGCCCAAGATCGACGTGCTCATTTCCGAGGCCAGCTCATCCCAACACACTCT 629
QY 552 ggaccacggttactgttactgttcttccaaactctgaattaggtgacgacggttgaagctaa 611
DB 630 CGACCCAGGCACTGCATCTTCCGAAGACAGCAATTTGGCGGATACCGTCCGAAGCCAA 689
QY 612 cttoactgttctgttgcgtccagctattagagctagattggaagctgactgtccaggtgt 671
DB 690 TTTTACCGCCACGCTGCTGCTCCCTCCATTCGTCAACGCTGTGGAAACGACTGTCCGGTGT 749
QY 672 tacttgaactgacgaagactgttactgttactgttactgttactgttactgttactgttactgtt 731
DB 750 GACTCTCAGACACACAGAGTGAACCTACCTACCTGATGGATGTGCTCTCGACACCATCTC 809
QY 732 tagaactctgaagctactgaattgtctccattctgtctgttcttactcactcagcagaatg 791
DB 810 CACCAGCACCGCTGACACACAGCTGTGCTCCCTTCTGTGACTGTTCACCCATGACCAATG 869
QY 792 gatccaatagactactgtcaaaagctgggttaagactactacggttactggtggtgtaaccc 851
DB 870 GATCACTACGACTACCTCCAGCTCTTGAAGAAAGTATTACGGCCATGGTCCAGGTAACCC 929
QY 852 attgggtccagctcaaggtgtgttctgcgttaacgaattgattgctagattgactcactc 911
DB 930 GCTGGCCGACCCAGGCGGTGCGGTACGTTACGAGCTCATGCGCCGTCTGACCCACTC 989
QY 912 tccagctcaagacacactctactaaccactttggaactcttaacccagctacttccc 971
DB 990 GCCTGTCACGATGACACAGTTCACACACACTTTGGACTCGAGCCGCGTACCTTTCC 1049
QY 972 attgaacgctactttgtactgctgactctctcactcagcaaacactatgatatattctt 1031
DB 1050 GCTCAACTCTACTCTCTACGGGACTTTTTCGATGACAAACGGCATCATCTCCATCTCTT 1109
QY 1032 cgtcttggtgtttgtacacggttaccacgaactgtctactactctgttgaactctatga 1091
DB 1110 TGTGATGCTGTGTGTACACAGGCACTAACCGCTATCTACACAGCGGTGGAGATATCAC 1169
QY 1092 agaaactgacggttactctgtcttctgactgttccactcgtcgtcgtcgtcgttactgtga 1151
DB 1170 CCAGACAGATGATCTGCTGCTGCTGAGCGGTTCGCTTGTGCTGCGCTTTGTGCTGCA 1229
QY 1152 aatgatgaatgtcaagctgaaagaaacacattggttagagtttgggttaacgacagagt 1211
DB 1230 GATGATGCTGTGTGTACACAGGCACTAACCGCTATCTACACAGCGGTGGAGATATCAC 1289
QY 1212 tgttccattgacggttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1271
DB 1290 TGTCCCGCTGCATGGGTGTCGGGTGATGATCTTTGGGGAGATGTACCCGGGATAGCTTGT 1349
QY 1272 tgaaggttctgttcttctgtctgtctgtctgtctgtctgtctgtctgtctgtctgtctgt 1325
DB 1350 GAGGGGGTGTAGCTTGTCTGTGCTGGGGGTGATTGGGGGGAGTGTGTGTGCTTA 1403

RESULT 4

US-08-693-709-1
; Sequence 1, Application US/08693709
; Patent No. 5770413
; GENERAL INFORMATION:
; APPLICANT: VAN OIJEN, ALBERT J.J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIMONS, PETER C.
; APPLICANT: VERMOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,709
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,424
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20011.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1401
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: 70...1401
; OTHER INFORMATION:
; NAME/KEY: Signal Sequence
; LOCATION: 1...72
; OTHER INFORMATION:
; US-08-693-709-1

Query Match 46.8%; Score 621.2; DB 1; Length 1404;
Best Local Similarity 67.0%; Pred. No. 5.7e-178;
Matches 881; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

QY 12 ttgtgacactgttgacggtgtgttaccactttccacagaaattctcacttgggggtac 71
DB 90 TTGGGATACGGTGCATCAGGGGTATCAATCTTCTCCGAGACTTCGATCTTTGGGGTCA 149
QY 72 ctactctccactctcttcttggcagcagactgtctatttctccagacttccacagca 131
DB 150 ATACCGACCGTCTCTCTCTGCGCAACGAATCGGTGATCTCCCGTAGGTGCGCCCG 209
QY 132 ctgtagatttacttctgttcaagtgttcttagacacggtgtctagatacccaactcttc 191

Thu Oct 18 11:34:44 2001

QY 192 tgcgttaaggtctactctgtctgttattgaagctattcaaaagaacgctactgctttaa 251
Db 270 CAAGGCAAGAATACTCGCTCTCATTCAGGAGATCCAGACGACGCGGACCACTTTGA 329
QY 252 gggtaagtagctcttcttgaagacttacacacacacacacacacacacacacacac 311
Db 330 CGGAAATATGCTTCTCTGAAGACATACACATACACATTCGGTTCAGATGACTGACTCC 389
QY 312 attcgtgaaacacaaatgtaactctgatttaagttctacagaagatacaagcctt 371
Db 390 CTTGGAGAACAGAGCTAGTCAACTCCGGCATCAAGTCTACACGCGTACGATCGCT 449
QY 372 ggcctagaagattgtccattcattagagctctctggtttctgacagagttattgctctgc 431
Db 450 CACAAGGAACATGTTCCATTCATCCGATCCTCTGGCTCCAGCGGCTGATCGCTCCGG 509
QY 432 tgaaggttcattgaaggtttccaaatctgcttaagttggtgacccaggttctcaaccaca 491
Db 510 CAAGAAATTCATGAGGGCTTCCAGAGACCAAGCTGAAGGATCCTCGTCCGACGCGCG 569
QY 492 ccaagctctccaggtatttaacgtgattccagaggaatccggttacacaacacacttt 551
Db 570 CCATCTGCGCCCAAGATCGAGTGGTCAATTCGAGGCGCAGCTCATCCAAACACACTCT 629
QY 552 ggaccaggttactgttactcttccgaagactctgaattaggtgacgacgttgaagctaa 611
Db 630 CGACCCAGGCACTGCACTCTCTTCGAAGACAGCGAATGGCCGATACCCGTCGAAGCCAA 689
QY 612 ctccactgcttctgctccagctattagagctagattggaagctgacttgcaggtgt 671
Db 690 TTTCCCGCCAGCTGCTCCCTCCATTCGTCAACGCTTGAGAACGACGCTGCTCCGGTGT 749
QY 672 tactttgactgacgaagacgttgttacttgatggacatgtgtccattccagactgtgcg 731
Db 750 GACTCTCACAGACACAGAAGTGAAGTCACTACCTCATGGACATGTCTCTTCGACACCATCTC 809
QY 732 tagaactctgaactgactgattgtctccattctgtcttctgctactcactcagcgaatg 791
Db 810 CACCAAGCAGGCTGACACCAAGCTGTCCCCCTCTGTGACCTGTTCACCCATGACGAATG 869
QY 792 gatccaatcacactacttgcgaagctgggttaagtaactaaggttacggtgctgtaaccc 851
Db 870 GATCAACTAGGACTACCTCCAGTCTCTGAAAGATTAATACGGCCATGTGTCAGGTAAACC 929
QY 852 attgggtccagctcaaggtgtgttgcgtacgaagattgattgactgactgactcactc 911
Db 930 GCTCGGCGCCGACCCAGGGGCTGGGTACGCTAAACGAGCTCATCGCCGCTCTGACCCACTC 989
QY 912 tccagttcaagaccacacttctacttaaccacacttttgactctaacccagctactttccc 971
Db 990 GCTGTCCACGATGACACCACTTCCACACACATTTGGACTCGAGCCGCGTACCTTTCC 1049
QY 972 attgaacgtactttgtaogctgactctctcagcaaacactatgatattattctt 1031
Db 1050 GCTCAACTCTACTCTACTACGGGAGCTTTTCGATGACAAACGCACTCATCTCACTCTCTT 1109
QY 1032 cuctttggttctgtaacaggttaccagccattgtctactactcttctgttgaactcttga 1091
Db 1110 TGTCTTAGGTCTGTACACGGGACCTAAGCCGCTATCTACCAGGACCGTGGAGATATCAC 1169
QY 1092 agaaactgacgttactctgtcttcttggactgttccattcgctgtagacttaagcttga 1151
Db 1170 CCAGACAGATGGATTCTGCTCTGTGGACGGTTCGCTTTCGCGCTTTGTACGTCGA 1229
QY 1152 aatgatgcaatgtcaagctgaaaggaacattgttagagttttggttaacgacagagt 1211
Db 1230 GATGATGTCAGTGCAGGCGGACGAGCGCGCTGGTCCGTGCTGTTGGTGAATGATCGGT 1289
QY 1212 tgttccattgacaggttctgctgtgacaaagttgggttagatgttaagagagacgacttgc 1271
Db 1290 TGTCCCGCTGCATGGGTGTCGCTTCTGTTGGGAGATGTACCCGGGATAGCTTTGT 1349

QY 1272 tgaagttgtcttcctagctagctggtggaactggtggaatggttcgctta 1325
Db 1350 GAGGGGTTGAGCTTCTAGATCTGGGGTGATTTGGCGGAGTGTGTTTCTTA 1403

RESULT 6
US-08-151-574-31
; Sequence 31, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seltin
; TITLE OF INVENTION: Cloning and Expression of Microbial
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; IMMEDIATE SOURCE:
; LIBRARY: lambda AF
; CLONE: pAF2-3, pAF2-6, pAF2-7
; FEATURE:
; NAME/KEY: exon
; LOCATION: 210..253
; FEATURE:
; NAME/KEY: intron
; LOCATION: 254..355
; FEATURE:
; NAME/KEY: exon
; LOCATION: 356..1715
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(210..253, 356..1715)
; OTHER INFORMATION: /codon_start= 210

Query Match		46.88;	Score 621.2;	DB 1;	Length 6756;
Best Local Similarity		67.08;	Pred. No. 1.2e-177;		
Matches 881;		Conservative 0;	Mismatches 433;	Indels 0;	Gaps 0;
Qy	12	tgtgacactgttgacggtgttaccgaatgtttcccaagaattttcccaagaattttccgaagtgtccgaagtac	71		
Db	401	TTGCCGATACGGTTCGATCAGGGGTATCAATGCTTCTCGAGACTTCGCATCTTGGGTGTCATCTTGGGTGTC	460		
Qy	72	ctactctccatactctctcttggcagcgaatctgctattttcccaagaattttccgaagtgtccgaaga	131		
Db	461	ATAGCAGCGTTCCTTCTCTGGCAACGAATCGGTCACTCCCGCTAGAGTGCCTCCCGCGG	520		
Qy	132	ctgtagagttactttcttcttggcagcgaatgtttgtctagacacggtgtctagataccccaaactcttc	191		
Db	521	ATGCGAGAGTCACTTTGCTCAGGTCTCTCCGCTCATGGAGCGGTATCCCGACCGCACTC	580		
Qy	192	tgcgtctaaagcttactctgctttgattgaagctatttcaaaagaacgtactgctttctcaa	251		
Db	581	CAAGGGCAAGAAATACCTCCGCTCTCAATGAGGAGATCCAGAGAACCGCACCATCTTGA	640		
Qy	252	gggtaaagctgttcttgaagacttacaactacactttgggtgctgacagacttgaactcc	311		
Db	641	CGGAAAAATAGCCTTCTCTGAAGACATACAACATACAGCTTGGGTGCAGATGACTGACTGCC	700		
Qy	312	attcgctgaacacaaatggtaactctgtgttaagtctctacagaagatacaaggtctt	371		
Db	701	CTTCGGAGAACAGAGCTAGTCAACTCCGGGCATCAAGTTCTACCAAGCGGTACGAATCGCT	760		
Qy	372	ggcttagaagattgttccattcaattagacttctggttctgacagagttattgctctgc	431		
Db	761	CACAAAGGAACATCGTTCATTCATCCGATCTCTGGCTCCAGCCGGGTGATCGGCTCCGG	820		
Qy	432	tgaaggttcaattgaaggtttccaatctgtctaagttggctgacccaggttctcaaccaca	491		
Db	821	CAAGAAATTCATCGAGGGTTCAGAGCACCAAGCTGAAGGATCTCTGTGCGCGCCCGG	880		
Qy	492	ccaagcttctccagttattaaagctgatacttcagaagaatccggtttacaacaacacttt	551		
Db	881	CCAATGTCGCCCCAGATCGAGTGGTCAATTCGAGGCCAGCTCATCCAACACACTCT	940		
Qy	552	ggaccacggtactgttactgctttcgaagactctgaaatagggtgacagcgttgaagctaa	611		
Db	941	CGACCCAGGCACTGCACCTGTCTTCAAGACAGCGAATTGCCCGATACCGTCGAGGCGAA	1000		
Qy	612	cttcactgctttgttcgctccagctattagagctagattggaagctgacttgcaggtgt	671		
Db	1001	TTTACCGCGCACTGCTGCTCCCTCCATTCGTTCAGCTGTGAGAACGACCTGTCCGCTGT	1060		
Qy	672	tactttgactgacgaagacgttttacttcatgtatgacatgtgtccattcgacactgtcgc	731		
Db	1061	GACTCTCAGACACAGAAAGTGAACCTACTCATGGCANATGTCTCTTCGACACCACTC	1120		
Qy	732	tagaactctgacgtactgtaattgtctccattctgtgctttgttcaactcacgacgaatg	791		
Db	1121	CACAGACCGTCGACACCAAGCTGTCCCTTCTGTGACCTGTTCACCCATGACGAATG	1180		
Qy	792	gatccaatacagactactgcaaacgttggtaagtactacggttaccggtgctggttaacc	851		

```

RESULT 7
US-08-419-448-31
; Sequence 31, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F. M. Van Gorcum
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G. M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,448
; FILING DATE: 10-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; INFORMATION FOR SEQ ID NO: 31:

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8 JUL 54

1089 tgaagaaactgacggttactctgtcttctgtgactgttccattcgtctgtagagcttaagt 1148
1149 tgaatgatgcaatgcaagctgaaagaaacattggttagagtttgggttaacgacag 1208
1748 CGAGATGATGCAATGCGACGGCCGACAGAGCGCGTGGTGGTCCGTGCTTGGTTAAATGATCG 1807
1209 agttgtccatgacggttggctgtgctgttgacaaagttgggttagatgtaagagagagactt 1268
1808 CGTTGCCCCCTGCATCGGTGTCCATTTGATGCTTTGGGGAGATGTACCCGGGATAGCTT 1867
1269 cgttgaaggtttgtcttctgctagatctctgtgttaactgggtgtaagtcttgcetta 1325
1868 TGTGAGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTGGGGGAGTGTCTGCTTA 1924

RESULT 11
US-09-155-855-4
; Sequence 4, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1332)
US-09-155-855-4

Query Match 46.0%; Score 609.8; DB 3; Length 1332;
Best Local Similarity 66.4%; Pred. No. 1.5e-174;
Matches 875; Conservative 0; Mismatches 442; Indels 0; Gaps 0;

9 ctctgtgacactgttgacggtgttaccatgtttccagaaatttctcaacttctgtggg 68
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69 tacctactctcatctctctgtgacgaaatctgtatttctccagacgttccaga 128
75 ccaatcagcgcgtctcttctctgcaacaaatcgccatctccctgtgttctcgc 134
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249 caagggtgaagtagcgtttcttgaagacttaacatacactttgggtgtgtagacacttgc 308
255 cgagggaaataatgctcttctgaagacatacaactacagcgtggcggtgtagctgac 314
309 tccattcgtgaaacaaatggttaactctgttattgaatttctacagaagatacaaggc 368

315 tcccttcgagagcaggagctgttccaaactccggtccaaacttctaccagcgatacgaatc 374
369 ttggctagaaaaagattgtccattcattagagcttctgttctgacagagattattgtcttc 428
375 gctcacaagaacattgtccctgttccatcccatctcaggtctccagcgcgtgattgcttc 434
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1269 cgttgaaggtttgttctcgttagactctgtgtgaactgggtggaatgttctgcctta 1325
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RESULT 12
US-09-155-855-5
; Sequence 5, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:

[illegible]

Thu Oct 18 11:34:44 2001

Query Match 25.1%; Score 333.2; DB 2; Length 2200;
Best Local Similarity 56.6%; Pred. No. 6.1e-91;
Matches 745; Conservative 0; Mismatches 523; Indels 48; Gaps 5;

1207 ACTAAA---CACATGCGGGTGTGAACCTCACCTTGGAGGATGTCCCGTTGTTTCATGGAT 1263
709 atgtgtccattgacactgt-----cgctagaaacttctgacgctactgaattgtctcca 762
1264 CTTTGTCCGTTTACACGGTGGGCTCGACCCAGTCTTTTCCACGGCAGCTCTCTCCG 1323
763 ttctgtgtctttgttccactcacgcaaatgagatgacactactactgcaaaagtgtggtt 822
1324 TTTTGTACATTGTTACGCGCGGAGATTGGATGGCTTACGATTACTACTACACCTCGAC 1383
823 aagtactacggttacggtgtgtgttaacccattgggtccacactcaagtgtgtgttgcgt 882
1384 AAATACTACAGCCACGGCGGCGGATTTGGCCCGCTCCCGCGCGTTCGGGTTCGTC 1443
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1444 AACGAGCTGATTGGCGGTATGACGGGAAATCTTCCCGTCAAGGACACACACAGTCAAC 1503
940 cacactttggacttaacccagctactttcccatctgaacgctactttgtacgctgacttc 999
1504 CACACTCTCGATGACAAACCCGGAACCTTCCCGTTGGACGCTGTCTTACGCGACTTT 1563
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1114 tcttgactgttccattgcttagacttacttgaatgacatgacatgacatgacatgacatgac 1173
1684 TCGTGACGGTGGCGGCTTCGACGAGGCGGATGTGGAGTTCCTGCGATGTGACACGGAA 1743
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1204 gacagattgttccattgacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1263
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1264 gacttctgtaaggttcttcttctgcttagatctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1319
1864 GAGTGAATGAGGACTCACGTTGCTGACAGGGGTGGGCTTGGATTCGCTGCTT 1919

RESULT 14
US-09-163-642-1
Sequence 1, Application US/09163642
Patent No. 6221644
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62216440 No. 6221644disk of No. 6221644th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,642
FILING DATE:

Thu Oct 18 11:34:44 2001

FILING DATE: 07-MAY-1997
 APPLICATION NUMBER: 60/046,081
 FILING DATE: 09-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Gregg, Valeta A
 REGISTRATION NUMBER: 35,127
 REFERENCE/DOCKET NUMBER: 5101.200-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1320 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-221-654-1

Query Match 9.3%; Score 122.8; DB 3; Length 1320;
 Best Local Similarity 55.7%; Pred. No. 1.6e-27;
 Matches 263; Conservative 0; Mismatches 197; Indels 12; Gaps 1;

Qy	585	tgaattagtgacgacgttgaaagctaaccttcaactgcttctgttgcctccagctattagagc	644
Db	594	TGAAGTGGATGGTGACGAATCCACAACGGTGGTGGGGGCTTTTGGCCCGCAACATCACCGC	653
Qy	645	tagattgaaagctgactgccagggtgttactttgactgacgaagacgtttgttactttgat	704
Db	654	GCGATTGAACGCTGCTGCGCGGAGTGCCAACTCTCAGACAGCGACGGCGCTCACTCTCAT	713
Qy	705	ggacatgtgtccattgcacactgtgcgtagaacttctgacgtactgaattgtctccatt	764
Db	714	GGATATGTGCCCGTTCGACACTCTCAG-----CTCCGGGAACGCCAGCCCCCTT	761
Qy	765	ctgtgcttcttcaactcacacgaatggatccaatcagactacttgcaagcttgggttaa	824
Db	762	CTGTGACCTATTACCGCGGAGGAGTATGTGCTGAGGAGTACTACTATGACCTCGACAA	821
Qy	825	gtactacggttacggtgtgtgtaaccattgggtccagctcaagggtgtgtgttgcgttaa	884
Db	822	GTACTATGGCACGGGCCCCGGGAACGCTCTCGGTCTCTGTCAGGGCGTCGGATACGTCAA	881
Qy	885	cgaattgattgctagattgactcaactctccagttccaagacacacacttctactaaccacac	944
Db	882	TGAGCTGCTTGCACGCTTGACCGGCCAAGCCGTTTCGAGACGACGACGACGACGCCAC	941
Qy	945	tttgactctaacccagctactttcccatggaacgctactttgtacgctgacttctctca	1004
Db	942	GCTCGACAGCGACCCCTGCAACATTCGCCGTGAACCGTACGTTCTACGCGACTTCTCGCA	1001
Qy	1005	cgacaacactatgatattttcttgcgtttgtgggtttgtacaacgggtacc	1056
Db	1002	TGATAACACCATGTGGCCATCTTTTGGGGCGCTCGGGCTCTTCAACGCCACC	1053

Search completed: October 16, 2001, 12:05:51
 Job time: 545 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 12:13:46 ; Search time 573.71 Seconds
(without alignments)
1451.252 Million cell updates/sec

Title: US-09-488-265-28_COPY_79_1404

Perfect score: 1326

Sequence: 1 aattctcactcttgacac.....gggctgaatttcgcttaa 1326

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1326	100.0	1404	20	AAZ31520
2	1326	100.0	1404	21	AAZ31520
3	1326	100.0	1404	21	AAZ31520
4	1310	98.8	1404	21	AAZ31520
5	1306.8	98.6	1404	21	AAZ31520
6	1282.8	96.7	1426	20	AAZ31520
7	1282.8	96.7	1426	20	AAZ31520
8	1282.8	96.7	1426	21	AAZ31520
9	1282.8	96.7	1426	21	AAZ31520
10	1249.2	94.2	1404	20	AAZ31520
11	1249.2	94.2	1404	21	AAZ31520

12	1249.2	94.2	1404	21	AAZ31520
13	1246	94.0	1404	21	AAZ31520
14	1242.8	93.7	1404	21	AAZ31520
15	1239.6	93.5	1426	21	AAZ31520
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17	1214	91.6	1426	20	AAZ31520
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19	1214	91.6	1426	21	AAZ31520
20	621.2	46.8	1404	12	AAQ11175
21	621.2	46.8	1404	18	AAZ31520
22	621.2	46.8	1404	20	AAZ31520
23	621.2	46.8	1404	20	AAZ31520
24	621.2	46.8	1404	20	AAZ31520
25	618	46.6	1404	18	AAZ31520
26	617.8	46.6	1404	18	AAZ31520
27	617.8	46.6	1404	18	AAZ31520
28	601.8	45.4	1515	18	AAZ31520
29	595.4	44.9	1404	20	AAZ31520
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31	595.4	44.9	1404	20	AAZ31520
32	580.6	43.8	1571	19	AAZ31520
33	580.6	43.8	1571	19	AAZ31520
34	578.4	43.6	1931	19	AAZ31520
35	578.4	43.6	1931	19	AAZ31520
36	548.8	41.4	1912	17	AAZ31520
37	544.4	41.1	1845	19	AAZ31520
38	542.8	40.9	1845	19	AAZ31520
39	522.4	39.4	1567	19	AAZ31520
40	522.4	39.4	1567	19	AAZ31520
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43	500.4	37.7	1464	22	AAZ31520
44	500.4	37.7	1464	22	AAZ31520
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ALIGNMENTS

RESULT 1

AAZ31520

ID AAZ31520 standard; DNA; 1404 BP.

AC AAZ31520;

DT 06-JAN-2000 (first entry)

DE Consensus phytase-1-thermo(8)-Q50T-K9IA coding sequence.

DE Phytase; animal feed preparation; thermostable phytase; transgenic plant;

DE Consensus sequence; ds.

OS Synthetic.

PN WO9948380-A1.

PD 30-SEP-1999.

PF 22-MAR-1999; 99WO-DK00154.

PR 23-MAR-1998; 98DK-0000407.

PR 19-JUN-1998; 98DK-0000806.

PR 18-SEP-1998; 98DK-0001176.

PR 22-JAN-1999; 99DK-0000091.

PR 22-JAN-1999; 99DK-0000093.

PA (NOVO) NOVO-NORDISK AS.

PI Petersen S;

PI WPI; 1999-591030/50.

DR P-PSDB; AAY43169.

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

DR

preparing animal feed using a thermostable phytase

Introduction

This sequence encodes the consensus phytylase-1-thermo(8)-O50T-K91A. The invention relates to a process for preparing animal feed by agglomerating feed ingredients with a thermostable phytylase, which is added before or during agglomeration. The thermostable phytylase is useful for expression in transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytylase allows animal feed to be produced more efficiently, in addition to improved phytylase-expressing transgenic plants. These plants provide a feed ingredient and a feed additive (phytylase) simultaneously.

ingredient and a rock substance (1-17-18).

```

Query Match      100.0%; Score 1326; DB 20; Length 1404;
Best Local Similarity 100.0%; pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Sequence 1404 BP; 329 A; 319 C; 304 G; 452 T; 0 other;

```

1 aattctcactcttqtgacactgttgacggtggttaccaatgtttcccagaaatttctcac 60

100

b
79 aattctactcttgtgacactgttgacggtggttaccgaatgtttcccgagaaatttctcac

126

61 ttgtgggtacctactctccatacttctcttcttggcagacgaatctgctatttctccagac

198

b 139 ttgtgggtacctaactctccatacttctcttttggcagacgaacccccccagac

...ctctacacggtctctagatac 180

y
121 gttccagacgactgttagagctaccctcgcctcaaggccccggaccacgcccgaagt

100 -ttccggcggcctatagaaattactttcattcaagttttgtctagacacgggtgctagatac 258

[illegible]

191 ccaacttctctacgtctaaaggttactctgcttctgattgaagctattcaaaagaacgct 240

[illegible]

h 259 ccaacttcttctacgctctaaggcttactctgctttgattgaagctattcaaaagaacgct 318

100

241 actgcttcaagggtaaagtaacgctttcttgaagacttacaactacactttgggtgctgac 300

319 actgcttcaagggttaagtacgctttcttgaagacttacaactacactttgggtgctgac 370

301 gactgactccattcgggtgaaaccaaataagttctacagaa

43

bb 379 gacttgactccattcgggtgaaaaccacadtggttadcttcctggtcatcaagcttcctcctggaaga

[illegible][illegible]

420 +-----+cccttgccttcattcatttagagcttctggttctgacagaqt 49

[illegible]

DR P-PSDB; AAB20526.

PT Novel phytases with improved properties such as temperature stability,
PT pH stability and substrate specificity, for use in pharmaceuticals and
PT compound foods and feeds -

PS Claim 10; Fig 7a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present invention.

Sequence 1404 BP; 329 A; 319 C; 304 G; 452 T; 0 other;

```

Query Match      100.0%; Score 1326; DB 21; Length 1404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1	aa	tctcaactctt	gtgacac	gtgtga	cgggtgt	tacca	atgttt	ccacaga	aaattt	ctcac	60
79	db	aatctcaactctt	gtgacact	gtgtga	cgggtgt	tacca	atgttt	ccacaga	aaattt	ctcac	138
61	py	tgtgggggt	tacctac	tctccat	ctactct	ttctt	gtgcag	cgaatct	gtctatt	ctccag	120
139	db	tgtgggggt	tacctac	tctccat	ctactct	ttctt	gtgcag	cgaatct	gtctatt	ctccag	198
121	py	gttcaga	gaactgt	tagagt	tactt	tcgtt	caaagt	ttt	gtctaga	cacagct	180
199	db	gttcaga	gaactgt	tagagt	tactt	tcgtt	caaagt	ttt	gtctaga	cacagct	240
181	py	ccaactt	cttct	gcgtcta	aggtta	ctctct	gtt	gattga	agctatt	caaaaga	360
259	db	ccaactt	cttct	gcgtcta	aggtta	ctctct	gtt	gattga	agctatt	caaaaga	318
241	py	actgctt	tcaagg	gttaagt	taagct	ttctt	gaagact	taca	actacac	ctt	300
319	db	actgctt	tcaagg	gttaagt	taagct	ttctt	gaagact	taca	actacac	ctt	378
301	py	gacttgac	tccatt	cgggtga	aaaccaa	atggt	taact	ctb	gtgtatt	aa	420
379	db	gacttgac	tccatt	cgggtga	aaaccaa	atggt	taact	ctb	gtgtatt	aa	438
361	py	tacaag	gctt	gtgc	taga	aatg	tgtcc	att	gaagctt	ctct	420
439	db	tacaag	gctt	gtgc	taga	aatg	tgtcc	att	gaagctt	ctct	498
421	py	attgctt	ctgt	gaaa	gttca	atg	ctaa	ttct	gaa	gctt	480
499	db	attgctt	ctgt	gaaa	gttca	atg	ctaa	ttct	gaa	gctt	558
481	py	tctcaac	caacac	caagctt	ctccag	gttata	aac	gta	ctat	cc	540
559	b	tctcaac	caacac	caagctt	ctccag	gttata	aac	gta	ctat	cc	618
541	y	aaaca	caactt	gtgg	accac	ggtg	ta	ctgtt	ctt	ga	600
619	b	aaaca	caactt	gtgg	accac	ggtg	ta	ctgtt	ctt	ga	678
601	y	gttga	agctaa	ctta	ctgctt	gtt	ctgc	gtt	ctgc	gtt	660
679	b	gttga	agctaa	ctta	ctgctt	gtt	ctgc	gtt	ctgc	gtt	738

Db 1099 tctattttctcgtcttgggtttgtacacggtacacagccattgctctactctgtt 1158
 Qy 1081 gaactattgaagaaactgacggttactctgtcttcttggactgttccattcgtctaga 1140
 Db 1159 gaactattgaagaaactgacggttactctgtcttcttggactgttccattcgtctaga 1218
 Qy 1141 gctacgttgaatgatgcaatgcaagctgaaagaaacacattggttagagtttggtt 1200
 Db 1219 gctacgttgaatgatgcaatgcaagctgaaagaaacacattggttagagtttggtt 1278
 Qy 1201 aacgacagagtgttccattgacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
 Db 1279 aacgacagagtgttccattgacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1338
 Qy 1261 gacgacttctgaaagtttcttctcgtctagatctgtgtgtgtgtgtgtgtgtgtgtgt 1320
 Db 1339 gacgacttctgaaagtttcttctcgtctagatctgtgtgtgtgtgtgtgtgtgtgtgt 1398
 Qy 1321 gcttaa 1326
 Db 1399 gcttaa 1404

RESULT 6
 AAZ27423
 ID AAZ27423 standard; cDNA; 1426 BP.
 AC AAZ27423;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Ascomycete consensus phytase coding sequence.
 XX
 KW Phytase; variant; enzyme; phosphorus liberation; phytase substrate;
 KW Phytase level reduction; animal manure; food preparation;
 KW soy processing; inositol manufacture; ss.
 XX
 OS Synthetic.
 XX
 PN WO9949022-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 22-MAR-1999; 99WO-DK00153.
 XX
 PR 23-MAR-1998; 98DK-0000407.
 PR 19-JUN-1998; 98DK-0000806.
 PR 18-SEP-1998; 98DK-0001176.
 PR 22-JAN-1999; 99DK-0000091.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Svendsen A;
 XX
 DR WPI; 1999-580444/49.
 DR P-PSDB; AAY39906.
 XX
 PT New variant phytase enzymes, used for liberating phosphorus from a
 PT phytase substrate, for reducing phytate levels in animal manure and in
 PT feed and food preparations -
 XX
 PS Disclosure; Fig 9f-g; 141pp; English.
 XX
 CC This sequence encodes the consensus Ascomycete phytase sequence.
 CC The invention relates to variant phytase enzymes with specific amino acid
 CC substitutions for improved properties. The phytase variants can be used
 CC for liberating phosphorus from a phytase substrate. They can be used for
 CC reducing phytate levels in animal manure. They can be used in feed or
 CC food preparations. The phytase DNA can also be used to produce transgenic
 CC plants which can be used in feeds or foods. The phytase variants can also
 CC be used in soy processing and in the manufacture of inositol or
 CC derivatives. The phytase variants can have altered activities such as pH

CC stability, temperature stability, pH profile, temperature profile,
 CC specific activity (in particular in relation to pH and temperature),
 CC substrate specificity, substrate cleavage pattern, substrate binding,
 CC position specificity, the velocity and level of release of phosphate
 CC from corn, reaction rate, phytase degradation rate and end level of
 CC released phosphate reached.
 XX
 SQ Sequence 1426 BP; 338 A; 311 C; 308 G; 469 T; 0 Other;
 Query Match 96.7%; Score 1282.8; DB 20; Length 1426;
 Best Local Similarity 98.0%; Pred. No. 0;
 Matches 1299; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
 Qy 1 aattctcactcttctgacactcttccacggtgttaccacgttttccacgaatttccac 60
 Db 90 aattctcactcttctgacactcttccacggtgttaccacgttttccacgaatttccac 149
 Qy 61 ttgtggggttacctactctccatactctcttcttggcagacgaatctgtctatttccacag 120
 Db 150 ttgtggggttccaatactctccatactctcttcttggcagacgaatctgtctatttccacag 209
 Qy 121 gtccacagcactgtagagttaacttcttccaaagttttcttagacacggtgtctagatc 180
 Db 210 gtccacagcactgtagagttaacttcttccaaagttttcttagacacggtgtctagatc 269
 Qy 181 ccaactcttctcgctcctaaagcttactctgttcttggattgaagctattcacaagaacgct 240
 Db 270 ccaactcttctcctaaagcttactctgttcttggattgaagctattcacaagaacgct 329
 Qy 241 actgttttccaaaggttaagtacgcttcttgaagacttacaactacacttgggtgtctgac 300
 Db 330 actgttttccaaaggttaagtacgcttcttgaagacttacaactacacttgggtgtctgac 389
 Qy 301 gacttgactcctacgttgaaacacaaatggttaactctgtgtattgaattacacagaaga 360
 Db 390 gacttgactcctacgttgaaacacaaatggttaactctgtgtattgaattacacagaaga 449
 Qy 361 tacaaggcttggctagaagaattgttccattcatttagacttctgttctgtacagagtt 420
 Db 450 tacaaggcttggctagaagaattgttccattcatttagacttctgttctgtacagagtt 509
 Qy 421 attgctctgctgaaagttcattgaagggttccaatctgctgaagttggctgacccaggt 480
 Db 510 attgctctgctgaaagttcattgaagggttccaatctgctgaagttggctgacccaggt 569
 Qy 481 tctcaacacacacacacacacacacacacacacacacacacacacacacacacacacac 540
 Db 570 tctcaacacacacacacacacacacacacacacacacacacacacacacacacacacac 629
 Qy 541 aacaacacacacacacacacacacacacacacacacacacacacacacacacacacac 600
 Db 630 aacaacacacacacacacacacacacacacacacacacacacacacacacacacacac 689
 Qy 601 gttagaacttaacttctgctgttctgctgttctgctgttctgctgttctgctgttctgct 660
 Db 690 gttagaacttaacttctgctgttctgctgttctgctgttctgctgttctgctgttctgct 749
 Qy 661 ttgcaggtgttacttctgactgacgaagacgttctgttcttctgtgtgtgtgtgtgtgt 720
 Db 750 ttgcaggtgttacttctgactgacgaagacgttctgttcttctgtgtgtgtgtgtgtgt 809
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 Db 810 gaaactgttctgtagaacttctgactgacgttctgttcttctgttctgttctgttctgtt 869
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 Qy 841 gctggttaacccattgggttcacagctcaaggttgggttctgtctgaacgaattgattgctaga 900
 Db 930 gctggttaacccattgggttcacagctcaaggttgggttctgtctgaacgaattgattgctaga 989

Thu Oct 18 11:34:43 2001

QY 901 ttgaactcactctccaggttcaagaccacacacttctactaaccacacacttggactcttaaccca 960
DB 990 ttgactagatctccagttcaagaccacacttctactaaccacacacttggactcttaaccca 1049
QY 961 gctacttccattgaacgctacttctgacgctgacttctctcagacacacactatgata 1020
DB 1050 gctacttccattgaacgctacttctgacgctgacttctctcagacacacactatgatt 1109
QY 1021 tctatttctctgcttgggttctgaacgctgacttctctcagacacacacttctcttct 1080
DB 1110 tctatttctctgcttgggttctgaacgctgacttctctcagacacacacttctcttct 1169
QY 1081 gaactattgaagaactgacggttactctgcttcttctgactgttccactgctgctaga 1140
DB 1170 gaactattgaagaactgacggttactctgcttcttctgactgttccactgctgctaga 1229
QY 1141 gcttaagttgaatgatgaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 1200
DB 1230 gcttaagttgaatgatgaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 1289
QY 1201 aacgacagagttgttcattgacggttctgctgttgacaaagtgggtgacagatgaagaga 1260
DB 1290 aacgacagagttgttcattgacggttctgctgttgacaaagtgggtgacagatgaagaga 1349
QY 1261 gacgactctgtgaaggttcttctgctgactgactgctgctgctgctgctgctgctgct 1320
DB 1350 gacgactctgtgaaggttcttctgctgactgactgctgctgctgctgctgctgctgct 1409
QY 1321 gcttaa 1326
DB 1410 gcttaa 1415
RESULT 7
ID AAX23022 standard; DNA: 1426 BP.
XX AC AAX23022;
XX DT 11-JUN-1999 (first entry)
XX DE Fungal phytase gene consensus DNA.
XX KW Phytase; consensus: myo-inositol hexakisphosphate; hydrolysis; food;
XX KW feed additive; variant; muten; feed; pharmaceutical; ds.
XX OS Fungi.
XX FH Key
XX FT CDS
XX FT Location/Qualifiers
XX FT 12..1415
XX FT /*tag= a
XX FT /product= "phytase"
XX EP897985-A2.
XX PN 15-JUL-1998; 98EP-0113176.
XX PD 24-FEB-1999.
XX PF 15-JUL-1998; 98EP-0113176.
XX PR 24-JUL-1997; 97EP-0112688.
XX PA (HOFF) HOFFMANN LA ROCHE AG F.
XX PI Lehmann M;
XX WP1; 1999-134647/12.
XX DR P-PSDB; AAW53380.
XX PT Preparation of a consensus protein, especially a phytase - using
XX PT programs to compare evolutionary similarity of sequences
XX PS Claim 8; Fig 2; 30pp; English.

XX This invention describes a novel process for the preparation of a
CC consensus protein. The specific example given in the specification is
CC that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses
CC phytase to valuable feed additives, with a fully defined amino acid
CC sequence given in the specification, or variant or muten. The method is
CC useful for improving protein properties by altering their sequence. The
CC consensus protein and muten are useful in food, feed or pharmaceutical
CC compositions. This sequence encodes the consensus phytase protein used
CC in the method of the invention.
XX
SQ Sequence 1426 BP; 338 A; 311 C; 308 G; 469 T; 0 other;
Query Match 96.7%; Score 1282.8; DB 20; Length 1426;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1299; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 1 aattctcactcttgcacactgttgacggtgtgttaccacatgtttccacagaaattctcac 60
DB 90 aattctcactcttgcacactgttgacggtgtgttaccacatgtttccacagaaattctcac 149
QY 61 ttgtgggttaactactctccactctctcttcttgcagacgaatctgctatttctccagac 120
DB 150 ttgtgggttaactactctccactctctcttcttgcagacgaatctgctatttctccagac 209
QY 121 gttccagacgactgtagagttacttcttcaagtgtttgtctagacacggtgctagatcac 180
DB 210 gttccagacgactgtagagttacttcttcaagtgtttgtctagacacggtgctagatcac 269
QY 181 ccaactcttctgcttaaggttactctcttcttgaagacttcaactacacttgggtgctgac 240
DB 270 ccaactcttctgcttaaggttactctcttcttgaagacttcaactacacttgggtgctgac 329
QY 241 actgtcttcaaggttaagtaagcttcttgaagacttcaactacacttgggtgctgac 300
DB 330 actgtcttcaaggttaagtaagcttcttgaagacttcaactacacttgggtgctgac 389
QY 301 gacttgactccattcgttgaaacccaaatggttaactctggttatttaagttctacagaaga 360
DB 390 gacttgactccattcgttgaaacccaaatggttaactctggttatttaagttctacagaaga 449
QY 361 tacaaggttctgctagaaagattgttccattcattagacttctggttctgacagagtt 420
DB 450 tacaaggttctgctagaaagattgttccattcattagacttctggttctgacagagtt 509
QY 421 attgcttctgctgaaaggttcaattgaaggttcccaatctgctaaagtgtggtgacccaggt 480
DB 510 attgcttctgctgaaaggttcaattgaaggttcccaatctgctaaagtgtggtgacccaggt 569
QY 481 tctcaaccacacacacacacacacacacacacacacacacacacacacacacacacacacac 540
DB 570 tctcaaccacacacacacacacacacacacacacacacacacacacacacacacacacacac 629
QY 541 aacaacacacacacacacacacacacacacacacacacacacacacacacacacacacac 600
DB 630 aacaacacacacacacacacacacacacacacacacacacacacacacacacacacacac 689
QY 601 gttgaagctaaacttcaactcttctgctgacgacgacgacgacgacgacgacgacgacgac 660
DB 690 gttgaagctaaacttcaactcttctgctgacgacgacgacgacgacgacgacgacgacgac 749
QY 661 ttgcccaggttacttctgctgacgacgacgacgacgacgacgacgacgacgacgacgacgac 720
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QY 721 gacactgctgtagaacttctgctgacgacgacgacgacgacgacgacgacgacgacgacgac 780
DB 810 gaaactgttctgtagaacttctgctgacgacgacgacgacgacgacgacgacgacgacgacgac 869
QY 781 cagacgaatggagacacacacacacacacacacacacacacacacacacacacacacacacac 840
DB 870 cagacgaatggagacacacacacacacacacacacacacacacacacacacacacacacacac 929

Qy	841	gctggaaccattgggtccagctcaaggtgttggtttcgtcaacgaattgattgctaga	900
Db	930	gctggtgaaccattgggtccagctcaaggtgttggtttcgtcaacgaattgattgctaga	989
Qy	901	ttgactcaactctccagttcaagaccacacttctactaaccacactttggactctaaaccca	960
Db	990	ttgactagatctccagttcaagaccacacttctactaaccacactttggactctaaaccca	1049
Qy	961	gctactttccattgaacgctactttgtacgtgacttctctcacgacaaacactatgata	1020
Db	1050	gctaactttccattgaacgctactttgtacgtgacttctctcacgacaaacactatgata	1109
Qy	1021	tctattttctcgtttgggtttgtacaacggtgacacagccatgtctactactcttggtt	1080
Db	1110	tctaattttctcgtttgggtttgtacaacggtgactgtccattgtctactactcttggtt	1169
Qy	1081	gaatctattgaagaaactgacggttactctgctctttggactgtccattcgctgctaga	1140
Db	1170	gaatctattgaagaaactgacggttactctgctctttggactgtccattcgctgctaga	1229
Qy	1141	gcttaagttgaatatgataatgcaatgtcaagctgaaaaggaaacctggttagagttttggtt	1200
Db	1230	gcttaagttgaatatgataatgcaatgtcaagctgaaaaggaaacctggttagagttttggtt	1289
Qy	1201	aacgcagaggtttgttcattgacggtttgtcgtgtgacaagttgggttagatgataagaga	1260
Db	1290	aacgcagaggtttgttcattgacggtttgtcgtgtgacaagttgggttagatgataagaga	1349
Qy	1261	gacgacttcgttgaaggtttgtcttcttcgtatgatactggtgaactgggctgaatttctc	1320
Db	1350	gacgacttcgttgaaggtttgtcttcttcgtatgatactggtgaactgggctgaatttctc	1409
Qy	1321	gcttaa	1326
Db	1410	gcttaa	1415

RESULT 8

AAA73231
ID AAA73231 standard; DNA; 1426 BP.

AC AAA73231:

DT 05-DEC-2000 (first entry)

Consensus phytase polynucleotide sequence SEQ ID NO:15.

KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW temperature stability; pH profile; temperature profile; reaction rate;
KW specific activity; substrate specificity; substrate cleavage pattern;
KW substrate binding; position specificity; phytate degradation rate;
KW food; feed; phytate; manure; ds.

AA	Synthetic.
OS	

AX
PN WO200043503-A1.

XX
PD 27-JUL-2000.

XX
PF 21-JAN-2000; 2000WO-DK00025.

XX
22- JAN-1000- 0000 00000000

PR	22-JAN-1999;	99DK-0000092.
PR	21-SEP-1999;	99DK-0001340.

XX
PA (NOVO) NOVO NORDISK AS.

Lehmann M:

XX
XX

XXXXXXXXXXXX

DR WPI; 2000-491161/43.
DR P-PSDB: AAR20515

XX
A 1000, AAB20313.

PT Novel phytases with improved properties such as temperature stability,

PT PT XX PS XX CC CC CC CC CC CC CC CC CC CC CC CC CC CC XX SQ

Query Match 96.7%; Score 1282.8; DB 21; Length 1426;
Best Local Similarity 98.0%; Pred. NO. 0;
Matches 1299; Conservative 0; Mismatches 27; Indels 0; Cons 0.

QY	1	aattctcactcttggacactgttgacggttggttaccaatgtttccagaaattttctc	60
Db			
Db	90	aattctcactcttggacactgttgacggttggttaccaatgtttccagaaattttctc	149
QY	61	ttgtgggttacctctccatactctctttggcagacgaatctgtattttctccagac	120
Db			
Db	150	ttgtgggtcaatactctccatactctctttggaacgaatctgtattttctccagac	209
QY	121	gttcacagacactgtagagtttaactttcgttccaaagtttctctagacacggtgtcagatac	180
Db			
Db	210	gttcacagacactgtagagtttaactttcgttccaaagtttctctagacacggtgtcagatac	269
QY	181	coaaactttctcgctctaaagcttactctgtcttgattgaagctattcaaaagaacgct	240
Db			
Db	270	ccaactttctaaagctaaaggcttactctgcttggattgaagctattcaaaagaacgct	329
QY	241	actgotttcaaaggttaagtcagctttcttgaagactttacaactcacactttgggtgctgcac	300
Db			
Db	330	actgotttcaaaggttaagtcagctttcttgaagacttacaactcacactttgggtgctgcac	389
QY	301	gacttgactccaactcgttgaaacccaaatggttaactctc59tattaaagttctacagaaga	360
Db			
Db	390	gacttgactccaactcgttgaaacccaaatggttaactctggtatttaagtctacagaaga	449
QY	361	tacaagctttggctagaaagattgtccaactcattagagcttctgtgtctacagagtt	420
Db			
Db	450	tacaagctttggctagaaagattgtccaactcattagagcttctgtgtctacagagtt	509
QY	421	attgctctgctgaaaagtttcattgaaggtttccaactgctaagtgtgctgaccacaggt	480
Db			
Db	510	attgctctgctgaaaagtttcattgaaggtttccaactgctaagtgtgctgaccacaggt	569
QY	481	tctcaaccacacaaagctctccagttattaaacgtgatcatctccagaaggaatccgggttac	540
Db			
Db	570	tctcaaccacacaaagctctccagttattaaacgtgatcatctccagaaggaatccgggttac	629
QY	541	aacaacactttgaccacaggtactgtactgctttcgaagactctgaattaggtgacacac	600
Db			
Db	630	aacaacactttgaccacaggtactgtactgctttcgaagactctgaattaggtgacacac	689
QY	601	gttgaagctaaacttcaactgctttgttgcgtccagactatttagagctagattggaagctgac	660
Db			
Db	690	gttgaagctaaacttcaactgctttgttgcgtccagactatttagagctagattggaagctgac	749
QY	661	tggccaggtgttactttgactacgaagaacggtgtgttacttgatggacatgtgtccattc	720
Db			
Db	750	ttyccacgggtgttactttgactgaacgaacggtgtgttacttgatggacatgtgtccattc	809

[illegible]

Qy	1201	aacgacagagtgttccattgcacgggttgctgttgacaagtgggtagatgaagaga	1260
Db	1290	aacgacagagtgttccattgcacgggttgctgttgacaagtgggtagatgaagaga	1349
Qy	1261	gacgacttcgtgaaggtttgtcttcctcagctagatctggtgaactggcgctgaattcttc	1320
Db	1350	gacgacttcgtgaaggtttgtcttcctcagctagatctggtgaactggcgctgaattcttc	1409
Qy	1321	gcttaa 1326	
Db	1410	gcttaa 1415	
RESULT 10			
AAZ31521			
ID	AAZ31521 standard; DNA; 1404 BP.		
XX	AAZ31521;		
XX			
DT	06-JAN-2000 (first entry)		
DE	Consensus phytase-10-thermo(3)-Q50T-K91A coding sequence.		
KW	Phytase: animal feed preparation; thermostable phytase; transgenic plant;		
KW	consensus sequence; ds.		
XX	Synthetic.		
OS			
PX	WO9948380-A1.		
XX			
PD	30-SEP-1999.		
XX			
PF	22-MAR-1999; 99WO-DK00154.		
XX			
PR	23-MAR-1998; 98DK-0000407.		
PR	19-JUN-1998; 98DK-0000806.		
PR	18-SEP-1998; 98DK-0001176.		
PR	22-JAN-1999; 99DK-0000091.		
PR	22-JAN-1999; 99DK-0000093.		
XX			
PA	(NOVO) NOVO-NORDISK AS.		
XX			
PI	Petersen S;		
XX			
DR	WPI; 1999-591030/50.		
DR	P-PSDB; AAY43170.		
XX			
PT	Preparing animal feed using a thermostable phytase -		
XX			
PS	Example 3; Fig 10; 7lpp; English.		
XX			
CC	This sequence encodes the consensus phytase-10-thermo(3)-Q50T-K91A.		
CC	The invention relates to a process for preparing animal feed by		
CC	agglomerating feed ingredients with a thermostable phytase, which is		
CC	added before or during agglomeration. The thermostable phytase is useful		
CC	for expression in transgenic plants. These plants are useful in the		
CC	preparation of animal feed itself. The thermostable phytase allows animal		
CC	feed to be produced more efficiently, in addition to improved animal		
CC	phytase-expressing transgenic plants. These plants provide a feed		
CC	ingredient and a feed additive (phytase) simultaneously.		
XX			
SQ	Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;		
Query Match 94.2%; Score 1249.2; DB 20; Length 1404;			
Best Local Similarity 96.4%; Pred. No. 0;			
Matches 1278; Conservative 0; Mismatches 48; Indels 0; Gaps 0;			
Qy	1	aattctcaactcttgtgacactgttgacggtgttacccaatgtttcccagaattttctcac	60
Db	79	aactctcaactcttgtgacactgttgacggtgttacccaatgtttcccagaattttctcac	138
Qy	61	tgttggggttaactactctccatactctcttcttggcagacgaactgtctatttctccagac	120

Best Local Similarity 96.4%; Pred. No. 0;
Matches 1278; Conservative 0; Mismatches 48; Indels 0; Cans 0.

QY	1	aattctcaactctgtgacactgttgacggttggttaccaatgtttccagaaaatttctcag	60
Db	79	aactctcaactctgtgacactgttgacggttggttaccaatgtttccagaaaatttctcag	138
QY	61	ttgtggggtacactctccataactctcttttggcagacgaatctgctattttccagac	120
Db	139	ttgtggggtacatactctccactctctcttttggcagacgaatctgctattttccagac	198
QY	121	gttcacagcagactgtagagtttaactttcgtttcaagtttgtctctagacacggtgctagatac	180
Db	199	gttccaaaaggggtgtgagagtttaactttcgtttcaagtttgtctctagacacggtgctagatac	258
QY	181	ccaaactctctcgtctaaagcttaactctgctttgattgaagctattccaaagaacgct	240
Db	259	ccaaactctctcgtctaaagcgtaactctgctttgattgaagctattccaaagaacgct	318
QY	241	actgctttcaagggtagaagtaagctttcttgaagacttacaactacactttgggtgctgac	300
Db	319	actgctttcaagggtagaagtaagctttcttgaagacttacaactacactttgggtgctgac	378
QY	301	gacttgactccatctcgtgaaaaccaaatgtttaactcttggtattaagtctctacagaaga	360
Db	379	gacttgactccatctcgtgaaaaccaaatgtttaactcttggtattaagtctctacagaaga	438
QY	361	tacaaggctttgggtgaaagattgttccattcattagagctctcgtttctgacagagtt	420
Db	439	tacaaggctttgggtgaaagattgttccattcattagagctctcgtttctgacagagtt	498
QY	421	attgctctcgtgaaaagttcattgaaggtttccaaactcgttaagtgggtgaccaggt	480
Db	499	attgctctcgtgaaaagttcattgaaggtttccaaactcgttaagtgggtgaccaggt	558
QY	481	tctcaacacacaaagctctccagttattaaactgatacttccagaagagatcccggttac	540
Db	559	gtcaaccacacaaagctctccagttattaaactgatacttccagaagagatcccggttac	618
QY	541	aacaaacactttgacacacggtactctgactgctttcggaagactctgaattggtgaagac	600
Db	619	aacaaacactttgacacacggtttgtgtactgctttcggaagactctgaattggtgacgac	678
QY	601	gttgaagctaacttcaactcgttttgcctccagctattagactagattgggaagctgac	660
Db	679	gttgaagctaacttcaactcgttttgcctccagctattagactagattgggaagctcacc	738
QY	661	ttgcacggtgttaactttgactaacgaagacggtgtgttacttgatggacatgtgccattc	720
Db	739	ttgcacggtgttaactttgactaacgaagacggtgtgttacttgatggacatgtgccattc	798
QY	721	gacactgtcgtagaactctgacgctaactgaattgtctccattctcgtttgttctcaact	780
Db	799	gacactgtcgtagaactctgacgctaactgaattgtctccattctcgtttgttctcaact	858
QY	781	cacgaagaaatggatccaatcacgaactacttgaaaagctttgggaagtaactacoggttacggt	840
Db	859	cacgaagaaatggatccaatcacgaactacttgaaaagctttgggaagtaactacoggttacggt	918
QY	841	gctgggtaaccactttgggtccagctcaaggtgtgggtttcgcgtcaacgaattgattgctaga	900
Db	919	gctgggtaaccactttgggtccagctcaaggtgtgggtttcgcgtcaacgaattgattgctaga	978
QY	901	ttgaactcaactctccagttcaagacacacactctctactaacacacatttgggactctaacca	960
Db	979	ttgaactcaactctccagttcaagacacacactctctactaacacacatttgggactctaacca	1038
QY	961	gctactttcccattgaaacgctactttgtacgctgacttctctcaacgacacactatgata	1020
Db	1039	gctactttcccattgaaacgctactttgtacgctgacttctctcaacgacacactatgata	1098
QY	1021	tctattttcttcgctttgggtttgtcaacggttaccagaacattgttctactactctgttt	1080

Db	1099	tctatttcttcgcttgggttgtaacaacggtactaaagccattgtctactacttcigt	1155
QY	1081	gaatcatttgaagaactgacggttactctgcttcttggaactgttccattcgctgctaga	1140
Db	1159	gaatcatttgaagaactgacggttactctgcttcttggaactgttccattcgctgctaga	1218
QY	1141	gcttacggtgaaatgatgcgaatgcaagctgaaaaagaaacccattggttagagtttgggt	1200
Db	1219	gcttacggtgaaatgatgcgaatgcaagctgaaaaagaaacccattggttagagtttgggt	1278
QY	1201	aacgcacagagttgtccattgcaagttgctgttgacaagtgtggtagatgaagaga	1260
Db	1279	aacgcacagagttgtccattgcaagttgctgttgacaagtgtggtagatgaagaga	1338
QY	1261	gacgaacttcggtgaaagttgtcttcctcgctagatcgtgtggaactcggtgaatgttcc	1320
Db	1339	gacgaacttcggtgaaagttgtcttcctcgctagatcgtgtggaactcggtgaatgttcc	1398
QY	1321	gcttaa 1326	
Db	1399	gcttaa 1404	
RESULT 12			
AAZ59716			
ID	AAZ59716 standard; DNA; 1404 BP.		
AC	AAZ59716;		
XX			
DT	19-APR-2000 (first entry)		
XX			
DE	DNA encoding a mutant phytase-10, phytase-10-thermo[3]-Q50T-K91A.		
XX			
KW	Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;		
KW	thermostable; animal feed; monogastric animal; phytate phosphorus;		
KW	phosphate availability; consensus; mutant; ds.		
XX			
OS	Aspergillus terreus 9A1.		
OS	Aspergillus terreus cbs16.46.		
OS	Aspergillus niger var. awamori.		
OS	Aspergillus niger str. NRRL3135.		
OS	Aspergillus fumigatus ATCC13073.		
OS	Aspergillus fumigatus ATCC32722.		
OS	Aspergillus fumigatus ATCC58128.		
OS	Aspergillus fumigatus ATCC26906.		
OS	Aspergillus fumigatus ATCC32239.		
OS	Emericella nidulans.		
OS	Talaromyces thermophilus ATCC20186.		
OS	Mycelophthora thermophila.		
OS	Paxillus involutus NN005693.		
OS	Trametes pubescens NN9343.		
OS	Agrocybe pediades NN009289.		
OS	Peniophora lycii NN006113.		
OS	Thermomyces lanuginosa.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
XX	CDS	1..1404	
FT	FT	/*tag= a	
FT	FT	/product= "Phytase-10-thermo[3]-Q50T-K91A"	
XX			
PN	EP969089-A1.		
XX			
PD	05-JAN-2000.		
XX			
PF	23-JUN-1999; 99EP-0111949.		
XX			
PR	29-JUN-1998; 98EP-0111960.		
XX			
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.		
XX			
PI	Brugger R, Lehmann M, Wyss M;		
XX			

DR WPI: 2000-099429/09.
 XX New stabilized enzyme formulation, useful for feed compositions for
 PT monogastric animals -
 XX Example 5; Fig 19; 101pp; English.
 XX The invention relates to a novel stabilised dry or liquid enzyme
 CC formulation, comprising phytase (myo-inositol hexakisphosphate
 CC phosphohydrolase) and one or more stabilising agents including
 CC xylitol or ribitol; polyethylene glycols with a molecular weight of 600
 CC to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
 CC glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
 CC The stabilised phytase formulation is used in a method for preparing a
 CC feed composition for monogastric animals (e.g., pigs, poultry) and
 CC provides a monogastric animal with its dietary requirements of
 CC phosphorus. Although a large amount of phosphate is present in animal
 CC feed in the form of phytate phosphorus, monogastric animals are unable
 CC to utilise this form of phosphate, resulting in the addition of extra
 CC phosphate to the feed of such animals. Phytase enhances the nutritional
 CC value of plant material without the need for adding additional phosphate
 CC to the feed. The level of phosphate pollution in the environment is
 CC reduced by adding phytase to animal feed, as the animal can make use of
 CC the inorganic phosphate liberated from phytate phosphorus using the
 CC enzyme. The phytase formulation of the invention has an improved
 CC thermostability and can therefore remain stable during long-term storage
 CC and can withstand feed processing methods such as extrusion, expansion
 CC and pelleting. The present sequence represents DNA encoding a mutant
 CC phytase-10 consensus sequence, phytase-10-thermo[3]-Q50T-K91A, which has
 CC a temperature optimum and melting point 4 degrees Celsius higher than
 CC that of phytase-10 (AAV69566). Its specific activity with phytate as a
 CC substrate is also strongly increased.
 XX
 SQ Sequence 1404 BP: 329 A; 309 C; 308 G; 458 T; 0 other;

Query Match 94.2%; Score 1249.2; DB 21; Length 1404;
 Best Local Similarity 96.4%; Pred. No. 0;
 Matches 1276; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 aattctcactctgtgacactgttgacggtgtgtacacatgtttccacagaattttctc 60
 DB 79 aactctcactctgtgacactgttgacggtgtgtacacatgtttccacagaattttctc 138
 QY 61 ttgtgggtacctactctccatctctctttgtgacagcaactctgtatttctccagac 120
 DB 139 ttgtgggtacctactctccatctctctttgtgacagcaactctgtatttctccagac 198
 QY 121 gtccagacgactgtagattactctgttctcaagttttgtctagacacggtgctagatc 180
 DB 199 gtccagaggtgttagattactctgttctcaagttttgtctagacacggtgctagatc 258
 QY 181 ccaactctctcgtctaaaggttactctgttctgattgaagctattcaaaagacgct 240
 DB 259 ccaactctctcgtctaaaggttactctgttctgattgaagctattcaaaagacgct 318
 QY 241 actgctttcaaggttaagtagctctcttttgaagacttcaactacactttgggtgctgac 300
 DB 319 actgctttcaaggttaagtagctctcttttgaagacttcaactacactttgggtgctgac 378
 QY 301 gacttgactccattcgttgaaacacaaatgttcaactctggtatttaagttctacagaaga 360
 DB 379 gacttgactccattcgttgaaacacaaatgttcaactctggtatttaagttctacagaaga 438
 QY 361 tacaaggtttgctagaaagattgtccattcattagagcttctggttctgacagagtt 420
 DB 439 tacaaggtttgctagaaagattgtccattcattagagcttctggttctgacagagtt 498
 QY 421 attgcttctgctgaaagttcattgaaagtttccaatctgtaagtttggtgacccaggt 480
 DB 499 attgcttctgctgaaagttcattgaaagtttccaatctgtaagtttggtgacccaggt 558
 QY 481 tctcaacacacacaggtctctccagttatttaacgtgatcttccagaaggtatccggttac 540

DB 559 gctaaaccacacaaagcttctccagttatttaacggtattattccagaaggtgctggttac 618
 QY 541 acaaacacttttgaccacacggttactgttactgtcttgcgaagactctgaattaggtgacgac 600
 DB 619 acaaacacttttgaccacacggttactgttactgtcttgcgaagactctgaattaggtgacgac 678
 QY 601 gttgaagctaaactcactgctttgttctgcagctccagctatttagagctagattggaagctgac 660
 DB 679 gttgaagctaaactcactgctttgttctgcagctccagctatttagagctagattggaagctcac 738
 QY 661 ttgcaggtgttactttgactgacgaagacggtttgttactgttgacacatgtgtccattc 720
 DB 739 ttgcaggtgttactttgactgacgaagacggtttgttactgttgacacatgtgtccattc 798
 QY 721 gacactgtcgtagaactttgacgctactgacgaattgtctcattctgtgttcttcaact 780
 DB 799 gacactgttctagaactttgacgctactgacgaattgtctcattctgtgttcttcaact 858
 QY 781 cacgacgaatggatcccaatcagcactacttgcgaagcttgggttaagtactacggttacggt 840
 DB 859 cacgacgaatggatcccaatcagcactacttgcgaatcttgggttaagtactacggttacggt 918
 QY 841 gctggttaaccattgggtccagctcgaaggtgtgtgttgcgaagacgttgcgaattgattgctaga 900
 DB 919 gctggttaaccattgggtccagctcgaaggtgtgtgttgcgaagacgttgcgaattgattgctaga 978
 QY 901 ttgactcactctcagttcgaagacacacttctactaaccacactttggactctaaaccca 960
 DB 979 ttgactcactctcagttcgaagacacacttctactaaccacactttggactctaaaccca 1038
 QY 961 gctactctccattgacgctactttgtacgctgactctctcagcacaacactatgata 1020
 DB 1039 gctactctccattgacgctactttgtacgctgactctctcagcacaacactatgatt 1098
 QY 1021 tctatttctctgctgttgggtttgtacaacggtacacagccattgtctactactctgtt 1080
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 QY 1081 gaactattgaaagaactgaacggttactctgtcttctgtgactgttccattcgtgctaga 1140
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 QY 1141 gttcactgtgaatgatgcaatgtcaagctgaaaaaggaacacactgtttagatttgggt 1200
 DB 1219 gttcactgtgaatgatgcaatgtgaaagctgaaaggaacacactgtttagatttgggt 1278
 QY 1201 aacgacagagttgtccattgcaaggttgcgtgttgacaagttgggttagatgtaagaga 1260
 DB 1279 aacgacagagttgtccattgcaaggttgcgtgttgacaagttgggttagatgtaagaga 1338
 QY 1261 gacgactctggtgaaggtttgtcttctcgtagatctgttgtaactgggtgaaatgtttc 1320
 DB 1339 gacgactctggtgaaggtttgtcttctcgtagatctgttgtaactgggtgaaatgtttc 1398
 QY 1321 gcttaa 1326
 DB 1399 gcttaa 1404

RESULT 13
 AAA73293
 ID AAA73293 standard; DNA; 1404 BP.
 XX
 AC AAA73293;
 XX
 DT 05-DEC-2000 (first entry)
 XX
 DE Consensus phytase 10 thermo 5 Q50T K91A polynucleotide SEQ ID NO:96.
 XX
 KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 temperature stability; pH profile; temperature profile; reaction rate;
 specific activity; substrate specificity; substrate cleavage pattern;

us-09-488-265-28_copy_79_1404.rng

Thu Oct 18 11:34:43 2001

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 QY 1321 gcttaa 1326
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 Db 1410 gcttaa 1415

Search completed: October 16, 2001, 12:14:29
 Job time: 1063 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 15:47:58 ; Search time 12806.7 Seconds
(without alignments)
1601.526 Million cell updates/sec

Title: US-09-488-265-28_COPY_79_1404
Perfect score: 1326
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba1:*
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98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1282.8	96.7	1426	9	AX021809
2	798	60.2	1350	56	AF295325
3	621.2	46.8	1404	9	AF295325 Synthetic
4	621.2	46.8	1404	10	AF295325 Synthetic
5	621.2	46.8	1404	10	AF295325 Synthetic
6	621.2	46.8	1404	10	AF295325 Synthetic
7	621.2	46.8	1404	10	AF295325 Synthetic
8	621.2	46.8	1404	10	AF295325 Synthetic

9 621.2 46.8 6756 10 IL3429
10 619.4 46.7 1528 13 AF218813
11 617.8 46.6 2363 9 AR018076
12 617.8 46.6 2363 9 AR051916
13 617.8 46.6 2379 13 ASN53934
14 617.8 46.6 2379 13 ASN53934
15 609.8 46.0 1515 12 AB022700
16 609.8 46.0 1590 14 AB013315
17 600 45.2 1553 12 AB042805
18 580.6 43.8 1571 9 AX000634
19 580.6 43.8 1812 15 SFU59804
20 578.4 43.6 1931 9 AX000630
21 578.4 43.6 1931 14 ENU59803
22 548.8 41.4 1912 9 A46793
23 544.4 41.1 1845 9 AX000632
24 544.4 41.1 1845 15 TTU59802
25 522.4 39.4 1567 9 AX000636
26 522.4 39.4 1770 14 ATU60412
27 522.4 39.4 2327 9 A46783
28 522.4 39.4 2327 14 ATU59805
29 501 37.8 1922 10 AX085191
30 500.4 37.7 1464 10 AX085193
31 500.4 37.7 1584 10 AX085192
32 407.8 30.8 4898 10 AX085207
33 333.2 25.1 2200 9 AR031151
34 275 20.7 853 10 AX085213
35 274.2 20.7 860 10 AX085208
36 258.8 19.5 3995 9 A46785
37 258.8 19.5 3995 14 MTU59806
38 132.8 10.0 950 10 AX085210
39 91.8 6.9 1117 14 MGR299239
40 68 5.1 1404 14 SCU19789
41 64.2 4.8 1404 14 SCPH05A
42 64.2 4.8 1904 10 AX072908
43 64.2 4.8 2934 15 SCYBR093C
44 64.2 4.8 3913 14 SCPH035
45 64.2 4.8 69748 14 SCRACII

ALIGNMENTS

RESULT 1
AX021809
LOCUS AX021809 1426 bp DNA
DEFINITION Sequence 3 from Patent EP0897985.
ACCESSION AX021809
VERSION AX021809.1 GI:10045052
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1. (bases 1 to 1426)
AUTHORS Lehmann,M.
TITLE Consensus phytases
JOURNAL Patent: EP 0897985-A 3 24-FEB-1999;
HOFFMANN LA ROCHE (CH)
FEATURES Location/Qualifiers
source 1..1426
/organism="synthetic construct"
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BASE COUNT 338 a 311 c 308 g 469 t
ORIGIN

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Best Local Similarity 98.08; Pred. No. 0;
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 LOCUS AF295325 1350 bp mRNA SYN 18-OCT-2000
 DEFINITION Synthetic construct phytase mRNA, complete cds.
 ACCESSION AF295325
 VERSION AF295325.1 GI:10732782
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct.
 synthetic construct
 artificial sequence.
 1 (bases 1 to 1350)
 AUTHORS Yang, L., Chen, Z., Bei, J., Liao, L. and Wang, X.
 TITLE Synthetic sequence of phytase gene for expression in *Pichia pastoris*
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1350)
 AUTHORS Chen, Z.
 TITLE Direct Submission
 JOURNAL Submitted (11-AUG-2000) Animal Science Institute, Guangdong Academy of Agricultural Sciences, Guangzhou, Guangdong 510640, China
 REFERENCE 3 (bases 1 to 1350)
 AUTHORS Yang, L., Bei, J., Liao, L. and Wang, X.
 TITLE Direct Submission
 JOURNAL Submitted (11-AUG-2000) Biopharmaceutical Center, Zhongshan University, Guangzhou, Guangdong 510275, China
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 BASE COUNT 319 a 354 c 282 g 395 t
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 Best Local Similarity 75.3%; Pred. No. 6e-204;
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LOCUS I13430 1404 bp DNA PAT 26-JUL-1995
DEFINITION Sequence 33 from patent US 5436156.
ACCESSION I13430
VERSION I13430.1 GI:910771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1404)
AUTHORS Van Gorcom,R.F.M., Van Hartingsveldt,W., Van Paridon,P.A.,
Veenstra,A.E., Luiten,R.G.M. and Sellen,G.C.M.
TITLE Cloning and expression of phytase from aspergillus
JOURNAL Patent: US 5436156-A 33 25-JUL-1995;
FEATURES
Location/Qualifiers
source
BASE COUNT 293 a 436 c 344 g 331 t
ORIGIN
Query Match 46.8%; Score 621.2; DB 10; Length 1404;
Best Local Similarity 67.0%; Pred. No. 2.2e-156;
Matches 881; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

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QY 72 ctactctcactctctctgttgacagacgaatctgtattttccagacgttccagacga 131
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QY 132 ctgtagatgactctgttcaagttttgtctagacacggtgtagatcccaacttttc 191
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QY 192 tgcgtcaggtctactctgtcttgatgaagctattcaaaagacgtactgtttcaa 251
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LOCUS I33881 1404 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 19 from patent US 5593963.
ACCESSION I33881
VERSION I33881.1 GI:1824672
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Van Ooljen,A.J.J., Rietveld,K., Hoekema,A., Pen,J., Sijmons,P.C.
and Verwoerd,T.C.
TITLE Expression of phytase in plants
JOURNAL Patent: US 5593963-A 19 14-JAN-1997;
FEATURES
Location/Qualifiers
source
BASE COUNT 293 a 436 c 344 g 331 t
ORIGIN
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Query Match 46.8%; Score 621.2; DB 10; Length 1404;
Best Local Similarity 67.0%; Pred. No. 2.2e-156;
Matches 881; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

QY 12 ttgtgacactgttgacggtggttaacaaattttcccaagaatttctcactgtggtggtac 71
DB 90 TTGCGATAGCGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATCTTTGGGTCA 149
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LOCUS		A.niger phyA gene.				
DEFINITION		Z16414				
ACCESSION		Z16414.1	GI:2392			
VERSION		phyA gene.				
KEYWORDS		Aspergillus niger.				
SOURCE		Aspergillus niger				
ORGANISM		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.				
REFERENCE		1 (bases 1 to 2000)				
AUTHORS		van Hartingsveldt, W., Van Zeijl, C.M.J., Harteveld, M.G., Gouka, R.J., Sykerbuyk, M.E.G., Luiten, R.G.M., Van Paridon, P.A., Selden, G.C.M., Veenstra, A.E., Van Gorcom, R.F.M. and Van Den Hondel, C.A.M.J.				
TITLE		Cloning, molecular characterization and overexpression of the phytase gene (phyA) of Aspergillus niger				
JOURNAL		Gene (1992) In press				
AUTHORS		2 (bases 1 to 2000)				
TITLE		van Hartingsveldt, W.				
JOURNAL		Direct Submission				
FEATURES		Submitted (05-OCT-1992) Van Hartingsveldt W., TNO Medical Biological Laboratory, Lange Kleiweg 139, Rijswijk, the Netherlands				
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Best Local Similarity 67.0%; Pred No. 2.3e-156;
Matches 881; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

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VERSION M94550.1 GI:166520
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REFERENCE 1 (bases 1 to 2665)
AUTHORS Mullaney,E.J., Gibson,D.M and Ullah,A.H.
TITLE Positive identification of a lambda gt11 clone containing a region of
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JOURNAL Appl. Microbiol. Biotechnol. 35, 611-614 (1991)
MEDLINE 9200601
REFERENCE 2 (bases 1 to 2665)
AUTHORS Mullaney,E.J.
TITLE Sequence of the Aspergillus niger (ficcum) phytase gene
JOURNAL Unpublished (1992)
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ACCESSION A19451
VERSION A19451.1 GI:583193
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SOURCE synthetic construct.
ORGANISM artificial sequence.
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AUTHORS Veenstra,A.E., Luiten,R.G.M., van Hartingsveldt,W., van Paridon,P.A.,
Cloning and expression of microbial phytase
Patent: EP 0420358-A 40 03-APR-1991;
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Matches 881; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

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ACCESSION I13429
VERSION I13429.1 GI:910770
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AUTHORS Van Gorcom,R.F.M., Van Hartingsveidt,W., Van Paridon,P.A.,
Veenstra,A.E., Luiten,R.G.M. and Selten,G.C.M.
TITLE Cloning and expression of phytase from aspergillus
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Best Local Similarity 67.0%; Pred. No. 2.5e-156;
Matches 881; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

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QY	672	tactttgactgacgaagagctgttttaactgtatgacatgttccattcgcacactgtgc	731
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QY	732	tagaactctgacgtactgaaatgtctccattctgtctgtttgttcaactcagcaaatg	791
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QY	792	gatacaatacgaacttctgcaagcttgggttaagtactacggttaccggtgctggttaaccc	851
Db	1181	GATCAACTAGCACTACCTCCAGTCTTGAATAAGTATTAGCGGCATGGTGCAGGTAAACCC	1240
QY	852	attgggtccagctcaaggttgggttcgctaacgaattgattgcttagattgactcactc	911
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QY	912	tccagttcaagacacacacttctactaaccacactttggactctaaacccagctacttccc	971
Db	1301	GCCTGTCCACGATGACACCACTGTTCCAAACCACTTTTGGACTCGAGCCCGGCTACCTTCC	1360
QY	972	attgaagctactgttgaactgacttctcgcacacacactatgatctctatttctt	1031
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QY	1032	cgtttggtttgttacaacggttaccagccattgtctactacttctgttgaatctattga	1091
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QY	1092	agaactgaacggttactctgtcttctggaactgttccattcgtgcttagagcttaacttga	1151
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RESULT 10
AF218813
LOCUS

DEFINITION	Aspergillus niger myo-inositol hexaphosphate phosphohydrolyase precursor, gene, complete cds.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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ORGANISM	Aspergillus niger. Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
REFERENCE	1 (bases 1 to 1528) Hongning,W., Qi,W. and Jing,X. PCR, cloning and characterization of the phytase (phyA) gene of Aspergillus niger (China Strain) Unpublished																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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AUTHORS	Submitted (24-DEC-1999) Aniaml Sci. & Tech. College, Sichuan Agricultural University, Ya'an City, Sichuan Province 625014, P.R.China																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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REFERENCE	1..1528 /organism="Aspergillus niger" /db_xref="taxon:5061" /country="China" join(14..57,160..172) join(14..57,160..1519) /product="myo-inositol hexaphosphate phosphohydrolyase precursor" join(14..57,160..1519) /EC_number="3.1.3.8" /function="catalyzes the hydrolysis of phytic acid" /note="phytase" /codon_start=1 /product="myo-inositol hexaphosphate phosphohydrolyase precursor" /protein_id="AAF25481.1" /db_xref="GI:6694941" /translation="MGVSALLPLLYLLSGVTSGLAVPASRNQSTCDTVDGQCFSETSHNQVAPFFSLANESAI SPQAGCRVTFQVLSHGARYPTDKRKYISALIEIQUNATFDGKYAFKTYNSLGADLTLPFGEQELVNSGKIFYORYESLTNIPFIRSSGSRVATASGKKFIEGFQSTKLPDRAQSQSSPKIDVISEASSNNTLDPGCTVFEDSLADAVANETATFVPTIRORLENDLSGVSLTDEVTYLMDCMSFDITSTVDTKLSFPCDLFTHDEWINDYLSQKVKYVGHGAGNPLGPTQGVYANELIARLTSPVHDDTSNHTLDSNATFPLNLTLDIADFSDHNGIISILFALGLYNGTKPLSTTVQNIQT DGFSSATVPFASRLYVEMQCAEQEPLRVILVNDVRVPLHGPCVDALGRCTRDSEFV KGLSFARSGGDWAECEFA"																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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Query Match	46.7%; Score 619.4; DB 13; Length 1528;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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RESULT 11
AR018076

LOCUS AR018076 2363 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 7 from patent US 5780292.
ACCESSION AR018076
VERSION AR018076.1 GI:3973679
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2363)
AUTHORS Nevalainen,H.K.M., Paloheimo,M.T., Miettinen-Oinonen,A.S.K.,
Torckeli,T.K., Cantrell,M., Piddington,C.S., Rambosek,J.A.,
Turunen,M.K. and Fagerstrom,R.B.
TITLE Production of phytate degrading enzymes in trichoderma
JOURNAL Patent: US 5780292-A 7 14-JUL-1998;
FEATURES Location/Qualifiers
source 1..2363
BASE COUNT 559 a 732 c 510 g 562 t
ORIGIN /organism="unknown"

Query Match 46.6%; Score 617.8; DB 9; Length 2363;
Best Local Similarity 66.8%; Pred. No. 1.9e-155;
Matches 880; Conservative 0; Mismatches 437; Indels 0; Gaps 0;

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Db 592 CACTTGGGATACGGTCGATCAAGGGTATCAATGTTCTCCGAGACTTCGATCTTTGGGG 651
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Db 652 TCATATAGCGCGGTCTCTCTCTGGCAACGAATCGGCCATCTCCCTCTGATGTGCCGC 711
Qy 129 cgactgtagagttaactctgttcaagtttctgtacacggtgtctagataccacacttc 188
Db 712 CGGTTCGAGAGTCACTTTCGCTCAGGTCCTCTCCGTCATGGAGCGGGTATCCGACCGA 771
Qy 189 ttctgcttaagcttactctactctgttgaatgactattcaaaagacgtactgttt 248
Db 772 GTCCAAGGGCAAGAAATACCTCCGCTCTCATTTAGGAGATCCAGCAGAACGTGACCTT 831
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Db 892 TCCCTTCGGAGAGCAGGAGTAGTCAACTCCGCGCATCAAGTTCTACCGGATACGAATC 951
Qy 369 ttgggttagaagattgttccattcattagagcttctgttctgacagagttattgtcttc 428
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Db 1012 CGCGGAGAAATTCATTGAGGGCTTCCAGAGCACCAAGCTTGAAGGATCTCTGTCGCCAGCC 1071
Qy 489 acaccaagcttctccagttattaaocgtatccattccagaaggtatccggttacaacaacac 548
Db 1072 GGGCCAAATCGTCGCCCAAGATCGACGTGTCATTTCCGAGGCCAGCTCATCCCAACAACAC 1131
Qy 549 ttggaccacggttactgttactgtcttgcagacactctgaattaggtgacagacgttgaagc 608
Db 1132 TCTCGACCCAGGACCTCGACATGTCTTTTGAAGACAGCAATTTGGCCGATACCTGTCGAAGC 1191
Qy 609 taacttcactgttctgttctccagctatttagagctagattggagctgactgtaccagc 668
Db 1192 CAATTTACCGCCACGTTTCGCCCTTCCATTCGTAACGCTGAGAGACGACCTGCTCTGG 1251
Qy 669 tgttacttgcactgacgaagacgttgtttacttgcattgacatgtgtccattcgcactgt 728
Db 1252 CGTGACTCTCACAGACAGAAAGTAGCTACCTCATGTCATGTCATGTCCTCTCGACACCAT 1311

[illegible]

us-09-488-265-28_copy_79_1404.rge

Thu Oct 18 11:34:43 2001

...

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 16, 2001, 17:50:54 ; Search time 88.89 Seconds
(without alignments)
101.458 Million cell updates/sec

Title: US-09-488-265-26_COPY_1_438
Perfect score: 2307
Sequence: 1 MGVPVLLSTATLFGSGT.....EPLRVLYNDVVPLHCGV 438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCFUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2028	87.9	441	4	US-09-121-425-1
2	2016	87.4	467	4	US-09-121-425-2
3	1745	75.6	467	1	US-07-923-724-8
4	1745	75.6	467	2	US-08-609-426A-8
5	1745	75.6	467	2	US-08-374-652C-2
6	1733	75.1	467	1	US-08-151-574-32
7	1733	75.1	467	1	US-08-146-424-20
8	1733	75.1	467	1	US-08-693-709-2
9	1733	75.1	467	2	US-08-419-448-32
10	1733	75.1	467	2	US-08-819-825-3
11	1733	75.1	467	4	US-09-163-642-3
12	1726	74.8	467	4	US-09-155-855-3
13	1684	73.0	443	4	US-09-155-855-1
14	1679	72.8	443	4	US-09-155-855-2
15	1282	55.6	475	2	US-08-819-825-2
16	1282	55.6	475	4	US-09-163-642-2
17	802	34.8	439	3	US-08-993-359-24
18	802	34.8	439	3	US-09-221-654-2
19	802	34.8	439	3	US-08-989-358A-2
20	789.5	34.2	453	3	US-08-993-359-22
21	782.5	33.9	443	3	US-08-993-359-30
22	755	32.7	442	3	US-08-993-359-28
23	747	32.4	442	3	US-08-993-359-26
24	347	15.0	468	1	US-07-627-539G-2
25	346.5	15.0	479	1	US-07-923-724-2
26	346.5	15.0	479	2	US-08-609-426A-2
27	346.5	15.0	479	2	US-08-374-652C-4

28	342.5	14.8	446	1	US-07-627-539G-7	Sequence 7, Appli
29	185.5	8.0	92	3	US-08-993-359-32	Sequence 32, Appli
30	179	7.8	449	3	US-08-680-506-7	Sequence 7, Appli
31	121.5	5.3	318	3	US-08-680-506-3	Sequence 3, Appli
32	121	5.2	113	1	US-08-241-853-8	Sequence 8, Appli
33	121	5.2	113	2	US-08-850-917-8	Sequence 32, Appli
34	115	5.0	24	2	US-08-374-652C-32	Sequence 32, Appli
35	110	4.8	113	1	US-08-241-853-10	Sequence 10, Appli
36	110	4.8	113	2	US-08-850-917-10	Sequence 10, Appli
37	97	4.2	35	2	US-08-151-574-2	Sequence 2, Appli
38	97	4.2	35	2	US-08-419-448-2	Sequence 2, Appli
39	95.5	4.1	386	1	US-08-758-213-1	Sequence 1, Appli
40	95.5	4.1	386	2	US-08-692-787-48	Sequence 48, Appli
41	95.5	4.1	386	4	US-09-097-199-48	Sequence 48, Appli
42	95.5	4.1	515	2	US-09-146-283-2	Sequence 2, Appli
43	95.5	4.1	515	3	US-08-579-823A-2	Sequence 2, Appli
44	95.5	4.1	515	4	US-09-344-195-2	Sequence 2, Appli
45	93.5	4.1	675	4	US-09-171-878-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus Phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-1

Query Match 87.9%; Score 2028; DB 4; Length 441;
Best Local Similarity 92.5%; Pred. No. 3.3e-205;
Matches 381; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY	27	NSHSCDTVDGGYQCFFPEISHLMGQKSPFSLADESAISDPVKGCRVTFVQLSRHGARY	86
DB	1	NSHSCDTVDGGYQCFFPEISHLMGQKSPFSLADESAISDPVKGCRVTFVQLSRHGARY	60
QY	87	PTSSKSKYSALIEAQKNATAFKGYAFKTYNTLTGADLTPTGEOQMVNSGKIFYRR	146
DB	61	PTSSKSKAYSALIEAQKNATAFKGYAFKTYNTLTGADLTPTGEOQMVNSGKIFYRR	120
QY	147	YKALARKIVPFVRASGSDRVIASAEKFTGFSQAKLADFGANPHQASPVINVIIEGAGY	206
DB	121	YKALARKIVPFVRASGSDRVIASAEKFTGFSQAKLADFGANPHQASPVINVIIEGAGY	180
QY	207	NNTLHGCTAFEESLGGDDVEANFTAVFAPIRARLEAHLPGVNLTDDEVVNLMDMCPF	266
DB	181	NNTLHGCTAFEESLGGDDVEANFTAVFAPIRARLEAHLPGVNLTDDEVVNLMDMCPF	240
QY	267	DTVARTSDATLSPECDLFTHDEWIQYDYVLSLQKGYCYGAGNPLGPAQGVFNELLAR	326
DB	241	ETVARTSDATLSPECDLFTHDEWIQYDYVLSLQKGYCYGAGNPLGPAQGVFNELLAR	300
QY	327	LTHSPVQDHTSTNHTLSNPATFPLNATLYADFSDHNTMVSIFTFALGLYNGTKPLSTTSV	386

Db 301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360

QY 387 ESIEETDGYAASWTVPFAARAYVEMMQCAEKEPLRVRLVNDVRVPLHGGCV 438

Db 361 ESIEETDGYASWTVPFGARAYVEMMQCAEKEPLRVRLVNDVRVPLHGGCAV 412

RESULT

US-09-121-425-2

Sequence 2, Application US/09121425

Patent No. 6153418

GENERAL INFORMATION:

APPLICANT: Lehmann, Martin

TITLE OF INVENTION: Consensus Phytases

FILE REFERENCE: consensus phytases 13239

CURRENT APPLICATION NUMBER: US/09/121.425

CURRENT FILING DATE: 1998-07-23

EARLIER APPLICATION NUMBER: EPO 97112688.3

EARLIER FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 467

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-09-121-425-2

Query Match 87.4%; Score 2016; DB 4; Length 467;

Best Local Similarity 84.5%; Pred. No. 6.8e-204;

Matches 387; Conservative 13; Mismatches 16; Indels 40; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGTALGPRGNHSCDVTGQYQCFPEISHLWGQYSPFFSLADE 60

Db 1 MGVFVLLSIATLFGSTGTALGPRGNHSCDVTGQYQCFPEISHLWGQYSPFFSLEDE 60

QY 61 SATSPDVPKCRVTFVQVLSRHGARYPTSSKSKYSALIEATOKNATAPKGYAFKLTYN 120

Db 61 SATSPDVPDCCRVTFFQVLSRHGARYPTSSKSKYSA-----TYN 100

QY 121 YTLGADLTTPFGQOMVNSGKIFRYKALARKIVPFVRASGSDRVIASAEKFIQFQSA 180

Db 101 YTLGADLTTPFGQOMVNSGKIFRYKALARKIVPFIRASGSDRVIASAEKFIQFQSA 160

QY 181 KLADPGANPHQASPVIN-----VIIPEGAGYNNITLDHGLCTAFEE 220

Db 161 KLADPGSOPHQASPVIDLIEAIQKNATAFKGYAFKLTVIIPEGAGYNNITLDHGTCTAFED 220

QY 221 SELGDDVEANFTAVFAPPIDARLEAHLPGVNLDEVDVNLMDMCPDFTVARTSDATOLSP 280

Db 221 SELGDDVEANFTALFAPIDARLEADLPGLTDEVDVNLMDMCPETVARTSDATLSP 280

QY 281 FCDLTFHDEWITQDYLOSLGKYCYGAGNPLGPAQGVFNELIARLTHSPVDHTSTNH 340

Db 281 FCAFLTDEWRFQDYLOSLGKYCYGAGNPLGPAQGVFPANELIARLTHSPVDHTSTNH 340

QY 341 TLDNSNPATFPLNATLYADFSHDNTWISIFFALGLYNGTKPLSTTSVESIETDGYAASWT 400

Db 341 TLDNSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIETDGYASWT 400

QY 401 VPFAARAYVEMMQCAEKEPLRVRLVNDVRVPLHGGCV 438

Db 401 VPFGARAYVEMMQCAEKEPLRVRLVNDVRVPLHGGCAV 438

RESULT

US-07-923-724-8

Sequence 8, Application US/07923724

Patent No. 5780292

GENERAL INFORMATION:

APPLICANT: Nevalainen, Helena K.M.
 APPLICANT: Paloheimo, Marja T.
 APPLICANT: Miettinen-Oinonen, Arja S.K.
 APPLICANT: Torkkeli, Tuula K.
 APPLICANT: Cantrell, Michael
 APPLICANT: Piddington, Christopher S.
 APPLICANT: Rambosek, John A.
 APPLICANT: Turunen, Marja K.
 APPLICANT: Fagerstr m, Richard B.
 TITLE OF INVENTION: Production Of Phytase Degrading Enzymes
 TITLE OF INVENTION: in Trichoderma
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/923,724

FILING DATE: 31-JUL-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/496,155

FILING DATE: 19-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/044,077

FILING DATE: 29-APR-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UK 8610600

FILING DATE: 30-APR-1986

ATTORNEY/AGENT INFORMATION:

NAME: Cimbala, Michele A.

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 1050.0240004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2500

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-923-724-8

Query Match 75.6%; Score 1745; DB 1; Length 467;

Best Local Similarity 74.4%; Pred. No. 2.5e-175;

Matches 326; Conservative 43; Mismatches 69; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTGTALGPRGNHSCDVTGQYQCFPEISHLWGQYSPFFSLADE 60

Db 1 MGVSALLPLLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

QY 61 SAISPDVPKCRVTFVQVLSRHGARYPTSSKSKYSALIEATOKNATAPKGYAFKLTYN 120

Db 61 SAISPDVPAGCKRVTFQVLSRHGARYPTESKSKYSALIEATOKNATAPKGYAFKLTYN 120

QY 121 YTLGADLTTPFGQOMVNSGKIFRYKALARKIVPFVRASGSDRVIASAEKFIQFQSA 180

Db 121 YSLGADLTTPFGCEQELVNSGKIFRYQYESLTRNIIPIFIRSSGSSRVIASGEKFIQFQST 180

QY 181 KLADPGANPHQASPVINVIIPEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPP 240

Db 181 KLKDPRAQPGQSSPKIDVVVISEASSNNTLDPGTCTVFESELDADTVANFTATFAPSIR 240

QY 241 ARLEAHLPGVNLTDDEYVNLMDMPFDTVARTSDATQSPFCDLFTHDEWIOYDYLQSLG 300
Db 241 QRLNDLSGVTLDTEVYLMDCSPDTISTSTVDKLSFCDLFTHDEWIHYDYLQSLK 300
QY 301 KYXGAGNPLGPAQGVFNELIARLTHSPVODHTSTNHTLDSNPATPLNATLYADFS 360
Db 301 KYXGAGNPLGPAQGVFNELIARLTHSPVODHTSTNHTLDSNPATPLNATLYADFS 360
QY 361 HDNTMVSIFPAGLYNGTKPLSTTSVESTTEEDGYAASWTVPFAARAYVEMMQCAEQEP 420
Db 361 HDNGIISILFALGNGTKPLSTTTVENITQTDGFSASWTVPFASRLYVEMMQCAEQEP 420
QY 421 LVRVLNDRVPLHGGCV 438
Db 421 LVRVLNDRVPLHGGCV 438

RESULT 4

US-08-609-426A-8
; Sequence 8, Application US/08609426A
; Patent No. 5830733
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstrom, Richard B.
; APPLICANT: Houston, Christine S.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; NUMBER OF INVENTION: in Trichoderma
; CORRESPONDENCE ADDRESSES: 69
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,426A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,724
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Grant E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 1050.0080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-609-426A-8

Query Match 75.6%; Score 1745; DB 2; Length 467;
Best Local Similarity 74.4%; Pred. No. 2.5e-175;
Matches 326; Conservative 43; Mismatches 69; Indels 0; Gaps 0;

QY 1 MGVEVLLLSIATLFGSTGTAALPGRNHSCDVTVDGQYQCFPEISHLWGQSPFSFADE 60
Db 1 MGVSAYLLPLLYLLAGVTSLGAVPASRNQSTCDTVDGQYQCFSETSHLWGQYAPFSLANE 60
QY 61 SAISPDPVKGRVTFVQVLSRHGARYPTSSKSKYSALIEAIOKNAFAFGKYAFLKTYN 120
Db 61 SAISPDPVAGCRVTFQVLSRHGARYPTESKSKYSALIEAIOKNAFAFGKYAFLKTYN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRRYKAIARKIVPVRASGSDRVIASAEKFTGFSQA 180
Db 121 YSLGADDLTPFGEQELVNSGKIFRYRYSLTRNIPIRSGSSSRVIASEKFTGFSQA 180
QY 181 KLADPGANPHOASPVINVIPEGAGYNTLDHGLCTAFESSELCDDEYEAFTAVFAPPIR 240
Db 181 KLADPGANPHOASPVINVIPEGAGYNTLDHGLCTAFESSELCDDEYEAFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLTDDEYVNLMDMPFDTVARTSDATQSPFCDLFTHDEWIOYDYLQSLG 300
Db 241 QRLNDLSGVTLDTEVYLMDCSPDTISTSTVDKLSFCDLFTHDEWIHYDYLQSLK 300
QY 301 KYXGAGNPLGPAQGVFNELIARLTHSPVODHTSTNHTLDSNPATPLNATLYADFS 360
Db 301 KYXGAGNPLGPAQGVFNELIARLTHSPVODHTSTNHTLDSNPATPLNATLYADFS 360
QY 361 HDNTMVSIFPAGLYNGTKPLSTTSVESTTEEDGYAASWTVPFAARAYVEMMQCAEQEP 420
Db 361 HDNGIISILFALGNGTKPLSTTTVENITQTDGFSASWTVPFASRLYVEMMQCAEQEP 420
QY 421 LVRVLNDRVPLHGGCV 438
Db 421 LVRVLNDRVPLHGGCV 438

RESULT 5

US-08-374-652C-2
; Sequence 2, Application US/08374652C
; Patent No. 5834286
; GENERAL INFORMATION:
; APPLICANT: NEVALAINEN, HELENA K.M.
; APPLICANT: PALOHEIMO, MARJA T.
; APPLICANT: FAGERSTROM, RICHARD B.
; APPLICANT: MIETTINEN-OINONEN, ARJA S.
; APPLICANT: TURUNEN, MARJA K.
; APPLICANT: RAMBOSEK, JOHN A.
; APPLICANT: PIDDINGTON, CHRISTOPHER S.
; APPLICANT: HOUSTON, CHRISTINE S.
; APPLICANT: CANTRELL, MICHAEL A.
; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTASE DEGRADING
; TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,574
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-151-574-32

Query Match 75.6%; Score 1745; DB 2; Length 467;
Best Local Similarity 74.4%; Pred. No. 2.5e-175;
Matches 326; Conservative 43; Mismatches 69; Indels 0; Gaps 0;
QY 1 MGVFVLLSIATLFGSTGALPGRNHSCDVTGQYQCFPEISHLWQYSPFFSLADE 60
DB 1 MGVSALLPLVLLAGVTSGLAVPASRNQSCDVTGQYQCFSETSHLWQYAPFFSLANE 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKYKYSALIEAIQKNATAFKGYAFLKTYN 120
DB 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKYKYSALIEAIQKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQFQSA 180
DB 121 YSLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQFQST 180
QY 181 KLADPAGNPHQASPVINVIPEGAGYNNLTDLHGLCTAFEESELGDDVEANFTAVFAPPIR 240
DB 181 KLADPAGNPHQASPVINVIPEGAGYNNLTDLHGLCTAFEESELGDDVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPDFTVARTSDATQSPFCDLFTHDEWIOYDYLOSIG 300
DB 241 QRLNDLSGVTLDTEVTYLMDCSFDFTISTVDTKLSFCDLTHDEWIDYLOSIG 300
QY 301 KYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADFS 360
DB 301 KYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADFS 360
QY 361 HDNTWVSIFGALGYNKTKPLSTTSVESTETDGYAASWTVPFAARAYVEMMOCEAKEP 420
DB 361 HDNGIISILFALGYNKTKPLSTTTVENITQDGFSSAWTVPFASRLYVEMMOCEAKEP 420
US-08-374-652C-2

Query Match 75.1%; Score 1733; DB 1; Length 467;
Best Local Similarity 74.2%; Pred. No. 4.6e-174;
Matches 325; Conservative 43; Mismatches 70; Indels 0; Gaps 0;
QY 1 MGVFVLLSIATLFGSTGALPGRNHSCDVTGQYQCFPEISHLWQYSPFFSLADE 60
DB 1 MGVSALLPLVLLAGVTSGLAVPASRNQSCDVTGQYQCFSETSHLWQYAPFFSLANE 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKYKYSALIEAIQKNATAFKGYAFLKTYN 120
DB 61 SVISPEVAGCRVTFVQVLSRHGARYPTSSKSKYKYSALIEAIQKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQFQSA 180
DB 121 YSLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQFQST 180
QY 181 KLADPAGNPHQASPVINVIPEGAGYNNLTDLHGLCTAFEESELGDDVEANFTAVFAPPIR 240
DB 181 KLADPAGNPHQASPVINVIPEGAGYNNLTDLHGLCTAFEESELGDDVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPDFTVARTSDATQSPFCDLFTHDEWIOYDYLOSIG 300
DB 241 QRLNDLSGVTLDTEVTYLMDCSFDFTISTVDTKLSFCDLTHDEWIDYLOSIG 300
QY 301 KYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADFS 360
DB 301 KYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADFS 360
QY 361 HDNTWVSIFGALGYNKTKPLSTTSVESTETDGYAASWTVPFAARAYVEMMOCEAKEP 420
DB 361 HDNGIISILFALGYNKTKPLSTTTVENITQDGFSSAWTVPFASRLYVEMMOCEAKEP 420
US-08-151-574-32

Query Match 75.6%; Score 1745; DB 2; Length 467;
Best Local Similarity 74.4%; Pred. No. 2.5e-175;
Matches 326; Conservative 43; Mismatches 69; Indels 0; Gaps 0;
QY 1 MGVFVLLSIATLFGSTGALPGRNHSCDVTGQYQCFPEISHLWQYSPFFSLADE 60
DB 1 MGVSALLPLVLLAGVTSGLAVPASRNQSCDVTGQYQCFSETSHLWQYAPFFSLANE 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKYKYSALIEAIQKNATAFKGYAFLKTYN 120
DB 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKYKYSALIEAIQKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQFQSA 180
DB 121 YSLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQFQST 180
QY 181 KLADPAGNPHQASPVINVIPEGAGYNNLTDLHGLCTAFEESELGDDVEANFTAVFAPPIR 240
DB 181 KLADPAGNPHQASPVINVIPEGAGYNNLTDLHGLCTAFEESELGDDVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPDFTVARTSDATQSPFCDLFTHDEWIOYDYLOSIG 300
DB 241 QRLNDLSGVTLDTEVTYLMDCSFDFTISTVDTKLSFCDLTHDEWIDYLOSIG 300
QY 301 KYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADFS 360
DB 301 KYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADFS 360
QY 361 HDNTWVSIFGALGYNKTKPLSTTSVESTETDGYAASWTVPFAARAYVEMMOCEAKEP 420
DB 361 HDNGIISILFALGYNKTKPLSTTTVENITQDGFSSAWTVPFASRLYVEMMOCEAKEP 420
QY 421 LVRVLNDRVPLHGCPI 438
DB 421 LVRVLNDRVPLHGCPI 438
RESULT 6
US-08-151-574-32
Sequence 32, Application US/08151574
Patent No. 5436156
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt

QY 421 LVRVLVNDVVPLHGGCV 438
Db 421 LVRVLVNDVVPLHGGCV 438

RESULT 7
US-08-146-424-20
; Sequence 20, Application US/08146424
; Patent No. 5593963
; GENERAL INFORMATION:
; APPLICANT: VAN OIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,424
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: 44615-20011.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-146-424-20

Query Match 75.1%; Score 1733; DB 1; Length 467;
Best Local Similarity 74.2%; Pred. No. 4.6e-174;
Matches 325; Conservative 43; Mismatches 70; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTSGTALGRGSHSCDVTVDGYQCFPEISHLWGYSPFFSLADE 60
Db 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSCDVTVDGYQCFSETSLWGYAPFFSLANE 60
QY 61 SAISPDPVPGCRVTFVQVLSRHGARYPTSSKKYSALIEAIOKNATAFKGYAFLKTYN 120
Db 61 SVISPEVPAGCRVTFVQVLSRHGARYPTDSKKYSALIEIOQNATFPDGYAFLKTYN 120
QY 121 YTLGADLLTPGEGQMVNSGKIFKRYRKALARKIVPVRASGDRVIASAEKFIQFQSA 180
Db 121 YSLGADLLTPGEGQMVNSGKIFKRYRKALARKIVPVRASGDRVIASAEKFIQFQST 180
QY 181 KLADPGANPHQASPVINVIPEGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPP 240
Db 181 KLKDPRAQPGQSSPKIDVWISSESSNNLTDPGTCTVFDESELADTVEANFTAVFVPSIR 240
QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPEDTAVTSDATOLSPFCDLFTHDEWIQVLYQLSLG 300

Db 241 QRLNDLSGVTLTDTETVYLMDCSFDITSTSTVTKLSPCDLETHDEWINDYQLSLK 300
QY 301 KYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db 301 KYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNATLYADFS 360
QY 361 HDNTMVSIFFFALGLYNGTKPLSTTSVESIEETDGYAASWTVFPAARAYVEMMQCEAEKEP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTIVENITQTDGFSASAWTVFPAARAYVEMMQCEAEKEP 420
QY 421 LVRVLVNDVVPLHGGCV 438
Db 421 LVRVLVNDVVPLHGGCV 438

RESULT 8
US-08-693-709-2
; Sequence 2, Application US/08693709
; Patent No. 5770413
; GENERAL INFORMATION:
; APPLICANT: VAN OIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,709
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,424
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20011.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...23
; OTHER INFORMATION:
US-08-693-709-2

Query Match 75.1%; Score 1733; DB 1; Length 467;

Best Local Similarity 74.2%; Pred. No. 4.6e-174; Indels 0; Gaps 0; Mismatches 325; Conservative 43; Mismatches 70; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTSGTALPGRNHSHCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
DB 1 MGVSALLPLLYLLSGTSLGLAVPASRNQSSCDTVDQGYQCFSETSHLWGOYAPFFSLANE 60

QY 61 SAISPDVPGKCRVTFVQVLSRHGARYPTSSKKYSALIEAIQKNATAFKGYAFKLTYN 120
DB 61 SVISPEVPAGCRVTFQAQLSRHGARYPTDSKGYKYSALIEELQONATTFDGKYAFKLTYN 120

QY 121 YTLGADDLTPFGEQMVNSGKIFKYYRYKALARKIVPFVRASGSDRVIASAEKPIEGFQSA 180
DB 121 YSLGADDLTPFGEQELVNSGKIFQYRESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

QY 181 KLADPGANPHQASPVINVIIPGAGYNNITLDHGLCTAFEESELGDDVEANFTAFVPSIR 240
DB 181 KLKDPRAQPGQSSPKIDVIVISEASSNNTLDPGCTVFEDSELADTVVEANFTAFVPSIR 240

QY 241 ARLEAHLPGVNLTDDEVNLMDCPFDTVARTSDATQSPFCDLFTHDEWIQDYLYQSLG 300
DB 241 QRLNDLSGVTLDTEVTYLMDCSFDITSTVDTKLSPCDLFTHDEWINDYLYQSLK 300

QY 301 KYGYGAGNPLGPAQGVGFVNLIELARLTHSPVQDHTSNHTLDSNPATFPLNATLYADFS 360
DB 301 KYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

QY 361 HDNTWVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420
DB 361 HDNGIISILFALGLYNGTKPLSTTTVENITQDGFSSAWTVPFASRLYVEMMOCAEQEP 420

QY 421 LVRVLNDRVPLHGCV 438
DB 421 LVRVLNDRVPLHGCPV 438

RESULT 9
US-08-419-448-32
; Sequence 32, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcum
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seltin
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,448
; FILING DATE: 10-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500

Query Match 75.1%; Score 1733; DB 2; Length 467;
Best Local Similarity 74.2%; Pred. No. 4.6e-174;
Matches 325; Conservative 43; Mismatches 70; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTSGTALPGRNHSHCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
DB 1 MGVSALLPLLYLLSGTSLGLAVPASRNQSSCDTVDQGYQCFSETSHLWGOYAPFFSLANE 60

QY 61 SAISPDVPGKCRVTFVQVLSRHGARYPTSSKKYSALIEAIQKNATAFKGYAFKLTYN 120
DB 61 SVISPEVPAGCRVTFQAQLSRHGARYPTDSKGYKYSALIEELQONATTFDGKYAFKLTYN 120

QY 121 YTLGADDLTPFGEQMVNSGKIFKYYRYKALARKIVPFVRASGSDRVIASAEKPIEGFQSA 180
DB 121 YSLGADDLTPFGEQELVNSGKIFQYRESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

QY 181 KLADPGANPHQASPVINVIIPGAGYNNITLDHGLCTAFEESELGDDVEANFTAFVPSIR 240
DB 181 KLKDPRAQPGQSSPKIDVIVISEASSNNTLDPGCTVFEDSELADTVVEANFTAFVPSIR 240

QY 241 ARLEAHLPGVNLTDDEVNLMDCPFDTVARTSDATQSPFCDLFTHDEWIQDYLYQSLG 300
DB 241 QRLNDLSGVTLDTEVTYLMDCSFDITSTVDTKLSPCDLFTHDEWINDYLYQSLK 300

QY 301 KYGYGAGNPLGPAQGVGFVNLIELARLTHSPVQDHTSNHTLDSNPATFPLNATLYADFS 360
DB 301 KYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

QY 361 HDNTWVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420
DB 361 HDNGIISILFALGLYNGTKPLSTTTVENITQDGFSSAWTVPFASRLYVEMMOCAEQEP 420

QY 421 LVRVLNDRVPLHGCV 438
DB 421 LVRVLNDRVPLHGCPV 438

RESULT 10
US-08-819-825-3
; Sequence 3, Application US/08819825
; Patent No. 5866118
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,825
; FILING DATE: 18-MAR-1997
; CLASSIFICATION: 435

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4758.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-819-825-3

Query Match 75.1%; Score 1733; DB 2; Length 467;
Best Local Similarity 74.2%; Pred. No. 4.6e-174;
Matches 325; Conservative 43; Mismatches 70; Indels 0; Gaps 0;

QY 1 MGVFVLLSTATLFGSTGALPGRNHSCDVTGQYQCFPEISHLWGQYSPFFSLADE 60
Db 1 MGVSALLPLLYLSGVTSGLAVPASRNQSCDVTGQYQCFSETSHLWGQYAPFFSLANE 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKKYSALIEATQKNATAPKGYAFLKTYN 120
Db 61 SVISPEVPAGCRVTFQAQVLSRHGARYPTDSKGYKYSALIEEIQNATTFDGKYAFLKTYN 120
QY 121 YTLGADDLTPFGQQMVNSGKIFRYRYKALARKIVPFRASGSDRVIASAEKFIQFQSA 180
Db 121 YSLGADDLTPFGQELVNSGKIFRYQYESLNRIVPFRSSGSSRVIASGKKFIQFQST 180
QY 181 KLADPGANPHQASPVINVIIPGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLKDPRAQPGQSPKIDVIVSEASSNNTLDPGTCTVESELDATVEANFTAVFVPSIR 240
QY 241 ARLEAHLPGVNLTDDEVDVNLMDCPDFTVARTSDATQSPCDFLTHDEWIQDYQLQSLG 300
Db 241 QRLNDLSGVTLDTEVTYLMDCSFDTISTVDTKLSPCDFLTHDEWINDYQLQSLK 300
QY 301 KYGAGAGNPLGPTQGVYANELIARLTHSPVQDHTSNHTLDSNPATFPLNATLYADF 360
Db 301 KYHGAGNPLGPTQGVYANELIARLTHSPVQDHTSNHTLDSNPATFPLNATLYADF 360
QY 361 HDNTMVSIFFALGNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCEAEKEP 420
Db 361 HDNGIISILFALGNGTKPLSTTTVENITQTDGFSASWTVPFASRLYVENMOCQAEQEP 420
QY 421 LVRVLNDRVPLHGCGV 438
Db 421 LVRVLNDRVPLHGCPV 438

RESULT 11
US-09-163-642-3
; Sequence 3, Application US/09163642
; Patent No. 6221644
; GENERAL INFORMATION:
; APPLICANT: Berk, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6221644 No. 6221644disk of No. 6221644th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/163.642
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/819.825
; FILING DATE: 18-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4758.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-163-642-3

Query Match 75.1%; Score 1733; DB 4; Length 467;
Best Local Similarity 74.2%; Pred. No. 4.6e-174;
Matches 325; Conservative 43; Mismatches 70; Indels 0; Gaps 0;

QY 1 MGVFVLLSTATLFGSTGALPGRNHSCDVTGQYQCFPEISHLWGQYSPFFSLADE 60
Db 1 MGVSALLPLLYLSGVTSGLAVPASRNQSCDVTGQYQCFSETSHLWGQYAPFFSLANE 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKKYSALIEATQKNATAPKGYAFLKTYN 120
Db 61 SVISPEVPAGCRVTFQAQVLSRHGARYPTDSKGYKYSALIEEIQNATTFDGKYAFLKTYN 120
QY 121 YTLGADDLTPFGQQMVNSGKIFRYRYKALARKIVPFRASGSDRVIASAEKFIQFQSA 180
Db 121 YSLGADDLTPFGQELVNSGKIFRYQYESLNRIVPFRSSGSSRVIASGKKFIQFQST 180
QY 181 KLADPGANPHQASPVINVIIPGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLKDPRAQPGQSPKIDVIVSEASSNNTLDPGTCTVESELDATVEANFTAVFVPSIR 240
QY 241 ARLEAHLPGVNLTDDEVDVNLMDCPDFTVARTSDATQSPCDFLTHDEWIQDYQLQSLG 300
Db 241 QRLNDLSGVTLDTEVTYLMDCSFDTISTVDTKLSPCDFLTHDEWINDYQLQSLK 300
QY 301 KYGAGAGNPLGPTQGVYANELIARLTHSPVQDHTSNHTLDSNPATFPLNATLYADF 360
Db 301 KYHGAGNPLGPTQGVYANELIARLTHSPVQDHTSNHTLDSNPATFPLNATLYADF 360
QY 361 HDNTMVSIFFALGNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCEAEKEP 420
Db 361 HDNGIISILFALGNGTKPLSTTTVENITQTDGFSASWTVPFASRLYVENMOCQAEQEP 420
QY 421 LVRVLNDRVPLHGCGV 438
Db 421 LVRVLNDRVPLHGCPV 438

RESULT 12
US-09-155-855-3
; Sequence 3, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya

```

```
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-09-155-855-3

Query Match          74.8%; Score 1726; DB 4; Length 467;
Best Local Similarity 73.1%; Pred. No. 2.5e-173;
Matches 320; Conservative 49; Mismatches 69; Indels 0; Gaps 0;

QY 1 MGVSALLPLLLSGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFSLANK 60
Db 1 MGVSALLPLLLSGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFSLANK 60
QY 61 SAISPDVPGKCRVTFQVLSRHGARYPTSSKSKYSALIEATOKNATAFKGYAPLKTYN 120
Db 61 SAISPDVPGKCRVTFQVLSRHGARYPTSSKSKYSALIEATOKNATAFKGYAPLKTYN 120
QY 121 YTLGADDLTPFGCEQMVNSGIGFYRYKALARKIYVFRASGSDRVIAAEKFIQFQSA 180
Db 121 YTLGADDLTPFGCEQMVNSGIGFYRYKALARKIYVFRASGSDRVIAAEKFIQFQSA 180
QY 181 KLDADGANPHQASPVNWIPEGAGYNNITDGLCTAFESLGDVDEANFTAVFAPPIR 240
Db 181 KLDADGANPHQASPVNWIPEGAGYNNITDGLCTAFESLGDVDEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLTDVNVLMDCMCPDTVARTSDATQLSPFCDLFTHEWIDYQLQSLG 300
Db 241 ARLEAHLPGVNLTDVNVLMDCMCPDTVARTSDATQLSPFCDLFTHEWIDYQLQSLG 300
QY 301 KYGYGAGNPLGPAQGVGFVNELIAKTHSPVODHTSTNHTLDSNPATPLNATLYADES 360
Db 301 KYGYGAGNPLGPAQGVGFVNELIAKTHSPVODHTSTNHTLDSNPATPLNATLYADES 360
QY 361 HDNTWVSIFALGLYNGTKPLSTTSVESIEETDGYAASVTPFAARAYVEMMOCEAKEP 420
Db 361 HDNTWVSIFALGLYNGTKPLSTTSVESIEETDGYAASVTPFAARAYVEMMOCEAKEP 420
QY 421 LVRVLVNDVRVPLHGGCV 438
Db 421 LVRVLVNDVRVPLHGGCV 438

RESULT 13
US-09-155-855-1
; Sequence 1, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Aspergillus niger
; FEATURE:
; OTHER INFORMATION: Xaa at positions 2 & 3 may be any amino acid or unknown
; US-09-155-855-2
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Aspergillus niger
; US-09-155-855-1

Query Match          73.0%; Score 1684; DB 4; Length 443;
Best Local Similarity 74.8%; Pred. No. 6.1e-169;
Matches 308; Conservative 47; Mismatches 57; Indels 0; Gaps 0;

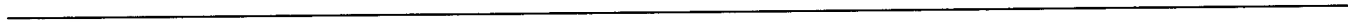
QY 27 NSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPGKCRVTFQVLSRHGARY 86
Db 3 NQSTCDTVDGGYQCFSETSHLWGQYAPFSLANKSAISPDVPGKCRVTFQVLSRHGARY 62
QY 87 PTSKSKKYSALIEATOKNATAFKGYAPLKTYNITLGGADDLTPFGCEQMVNSGIGFYRR 146
Db 63 PTDSKGGKYSALIEATOKNATTFEGKYAFUKTYNSLGADDLTPFGCEQMVNSGIGFYRR 122
QY 147 YKALARKIYVFRASGSDRVIAAEKFIQFQSAKLADPGANPHQASPVNWIPEGAGY 206
Db 123 YESLTRNIVPFISSGSSRVIAASGNKFIQFQSTKLKDPRAQPGQSPKIDVVISEASTS 182
QY 207 NNTLDHGLCTAFESLGDVDEANFTAVFAPPIRLEAHLPGVNLTDVNVLMDCMCP 266
Db 183 NNTLDHGLCTAFESLGDVDEANFTAVFAPPIRLEAHLPGVNLTDVNVLMDCMCP 242
QY 267 DTVARTSDATQLSPFCDLFTHEWIDYQLQSLGKYGYGAGNPLGPAQGVGFVNELIA 326
Db 243 DTISTVTDKLSFCDLFTHEWIDYQLQSLGKYGYGAGNPLGPAQGVGFVNELIA 302
QY 327 LTHSPVODHTSTNHTLDSNPATPLNATLYADESHDNTWVSIFALGLYNGTKPLSTTSV 386
Db 303 LTHSPVODHTSTNHTLDSNPATPLNATLYADESHDNTWVSIFALGLYNGTKPLSTTSV 362
QY 387 ESIBETDGYAASVTPFAARAYVEMMOCEAKEPLVRVLVNDVRVPLHGGCV 438
Db 363 ENITQTDGFSASVTPFAARAYVEMMOCEAKEPLVRVLVNDVRVPLHGGCV 414

RESULT 14
US-09-155-855-2
; Sequence 2, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Aspergillus niger
; FEATURE:
; OTHER INFORMATION: Xaa at positions 2 & 3 may be any amino acid or unknown
; US-09-155-855-2

Query Match          72.8%; Score 1679; DB 4; Length 443;
Best Local Similarity 75.1%; Pred. No. 2.1e-168;
Matches 307; Conservative 47; Mismatches 55; Indels 0; Gaps 0;
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us-09-488-265-26_copy_1_438.ra

Thu Oct 18 11:34:36 2001



Phytases

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 16, 2001, 17:52:48 ; Search time 101.07 Seconds
(without alignments)
330.112 Million cell updates/sec

Title: US-09-488-265-26_COPY_1_438

Perfect score: 2307
Sequence: 1 MGVFVLLSIATLFGSTSGT.....EPLRVLVNDRVPLHGGCV 438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1745	75.6	467	1 JN0889	3-phytase (EC 3.1.1.467)
2	1733	75.1	467	1 JN0656	3-phytase (EC 3.1.1.467)
3	1691	73.3	441	1 JN0482	3-phytase (EC 3.1.1.467)
4	391.5	17.0	467	1 PABYC	acid phosphatase (EC 3.1.1.467)
5	387.5	16.8	467	2 S53476	acid phosphatase (EC 3.1.1.467)
6	387.5	16.8	467	2 S48996	acid phosphatase (EC 3.1.1.467)
7	382.5	16.6	467	1 PABYC	acid phosphatase (EC 3.1.1.467)
8	355.5	15.4	468	2 S52495	acid phosphatase (EC 3.1.1.467)
9	350.5	15.2	479	1 JN0715	3-phytase (EC 3.1.1.467)
10	346.5	15.0	479	1 JN0890	acid phosphatase (EC 3.1.1.467)
11	338	14.7	468	2 JC4285	acid phosphatase (EC 3.1.1.467)
12	326	14.1	453	1 A25326	acid phosphatase (EC 3.1.1.467)
13	300	13.0	463	2 S14119	acid phosphatase (EC 3.1.1.467)
14	299	13.0	463	2 T39929	thiamin-repressibl
15	149	6.5	465	2 JE0369	histidine acid pho
16	147.5	6.4	468	2 A86233	hypothetical prote
17	134	5.8	755	2 T19118	acid phosphatase h
18	130	5.6	449	2 T15933	acid phosphatase h
19	120.5	5.2	423	2 A33395	acid phosphatase (
20	119	5.2	380	2 T15883	acid phosphatase (
21	112.5	4.9	421	2 S14742	acid phosphatase (
22	107.5	4.7	602	2 A36715	hypothetical prote
23	106.5	4.6	730	2 T16455	acid phosphatase (
24	105.5	4.6	423	1 S06167	exo-poly-alpha-gal
25	105	4.6	354	2 T21241	hypothetical prote
26	103.5	4.5	381	2 JH0152	acid phosphatase (
27	100.5	4.4	693	1 S61067	homoaconitate hydr
28	100.5	4.4	1225	2 T16346	hypothetical prote
29	100	4.3	438	2 S64682	acid phosphatase (

ALIGNMENTS

RESULT 1

JN0889
3-phytase (EC 3.1.1.3.8) A precursor - Aspergillus awamori
N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein
C:Species: Aspergillus awamori
C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999
C:Accession: JN0889
R:Pidlington, C.S.; Houston, C.S.; Palohelmo, M.; Cantrell, M.; Miettinen-Oinonen, A.
Gene 133, 55-62, 1993
A:Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-op
A:Reference number: JN0889; M01D:94040796
A:Accession: JN0889
A:Molecule type: DNA
A:Residues: 1-467 <PID>
A:Cross-references: GB:L02421; NID:q166518; PIDN:AAAL6898.1; PID:q166519
A:Experimental source: strain ALK0243
A:Note: part of the sequence, including the amino end of the mature protein, was conf
C:Comment: This enzyme catalyzes the conversion of phytate to inositol and inorganic
C:Genetics:
A:Gene: phyA
A:Introns: 15/2
C:Superfamily: yeast acid phosphatase
C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-467/Product: 3-phytase A #status experimental <MAT>
F:27,59,105,120,207,330,332,376,388/Binding site: carbohydrate (Asn) (covalent) #
F:81,361/Active site: Arg, His #status predicted
F:82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 75.6%; Score 1745; DB 1; Length 467;
Best Local Similarity 74.4%; Pred. No. 4.8e-133;
Matches 326; Conservative 43; Mismatches 69; Indels 0; Gaps 0;
QY 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTGGVQCPEIHLWGQSPFFSLADE 60
DB 1 MGVSALLPLVLLAGVTSGLAVPASRQSTCDTVDQGCFCSETSHLWGQYAPFFSLANE 60
QY 61 SAISPDVPGKCRVTFVQVLSRHGARYPTSSKKYSALIEAIOKNATAFKGKVAFLKTYN 120
DB 61 SAISPDVPGKCRVTFVQVLSRHGARYPTESKGGKYSALIEIQNVTFDGYAFLKTYN 120
QY 121 YTLGADDLTPFGEOQWNSGKIFRYRYKALARKIVPFVRASGSDRVTAASEKFTIEGQSA 180
DB 121 YSLGADDLTPFGELVNSGKIFRYRYKALARKIVPFVRASGSDRVTAASEKFTIEGQSA 180
QY 181 KLADPGANPHQASPVINVIPEAGYNNLTDLHGLCTAFEESELGDDVDVEANFTAFVAPPIR 240
DB 181 KLKDPRAQPGQSSPKIDWVISEASSNNLTDPGCTCTVFDESELADIVAEANFTAFVAPPIR 240
QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPFDVTARTSDATQLSPFCDLFTHDEWIOYDYLQSLG 300
DB 241 ARLEAHLPGVNLTDDEVVNLMDMCPFDVTARTSDATQLSPFCDLFTHDEWIOYDYLQSLG 300

Db 241 ORLENDLSGVTLTDEVTYLMDCSFDTISTSTVDTKLSPPCDLTFHDEWTHYDLSLQ 300

QY 301 KYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFS 360

Db 301 KYGAGNPLGPTGCGYANELIARLTHSPVHDDTSSNHTLDSNPATFPPLNATLYADFS 360

QY 361 HDNTWVSIFPAGLNGTKPLSTTSVESIETDGYAASWTVPFAARAYVEMMQCAEKEP 420

Db 361 HDNGIISILFALGNGTKPLSTTTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEP 420

QY 421 LVRVLNDRVPLHGGCV 438

Db 421 LVRVLNDRVPLHGGCV 438

RESULT 2

JN0656

3-phytase (EC 3.1.3.8) A precursor - Aspergillus niger

N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyaA protein

C:Species: Aspergillus niger

C:Date: 03-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999

A:Accession: JN0656; S28456

R:van Hartingsveldt, W.; van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk, M. A.M.J.

Gene 127, 87-94, 1993

A:Title: Cloning, characterization and overexpression of the phytase-encoding gene (phyA)

A:Reference number: JN0656; MUID:93252284

A:Accession: JN0656

A:Molecule type: DNA

A:Residues: 1-467 <VAN>

A:Cross-references: GB:216414; NID:92392; PIDN:CAA78904.1; PID:g2393

A:Experimental source: strain NRRL1315

A:Note: Parts of the sequence, including the amino end of the mature protein, were confirmed

C:Comment: This enzyme catalyzes the hydrolysis of phytic acid into myo-inositol and inositol

C:Genetics:

A:Gene: phya

A:Introns: 15/2

C:Superfamily: yeast acid phosphatase

C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phospho

F:1-2/Domain: signal sequence #status predicted <SIG>

F:24-467/Product: 3-phytase A #status experimental <MAT>

F:27,59,105,120,207,339,352,376,388/Binding site: carbohydrate (Asn) (covalent) #sta

F:81,361/Active site: Arg, His #status predicted

F:82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 75.1%; Score 1733; DB 1; Length 467;

Best Local Similarity 74.2%; Pred. No. 4.4e-132;

Matches 325; Conservative 43; Mismatches 70; Indels 0; Gaps 0;

QY 1 MGVPVLLSTATLFGSTSGTALGPRGNHSCDVTVDGGYQCFPEISHLWGQYSPFFSLADE 60

Db 1 MGVSALLPYLLSGVTSGLAVPASRNQSCDVTVDGGYQCFSETSHLWGQYAPFFSLANE 60

QY 61 SAISPDVPGKCRVTFVOVLSRHGARYPTSSKSKYKYSALTEAIOKNATAPKGYAFKLTYN 120

Db 61 SVISPEVAGCRVTFEAVLSRHGARYPTSSKSKYKYSALTEAIOKNATAPKGYAFKLTYN 120

QY 121 YTLGADDLTPFGEOQWNSGKIFKRYRKALARKIIVPEVRASGDRVIASAEKIEGFQSA 180

Db 121 YSLGADDLTPFGEOQWNSGKIFKRYRKALARKIIVPEVRASGDRVIASAEKIEGFQSA 180

QY 181 KLADPGANPHQASPVINVIIEGAGYNNLTDLGLCTAFEESELGDDVEANFTAVFAPPT 240

Db 181 KLADPGANPHQASPVINVIIEGAGYNNLTDLGLCTAFEESELGDDVEANFTAVFAPPT 240

QY 241 ARLEAHLPGVNLTDVNLMDCPDFTVARTSDATLSPCDLTFHDEWTHYDLSLQ 300

Db 241 ORLENDLSGVTLTDEVTYLMDCSFDTISTSTVDTKLSPPCDLTFHDEWTHYDLSLQ 300

QY 301 KYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFS 360

Db 301 KYGAGNPLGPTGCGYANELIARLTHSPVHDDTSSNHTLDSNPATFPPLNATLYADFS 360

QY 361 HDNTWVSIFPAGLNGTKPLSTTSVESIETDGYAASWTVPFAARAYVEMMQCAEKEP 420

Db 361 HDNGIISILFALGNGTKPLSTTTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEP 420

QY 421 LVRVLNDRVPLHGGCV 438

Db 421 LVRVLNDRVPLHGGCV 438

RESULT 3

JN0482

3-phytase (EC 3.1.3.8) A - Aspergillus ficum

N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyaA protein

C:Species: Aspergillus ficum

C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 07-May-1999

A:Accession: JN0482; PN0023

R:Ullah, A.H.J.; Dischinger Jr., H.C.

C:Biochem. Biophys. Res. Commun. 192, 747-753, 1993

A:Title: Aspergillus ficum phytase: Complete primary structure elucidation by chemi

A:Reference number: JN0482; MUID:93249451

A:Accession: JN0482

A:Molecule type: protein

A:Residues: 1-441 <ULL>

A:Note: authors state that the 9 Asn followed by Thr or Ser after an intervening resi

R:Ullah, A.H.J.; Cummins, B.J.; Dischinger Jr., H.C.

C:Biochem. Biophys. Res. Commun. 178, 45-53, 1991

A:Title: Cyclohexanedione modification of arginine at the active site of Aspergillus

A:Reference number: PN0023; MUID:91298982

A:Accession: PN0023

A:Molecule type: protein

A:Residues: 48-70 <ULL>

C:Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phyt

C:Superfamily: yeast acid phosphatase

C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph

F:4,36,82,97,184,207,316,329,353,365/Binding site: carbohydrate (Asn) (covalent) #sta

F:58,338/Active site: Arg, His #status predicted

F:59/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 73.3%; Score 1691; DB 1; Length 441;

Best Local Similarity 76.0%; Pred. No. 1e-128;

Matches 313; Conservative 41; Mismatches 58; Indels 0; Gaps 0;

QY 27 NSHSCDVTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPGKCRVTFVOVLSRHGARY 86

Db 4 NQSSCDVTVDGGYQCFSETSHLWGQYAPFFSLANESVISPVEPAGCRVTFEAVLSRHGARY 63

QY 87 PTSSKSKYSALTEAIOKNATAPKGYAFKLTYNITLGGADLTPFGEOQWNSGKIFKRYR 146

Db 64 PTSSKSKYSALTEAIOKNATAPKGYAFKLTYNITLGGADLTPFGEOQWNSGKIFKRYR 123

QY 147 YKALARKIIVPEVRASGDRVIASAEKIEGFQSAKLADPGANPHQASPVINVIIEGAGY 206

Db 124 YESLTRNIVPEIRSSGSRVIVASGKIEGFQSTKLADPGANPHQASPVINVIIEGAGY 183

QY 207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPIRARLEAHLPGVNLTDVNLMDMCP 266

Db 184 NNTLDHGLCTAFEESELGDDVEANFTAVFAPIRARLEAHLPGVNLTDVNLMDMCP 243

QY 267 DVARTSDATLSPCDLTFHDEWTHYDLSLQKYYGAGNPLGPAQGVFNELIAR 326

Db 244 DRISTSTVDTKLSPPCDLTFHDEWTHYDLSLQKYYGAGNPLGPAQGVFNELIAR 303

QY 327 LTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSHDNTWVSIFPAGLNGTKPLSTTSV 386

Db 304 LTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFSHDNTWVSIFPAGLNGTKPLSTTSV 363

QY 387 ESIEETDGYAASWTVPFAARAYVEMMQCAEKEPLRVVLNDRVPLHGGCV 438

Db 364 ENITQDGFSSAWTVPFASRLYVEMMQCAEQEPPLRVVLNDRVPLHGGCV 415

A:Accession: S59659
A:Molecule type: DNA
A:Residues: 1-16, 'L', 18-81, 'AR', 84-149, 'H', 151-467 <XUL>
A:Cross-references: EMBL:U19789; NID:g847754; PIDN:AAA73479.1; PID:g847755
C:Genetics:
A:Gene: SGD:PHO12
A:Cross-references: SGD:S0001258; MIPS:YHR215W
A:Map position: 8R
C:Superfamily: yeast acid phosphatase
C:Keywords: phosphoric monoester hydrolase

Query Match 16.8%; Score 387.5; DB 2; Length 467;
Best Local Similarity 26.4%; Pred. No. 1.9e-23;
Matches 115; Conservative 60; Mismatches 191; Indels 69; Gaps

QY 24 PRGNSHSODTVDDGQYQCQFPEISHLWGOYSPFFSLADESAISDPVPGKCRVTFVOVLSRHG 83
DB 21 PLGKLSDDIKTGTOFEIPEFL---GGSGPYISFFDCYGISRDLPESCEMKQVMQVGRHG 76
QY 84 ARYPTSSKSKYKSLIEAIOKNATPAKGYAFLK-----TYNTL-----GADDL 128
DB 77 ERYPTVSKAKSMTTWYKLSNYTGQFSGALSLINDDYEFFIRDTKNUEMETLANSVNVL 136
QY 129 TPF-GEQMVNSGKFKFRRYKALARKIVPF-VRASGDRVITASAEKFTGFSQSAKLADPG 186
DB 137 NPYTGEMAKHARDFLAQGYGVVENQTSFAVTSNSNRCHDTAQYFIDG-----LGDK- 190
QY 187 ANPHQASPVINII-----PEGAGYNNITDLHGLCTAPESLEGDDVEANFTAVFAPPIRA 241
DB 191 -----FNLSQTISEASAGANTLSAHHSCPAWDD-DYNDILKKYDTKYLSGIAK 2404
QY 242 RLEAHLPGVNLITDEDVNLMDMCPDFIVARTSDATQLSPFCDLFTHDSEWIOYDLSLGG 301
DB 241 RLNKENGLNLTSSDANTFFAWCAYELNAR----CYSIDICNIFTKDELVFRESYGQDLET 295
QY 302 YXGYGAGNPLGPAQGVGVNELIARLTHSPVDQHTSTNTLSDNPATPLNATLIYADFSH 361
DB 296 YYQTGPGYDVRSVGCANLFNASVKLLKESEVQDQ-----KVNLSFTH 337
QY 362 DNTWYSIFALGLYNGTKPLSTTSVESIEETDCYAAASWTVPFAARAYVEMMQCEAKEPL 421
DB 338 DTDILNLYLTGIDDDQNLLTAELVPPNENT--FHRSWYVPOGARVYITEKFQC--SNDTY 393
QY 422 VRVLNDRVYPLHGC 436
DB 394 VRYVINDAVVPIETC 408

RESULT 7
PABYCC
N:acid phosphatase (EC 3.1.3.2) precursor, constitutive - yeast (Saccharomyces cerevisiae)
A:Alternate names: acid phosphatase PHO3; protein YBR0813; protein YBR0922
C:Species: Saccharomyces cerevisiae
C:Date: 30-Sep-1991 #sequence.revision 09-Sep-1994 #text_change 05-Nov-1994
C:Accession: S48259; S45960; S05794; A25241; S44674
R:Mannhaupt, G.; Stucka, R.; Ehnlé, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A:Title: Analysis of a 70 kb region on the right arm of yeast chromosome 1
A:Reference number: S48255; MUID:95208357
A:Accession: S48259
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-467 <MAN>
A:Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g4760505
R:Feldmann, H.; Mannhaupt, G.; Schwarzlöse, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45927
A:Accession: S45960
A:Molecule type: DNA
A:Residues: 1-467 <FEZ>
A:Cross-references: EMBL:Z35961; NID:g536362; PIDN:CAA85045.1; PID:g536363

R;Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A:Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A:Reference number: S05794; MUID:85037940
A:Accession: S05794
A:Molecule type: DNA
A:Residues: 1-218, 'MKT', 222-467 <BAJ1>
A:Cross-references: EMBL:X01080; NID:g4148; PIDN:CAA25557.1; PID:g759281
A:Note: the authors translated the codon AAT for residue 134 as Asp and TAC for residue
R;Tait-Kanrad, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, C
Mol. Cell. Biol. 6, 1855-1865, 1986
A:Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within
A:Reference number: A93074; MUID:87064474
A:Accession: A25241
A:Molecule type: DNA
A:Residues: 1-44 <TAI>
C:Genetics:
A:Gene: SGD:PHO3; MIPS:YBR092c
A:Cross-references: SGD:S0000296; MIPS:YBR092c
A:Map position: 2R
C:Superfamily: yeast acid phosphatase
C:Keywords: glycoprotein; phosphatidine; phosphoprotein; phosphoric monoester hydrolase
F:1-17/Domain: signal sequence #status predicted <Sig>
F:18-467/Product: acid phosphatase, constitutive #status predicted <MAT>
F:75/Active site: His (phosphatidine intermediate) #status predicted
F:97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (coval
F:337/Active site: His #status predicted

Query Match 16.6%; Score 382.5; DB 1; Length 467;
Best Local Similarity 27.3%; Pred. No. 4.9e-23;
Matches 111; Conservative 59; Mismatches 179; Indels 57; Gaps 12;

QY 49 GQVSPFSLADESAISPDVPKGRVTFVQVLSRHGARYPTSSKSKYSALIEAIQKNATA 108
Db 42 GGAGPYFSPGDIYGRDLPCECKQLQMLARHGERYPTSKGATIMKTWYKLSNYTRQ 101
QY 109 FKGYAFLEK-TYNYTLGAD-----LTPF-GEQQMVNSGIGKPYRRYKALAR 152
Db 102 FNGSLFLNDDYEFFTRDDDDLEMETTFANSDNVNLPYTGEMDKARHAREFLAQGYWFE 161
QY 153 KIVPF-VRASGSDRVASAEKIEFGQSAKLADPGANPHQASPVINVIPEGAGYNNITLD 211
Db 162 NOTSPFIFAASERVHDTHAQYFDGL-----GDQFNISLQTVSEAMSAGA---NTLS 210
QY 212 HG-LCTAFESLGDVDEANTAVFAPPFIRARLEAHLPGVNLTDGVNLMQCPFDVA 270
Db 211 AGNACPGWDE-DANDDILDKYDTTLLDIAKLNKENGLNLSKDANTLFAWCAYELNA 269
QY 271 RTSATQLSPFCDLTHDEWIQDYQLSLGKYGYGAGNPLGPAQGVGVNLIARLTHS 330
Db 270 R-----GYSDVCDITFEDLVRSYGDVLSFYQDPCGYDMRSVGANLEFNATLKLKQS 324
QY 331 PVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTWVSTFFALGLYNGTKPLSTTSVESIE 390
Db 325 ETQD-----LKVMSLFTHTDILTTAGTIDDKNNLTAEYVPMFG 366
QY 391 ETDGYAASWTVPFAARAYVEMMQCAEKEPLRVLVNDRVYVPLHG 436
Db 367 NT--PHKSWYVPOGARVYTEKFC--SNDTYRVVINDAVVPIETC 408

RESULT 8
S52495
acid phosphatase homolog YDL024c - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D2815
C:Species: Saccharomyces cerevisiae
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C:Accession: S52495; S67556
R:Andre, B.; Vissers, S.; Urrestarazu, L.
submitted to the EMBL Data Library, February 1995
A:Reference number: The sequence of a 42 kb segment located on the left arm of chromosome IV
A:Residues: 20-101;133-146;376-399 <H2>

A:Accession: S52495
A:Molecule type: DNA
A:Residues: 1-468 <AND>
A:Cross-references: EMBL:Z48432; NID:g683669; PIDN:CAA88335.1; PID:g683673
A:Experimental source: strain S288C
R:Urrestarazu, L.A.; Andre, B.; Vissers, S.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67535
A:Accession: S67556
A:Molecule type: DNA
A:Residues: 1-468 <URR>
A:Cross-references: EMBL:Z74072; NID:g1430996; PIDN:CAA90583.1; PID:g1430997; MIPS:YD
A:Experimental source: strain S288C
C:Genetics:
A:Map position: 4L
C:Superfamily: yeast acid phosphatase

Query Match 15.4%; Score 355.5; DB 2; Length 468;
Best Local Similarity 25.4%; Pred. No. 7.5e-21;
Matches 108; Conservative 58; Mismatches 163; Indels 97; Gaps 12;

QY 49 GQVSPFSLADESAISPDVPKGRVTFVQVLSRHGARYPTSSKSKYSALIEAIQKNATA 108
Db 43 GGSAPYFSPGANYGIPTDIPGECRLTQVMIGRGERYPTRSEAKDIFVWYKISNYTGK 102
QY 109 FKGYAFLEK-TYNYTL-----GADDLTPF-GEQQMVNSGIGKPYRRYKALAR 152
Db 103 YEGSLSEFLNNGYEFFIPDESLEMETTLQNSIDVLPYTGEMNAKRHAREFLAKYKGLME 162
QY 153 KIVPF-VRASGSDRVASAEKIEFGQSAKLADPGANPHQASPVINVIPEGAGYNNITLD 211
Db 163 NCTNPFITFTNSKRIYTAQYFAEL-----GDGFNLSLQ 197
QY 212 HGLCTAFESLELG-----DDVEANTAVFAPPFIRARLEAHLPGVNL 253
Db 198 ----TLSENSSGANTLAAKSSCPNNSNANDILMSYSDYLENIDRLNDENKGNLS 253
QY 254 DEDVNLMDQCPDPTVARTSDATQLSPFCDLTHDEWIQDYQLSLGKYGYGAGNPLGP 313
Db 254 RKDAALFSCAFEL-----NAKYSNICIDIFSAAELIHSYETDLTSTFYQNGPGYKLIK 308
QY 314 AOGVGFVN---ELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTWVSIFF 370
Db 309 SIGANLENAIVKLIRQSAH-----LDQKVLSTFHTDILNLT 347
QY 371 ALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCAEKEPLRVLVNDRV 430
Db 348 TAGLIDTTRNLTTNHHVPRDHS--YHRSWIPOGARVYTEKFC--SNDSYVYVYVNDV 403
QY 431 VPLHG 436
Db 404 VPESC 409

RESULT 9
JN0715
3-phytase (EC 3.1.3.8) B precursor - Aspergillus ficum
N:Alternate names: pH 2.5-optimum acid phosphatase
C:Species: Aspergillus ficum
C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
C:Accession: JN0715; PNO594; PNO460
R:Ehrlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J
Biochem. Biophys. Res. Commun. 195, 53-57, 1993
A:Title: Identification and cloning of a second phytase gene (phyb) from Aspergillus
A:Reference number: JN0715; MUID:93371452
A:Accession: JN0715
A:Molecule type: DNA
A:Residues: 1-479 <EHR>
A:Cross-references: GB:I20567
A:Accession: PNO594
A:Molecule type: protein
A:Residues: 20-101;133-146;376-399 <H2>

R:Ullah, A.H.J.; Dischinger Jr., H.C.
 Biochem. Biophys. Res. Commun. 192, 754-759, 1993
 A:Title: Identification of active-site residues in *Aspergillus ficuum* extracellular pH 2
 A:Reference number: PNO460; MUID:93249452

A:Accession: PNO460
 A:Molecule type: protein
 A:Residues: 65-66,68-93 <ULL>

C:Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.3.2), hy
 C:Genetics:

A:Gene: phb
 A:Introns: 261/1; 300/2; 335/2

C:Superfamily: yeast acid phosphatase
 C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
 F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-479/Product: 3-phytase #status experimental <MAT>
 F:81.337/Active site: Arg, His #status predicted
 F:82/Active site: His (phosphohistidine intermediate) #status predicted

F:106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match 15.2%; Score 350.5; DB 1; Length 479;
 Best Local Similarity 27.9%; Pred. No. 2e-20;
 Matches 117; Conservative 53; Mismatches 159; Indels 91; Gaps 16;

QY 49 GOYSPFSLADESAISPDVPGKCRVTFQVLSRHGARYPTSSKSKY-SALIEAIQKNAT 107
 DB 53 GPYSERVSY-----GIARDPPTCEVDQVIMVKRGERYSPSAGKSIEEALAKVYSINTT 108

QY 108 AFKGYAFKTYNYTL-----GADDLT-PF-GEQMVNSGKIFRYRYKAL--ARKIVPF 157
 DB 109 EYKGLAFLNDWTYYVNPCEYNAETTSQYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168

QY 158 VRASGSDRVIASAEKFIQFQSAKLADPGANPHQASPVINVIPEGAGYNNTLDHGLCTA 217
 DB 169 F-SSGGRVETARKFGEF-----FGYNSTNAALNII 201

QY 218 FESELG-----DDVEANFTAVFAPPRI--ARLEAHLPGVNLTDDEVNLM 262
 DB 202 SESEVMGADSLTPTCDTNDQTTCDNLTYQLPQFKVAARLNQNPGLMTASDVYLMV 261

QY 263 MCPDFTVARTSQTLSPPCDLFTHEWTOYDYLQSLGKYGYGAGNPLGPAQGVGFVNE 322
 DB 262 MASFELNAR-----PFSNWINAFTQDEWSFGYVEDLNYYICAGPGDKNMAAVGAYANA 316

QY 323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFFAIGLY--NGTKP 380
 DB 317 SLTLLNQGP-----KEAGP-----LFFNLADHTNITPILALGVLIIPNEDLP 358

QY 381 LSTSVESIEETDGYAASWTVPFAARAYVEMMOCEA-----EKEPLVRVLNDRVVPVPHGC 436
 DB 359 L-----DRVAFGNPYSIGNIVPMGGHLLTIERLSQATALSDEGTYYRLVNEAVLPFNDC 413

RESULT 10
 JN0890
 acid phosphatase (EC 3.1.3.2) precursor - *Aspergillus awamori*
 C:Species: *Aspergillus awamori*
 C:Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999

C:Accession: JN0890
 R:Pidington, C.S.; Houston, C.S.; Palohelmo, M.; Cantrell, M.; Miettinen-Oinonen, A.; N
 Gene 133, 55-62, 1993
 A:Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-opti
 A:Reference number: JN0889; MUID:94040796

A:Accession: JN0890
 A:Molecule type: DNA
 A:Residues: 1-479 <PID>

A:Cross-references: GB:I02420; NID:q166481; PIDN:AAAL6897.1; PID:q166482
 A:Experimental source: strain ALK0243

C:Comment: The highly similar enzyme from *A. ficuum* has been shown to have 3-phytase (EC
 C:Genetics:

A:Gene: aph
 A:Introns: 261/1; 300/2; 335/2
 C:Superfamily: yeast acid phosphatase

C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-479/Product: 3-phytase #status predicted <MAT>
 F:81.337/Active site: Arg, His #status predicted
 F:82/Active site: His (phosphohistidine intermediate) #status predicted
 F:106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 15.0%; Score 346.5; DB 1; Length 479;
 Best Local Similarity 27.4%; Pred. No. 4.1e-20;
 Matches 115; Conservative 54; Mismatches 160; Indels 91; Gaps 15;

QY 49 GOYSPFSLADESAISPDVPGKCRVTFQVLSRHGARYPTSSKSKY-SALIEAIQKNAT 107
 DB 53 GPYSERVSY-----GIARDPPTCEVDQVIMVKRGERYSPSAGKDIEEALAKVYSINTT 108

QY 108 AFKGYAFKTYNYTL-----GADDLT-PF-GEQMVNSGKIFRYRYKAL--ARKIVPF 157
 DB 109 EYKGLAFLNDWTYYVNPCEYNAETTSQYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168

QY 158 VRASGSDRVIASAEKFIQFQSAKLADPGANPHQASPVINVIPEGAGYNNTLDHGLCTA 217
 DB 169 F-SSGGRVETARKFGEF-----FGYNSTNAALNII 201

QY 218 FESELG-----DDVEANFTAVFAPPRI--ARLEAHLPGVNLTDDEVNLM 262
 DB 202 SESEVMGADSLTPTCDTNDQTTCDNLTYQLPQFKVAARLNQNPGLMTASDVYLMV 261

QY 263 MCPDFTVARTSQTLSPPCDLFTHEWTOYDYLQSLGKYGYGAGNPLGPAQGVGFVNE 322
 DB 262 MASFELNAR-----PFSNWINAFTQDEWSFGYVEDLNYYICAGPGDKNMAAVGAYANA 316

QY 323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFFAIGLY--NGTKP 380
 DB 317 SLTLLNQGP-----AGSLFFENFAHDTNITPILALGVLIIPNEDLP 358

QY 381 LSTSVESIEETDGYAASWTVPFAARAYVEMMOCEA-----EKEPLVRVLNDRVVPVPHGC 436
 DB 359 L-----DRVAFGNPYSIGNIVPMGGHLLTIERLSQATALSDEGTYYRLVNEAVLPFNDC 413

RESULT 11

JC4285
 acid phosphatase (EC 3.1.3.2) precursor - yeast (*Pichia pastoris*)
 N:Alternate names: orthophosphoric monoester phosphohydrolase (acid optimum); Pho
 C:Species: *Pichia pastoris*

C:Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 29-Oct-1999
 C:Accession: JC4285

R:Payne, W.E.; Gannon, P.M.; Kaiser, C.A.
 Gene 163, 19-26, 1995
 A:Title: An inducible acid phosphatase from the yeast *Pichia pastoris*: Characterizati
 A:Reference number: JC4285; MUID:96001238

A:Accession: JC4285
 A:Molecule type: DNA
 A:Residues: 1-468 <PAY>

A:Cross-references: GB:U28658; NID:g881955; PIDN:AAA85503.1; PID:g881956
 A:Experimental source: GS115

C:Genetics:
 A:Gene: pho1
 C:Superfamily: yeast acid phosphatase
 C:Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydr
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-468/Product: acid phosphatase #status predicted <MAT>
 F:84/Active site: His (phosphohistidine intermediate) #status predicted
 F:163,196,256,321,360,453/Binding site: carbohydrate (Asn) (covalent) #status predict
 F:345/Active site: His #status predicted

Query Match 14.7%; Score 338; DB 2; Length 468;
 Best Local Similarity 25.8%; Pred. No. 1.9e-19;
 Matches 120; Conservative 75; Mismatches 180; Indels 90; Gaps 21;

QY 6 VLLSLATL---FGTSGTALPGRGNHSCDVTGGYQCFPEISHLWQGYSPF--FSLADE 60

Db 10 IILALATLQSFVAVELQHLVGVNDRIYPPORT--DQTNILRHUGGL-GPYIGYNGWGIAAE 67
QY 61 SAISPDVPKCRVTFVQVLSRAGRYPTSSKSKYKYSALIE-AIQKNATAFKGKYAFKTY 119
Db 68 SEI-----ESCITDQAHLLMRHGERYPSTNVGKQLEALYQKLLDADVEVPTGPLESFQDY 122
QY 120 NYTLG-----ADDLTPGEGQOMWNSGKIF-----YRRYKAL-----ARKTVFVFRASGSDR 165
Db 123 DYFVSDAAWYEQTTFKGYSLGNTAFDFGTTLRERYDHLINTSEEGKL--SVWAGSQER 180
QY 166 VIASAEKFIKGFOSAKLADPGANPHQASPVINVIPE--GAGYNTLDHGLCT-----A 217
Db 181 VDTAKYAGGFMKSNYTD-----WVEVVALEEKSOGLNSLTARISCPNYSNH 230
QY 218 FESEELGDDV---EAFNTAVFAPPPIRARLEAHLPGVNLNMDMCPEDTARTSD 274
Db 231 YKGDGFPNDIAEAD-----RNTLSPGPNITADDIPTIALYCGFELNVURGE- 278
QY 275 ATQLSPFCDLTHDEMIQDYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVOD 334
Db 279 -----SSFCVDLSREALLYTAYLRDLGWYNGVNGNPLGKTIGYVYAN----- 321
QY 335 HTSTNHTLDSNPATPLNATLVADPSHDNTMYSIFPAGLGLXNGTK-PLSTTSVESIEETD 393
Db 322 --ATROLLENTEAD-PRDYPLPFSFSDHDTDLQVFTSLGLENVTDLPL-----DOIQFQT 373
QY 394 GYAASWTVPFAARAYVEMMQC--EAEKPLRVLRVNDVRVPLHGC 436
Db 374 SFKSTETVPMGARLLTERLLCTVEGEKYYVTRILNDVAVPLSDC 418

RESULT 12

A25326
acid phosphatase (EC 3.1.1.3.2) precursor [similarity] - fission yeast (Schizosaccharomyces
C:Species: Schizosaccharomyces pombe
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: A25326; T50405
R:Elliot, S.; Chang, C.; Schweingruber, M.E.; Schaller, J.; Rickli, E.E.; Carbon, J.
J. Biol. Chem. 261, 2936-2941, 1986
A:Title: Isolation and characterization of the structural gene for secreted acid phosphatase
A:Reference number: A25326; MUID: 86140050
A:Accession: A25326
A:Molecule type: DNA
A:Residues: 1-453 <ELL>
A:Cross-references: GB:M11857; NID:g173422; PIDN:AAA35321.1; PID:g173423
R:Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrrell, B.G.
submitted to the EMBL Data Library, January 2000
A:Reference number: Z25068
A:Accession: T50405
A:Molecule type: DNA
A:Residues: 1-453 <RIE>
A:Cross-references: EMBL:AL137099; PIDN:CAB68657.1; GSPDB:GN00067; SPDB:SPBP4G3.02
A:Experimental source: strain 972h(-); clone p1 p4G3

C:Genetics:
A:Gene: pho1; SPDB:SPBP4G3.02
A:Map position: 2
C:Superfamily: yeast acid phosphatase
C:Keywords: phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F:68/Active site: Arg #status predicted
F:69/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 14.1%; Score 326; DB 1; Length 453;
Best Local Similarity 24.8%; Pred. No. 1.7e-18;
Matches 103; Conservative 63; Mismatches 201; Indels 48; Gaps 8;
QY 35 DGGYQCFPEISHLWQYSPFFSLADESAISPDVPGCRVTFVQVLSRAGRYPTSSSKSKK 94
Db 27 DKGDFDFKEHLTSKSPYHXPYF-----YGPSIDFPTTCKIKQVHTLQHGSRNPTGGNAAF 81
QY 95 YSALTEATQK-----NATAFKGKYAFKTYNTYL---GADDLTPFGGQOMWNSGK 142

Db 82 DAVGIANFOORLLGVSVPIDYSVSGNPLSFVPTWTPVTEAANADALSSSGRVLEFDMGRQ 141
QY 143 FYRRYKALARKIVPVRASGSDRVIAASAEKFTIEGFSQAKLADPGANPHQASPVINVIPE 202
Db 142 FYERHELFINASTNIYTAQQRVVDVSALWYGYGMF-----GEDVHNFTNYILVSENA 194
QY 203 GAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPPIRARLEAHLPGVNLNMDMCPEDV 262
Db 195 TAGSNLSYSSNACPASDADDTTPALEARNVYMPPIRQLRNPYFSVNLNNDILNLYG 254
QY 263 MCPEDTARTSDATQLSPFCDLTHDEMIQDYDYLQSLGKYYGYGAGNPLGPAQGVGFVNE 322
Db 255 ICSYELAQ-----DYSEFCKLNFSDVDFNFEYEGDLSFSYGMGNSVKWGSIFGCAVANS 309
QY 323 LIARLTHSPVODHTSTNHTLDSNPATPLNATLVADPSHDNTMYSIFPAGLGLXNGTKPLS 382
Db 310 LANSL--RSVENNTQ-----OVFFAETHDANIIPVETALGFFTDNTPEN 351
QY 383 TTSVESIEETDGYAASWTVPFAARAYVEMMQEAEKPLRVLRVNDVRVPLHGC 437
Db 352 PLPTSYQVHSHSMKASEFVFPFAGNLITELFOCEDSKY-YVRHLVNEEVFPPLSDCG 405
RESULT 13
S14119
acid phosphatase (EC 3.1.1.3.2) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 10-Dec-1999
C:Accession: S14119; T40455
R:Yang, J.; Schweingruber, M.E.
Curr. Genet. 18, 269-272, 1990
A:Title: The structural gene coding for thiamin-repressible acid phosphatase in Schiz
A:Reference number: S14119; MUID: 91064763
A:Accession: S14119
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-463 <YAN>
A:Cross-references: GB:X56939; NID:g5006; PIDN:CAA40258.1; PID:g5007
R:Lyne, M.; Rajandream, M.A.; Barrrell, B.G.; Baker, S.; Mungall, K.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z21931
A:Accession: T40455
A:Status: preliminary; translated from GB/EMBL/DDBY
A:Molecule type: DNA
A:Residues: 1-463 <LYN>
A:Cross-references: EMBL:AL034382; PIDN:CAA22278.1; GSPDB:GN00067; SPDB:SPBC428.03c
A:Experimental source: strain 972h-; cosmid c428
C:Genetics:
A:Gene: SPBC428.03c
A:Map position: 2
C:Superfamily: yeast acid phosphatase
C:Keywords: phosphoric monoester hydrolase

Query Match 13.0%; Score 300; DB 2; Length 463;
Best Local Similarity 25.4%; Pred. No. 2.2e-16;
Matches 104; Conservative 66; Mismatches 181; Indels 58; Gaps 14;

QY 51 YSPFFSLADESAISPDVPGCRVTFVQVLSRAGRYPTSS-----KSKYKYSALIE---- 100
Db 43 HEPYF-----NGPTTSPPECAIKQVHLQHGSRNPTGDDTATDVSSAQYIDIFQNKLL 97
QY 101 --ATOKNATAFKGKYAFKTYNTYL---GADDLTPGEGQOMWNSGKIFYRRYKALARKIV 155
Db 98 NGSPVNFYSYPENPLPVFKVHTVFIKAENADQLSSSGRIELFDLGRQVFRERYELEFDTDV 157
QY 156 PFVRASGSDRVIAASAEKFTIEGFSQAKLADPGANPHQASPVINVIPE--CAGYNTLDHC 213
Db 158 YDINTAQRVDSAEWFSYGM-----FGDDMQNKNF-----IVLPEDDSAGANSUAMY 208
QY 214 LCTAFEESELGDD--VEANFTA---VFAPPPIRARLEAHL-PGVNLNMDMCPEDT 268
Db 209 SCPVIEDNNIDENTEAAHTSWRNFLKPIANLKNLYFDSYGNLYTSDVRSLSYICVYEI 268

QY 269 VARTSDATQLSPFCDLTFHDEWIOYDYLQSLGKYGGAGNPLGPAQGVGVNELIARLT 328
 Db 269 ALRDN-----SDFCSLFTPSEFLNFEVDSLDYAYWGPASEWASTLGGAYVNNLANNL- 322
 QY 329 HSPVQDHTSTNHTLDSNPATPLNATLYADFSDHNTMVSIFFAALGYNGKPLSTTSVES 388
 Db 323 -----RKGVNASDRK-----VFLAFTHDSQIIPVEAALGFFPDITPEHPLPTDK 367
 QY 389 IEETDGYAASWTVPFAARAYVEMMOCEAEKEPLVRLVNDVRVPLHGC 437
 Db 368 NIITYSLKTSSTSVFPAGNLTLELFC-SDNKYYVRHLVNOQVYPLTDCG 415

RESULT 14
 T39929
 thiamin-repressible acid phosphatase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
 C:Accession: T39929
 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
 submitted to the EMBL Data Library, May 1998
 A:Reference number: Z21857
 A:Accession: T39929
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-463 <LYN>
 A:Cross-references: EMBL:AL023286; PIDN:CAA18863.1; GSPDB:GN00067; SPDB:SPBC21H7.03c
 A:Experimental source: strain 972h-; cosmid c21h7
 C:Genetics:
 A:Gene: SPDB:SPBC21H7.03c
 A:Map position: 2
 C:Superfamily: yeast acid phosphatase

Query Match 13.0%; Score 299; DB 2; Length 463;
 Best Local Similarity 24.7%; Pred. No. 2.7e-16;
 Matches 101; Conservative 68; Mismatches 182; Indels 58; Gaps 12;

QY 51 YSPFSLADESAISPDVPGCRVTFVQVLSRHRGARYPTS--SKSKYSA-----L 98
 Db 43 HEPYFDGLDSA-----FPETCIEQVHLLQHRGSRNPTGDTATDVSSQVLYNFOEKL 97
 QY 99 IEAIQKNATAFKYAFKLTNYTL---GADLTPFGQQMVNSGIRFYRYKALARKIV 155
 Db 98 NGSIPNFSYPENPLCFIKQWTPVIDAENADQLSSRGLFELDLGRQLYQRYKLFDSYV 157
 QY 156 PVRASGSDRVITASAEKTFEGFSQAKLADPGANPHQASPVINVIPEG--AGYNTLIDHG 213
 Db 158 YDINTAEQERVVESAkwFTYGLFGDKMYE-----KTNFILLISEGKAAGANSLSMYN 208
 QY 214 LCTAFEESEL---GDDVEANFTAVFAPPPIRARELAHL-PGVNLTDEVDVNLMDMCPDPT 268
 Db 209 ACPVFKDNFNHNATDAHAHWRNFIPEVYNRLAKYFDSSTYKLTINDVRSLFYICEYEI 268
 QY 269 VARTSDATQLSPFCDLTFHDEWIOYDYLQSLGKYGGAGNPLGPAQGVGVNELIARLT 328
 Db 269 AIKDH-----SDFCSIFTPEFLNFEVDSLDYAYWGPASEWASTLGGAYVNNLANNL- 322
 QY 329 HSPVQDHTSTNHTLDSNPATPLNATLYADFSDHNTMVSIFFAALGYNGKPLSTTSVES 388
 Db 323 -----RNYTNPDFDRK-----VFLAFTHDSQIIPVEAALGFFPDITPEHPLPTDK 367
 QY 389 IEETDGYAASWTVPFAARAYVEMMOCEAEKEPLVRLVNDVRVPLHGC 437
 Db 368 NIITYSLKTSSTSVFPAGNLTLELFC-SDNKYYVRHLVNOQVYPLTDCG 415

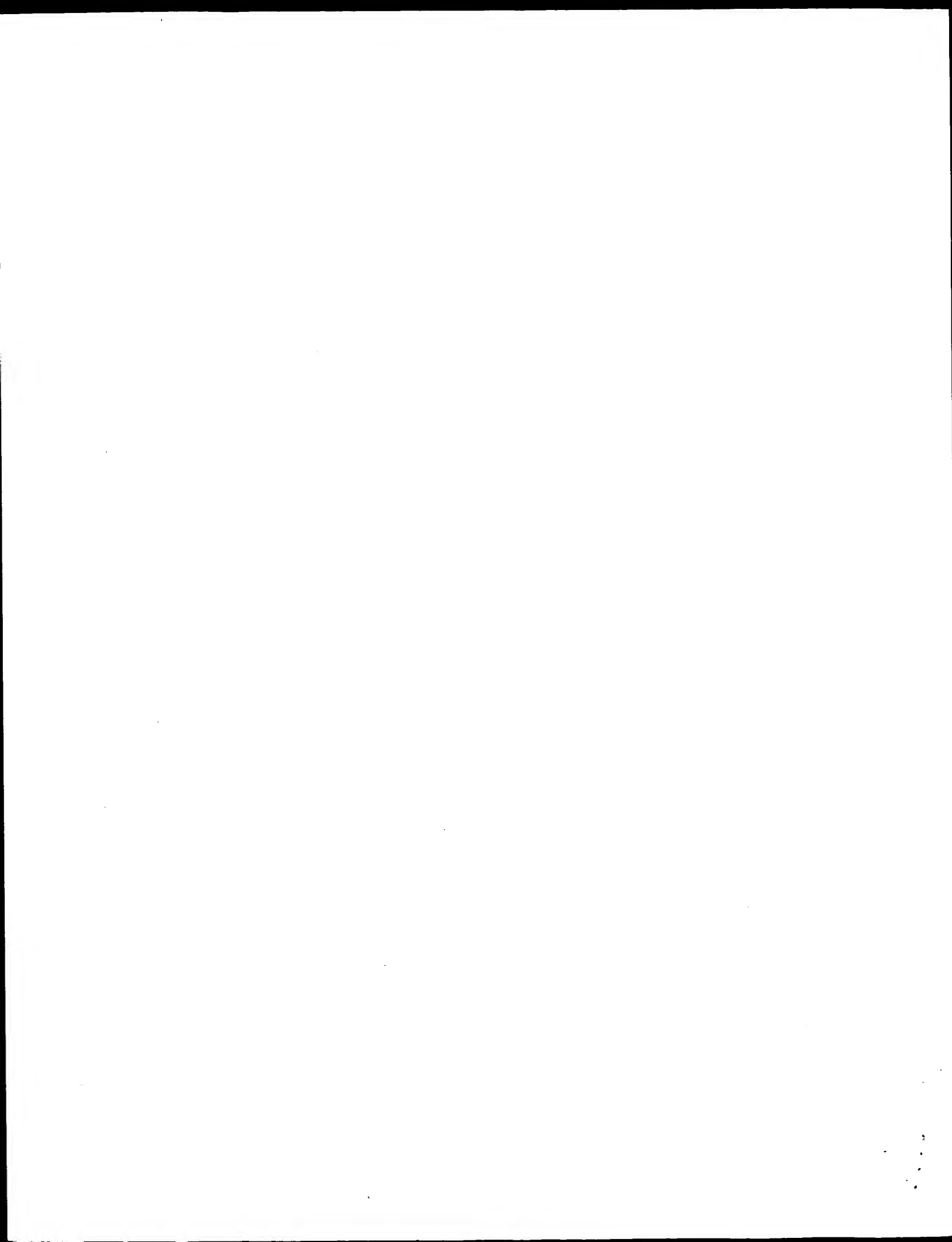
RESULT 15
 JEO369
 histidine acid phosphatase (EC 3.1.3.-) - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000

C:Accession: JEO369
 R:Mullaney, E.J.; Ullah, A.H.J.
 Biochem. Biophys. Res. Commun. 251, 252-255, 1998
 A:Title: Identification of a histidine acid phosphatase (phyA)-like gene in Arabidops
 A:Reference number: JEO369; MUID:99009256
 A:Accession: JEO369
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-465 <MUL>
 C:Superfamily: yeast acid phosphatase
 C:Keywords: phosphoric monoester hydrolase

Query Match 6.5%; Score 149; DB 2; Length 465;
 Best Local Similarity 21.9%; Pred. No. 0.00035;
 Matches 96; Conservative 64; Mismatches 194; Indels 84; Gaps 19;

QY 35 DGYGQCFPEISHLWNGOYSPFFSLADESAISPDVPGCRVTFVQVLSRHRGARYPTSCKSKK 94
 Db 16 DGGFDVRHHLSTV-TRYSTSKDVTQNLIEGSNVPSCTPIHLNLVARHGTRSPTKRLRE 74
 QY 95 YSAL---IEAIQKNATAFK-----GKYAFLKTYNTLGGADLTPFGQQMVNSGI 141
 Db 75 MESLAGRFKELVRDAEARKLPDSKIPGWLQWK--SPWEGKVGKGLIRQGEDELYQLGI 132
 QY 142 KYRYRYKALARK----IVPFVRASGSDRVIASAEKTFEGFSQAK-LADPGANPHQASPIV 196
 Db 133 RVREPFSLFEEDYHPDVTIRATQIPRASASAVAFGMGLFSEKGNLGPGRNRAFA--- 188
 QY 197 NVIIPEGAGYNTLIDHGLCTAFEESELGDDVEANFTAVFAPPPIRARELAHLPGVNLTD 256
 Db 189 --VTSENRASDTKLRFEC-----QNY-----KSYRKAKEPAVDKLEP 226
 QY 257 VVNLMDMC---PEDTVARTSDATQLSPFCDLTFHDEWIOYDYLQSLGKYGGAGNPLGP 313
 Db 227 VLNKITASVAKRYDLKFTKQDISSLWFLCKQVALLW-----TDDLEVLKGYGNSLY 281
 QY 314 AQGVGVNELIARLTISPVDHTSTNHTLDSNPATPLNATLYADFSDHNTMVSIFFA-L 372
 Db 282 KMGVPLLEDVL---HSMEEAIKAREEKLKLP--PGSYE-KARL--RFAHAETIVPPFCILL 332
 QY 373 GLYNGTKPLSTTSVEST-----ETDGYAASWTVPFAARAYVEMMOCEAEKEP 420
 Db 333 GLF-----LDGSEFEKIQKEKPLELPQPFPKTRDFRGSTMAPFGGNNILVLYSCPAESSP 387
 QY 421 --LVRLVNDVRVPLHGC 436
 Db 388 KYFQVVLNHEPIAVPGC 405

Search completed: October 16, 2001, 17:52:49
 Job time: 20208 sec



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OM protein - protein search, using sw model

Run on: October 16, 2001, 17:57:22 ; Search time 52.08 Seconds
(without alignments)
288.093 Million cell updates/sec

Title: US-09-488-265-26_COPY_1_438
Perfect score: 2307
Sequence: 1 MGVPVLLSLATLFGSTSGT.....EPLRVLVNDRVPLHGCGV 438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1745	75.6	467	1	PHYA-ASPAW
2	1733	75.1	467	1	PHYA-ASPAW
3	1689.5	73.2	463	1	PHYB-EMENI
4	391.5	17.0	467	1	PPA5-YEAST
5	387.5	16.8	467	1	PPAB-YEAST
6	387.5	16.8	467	1	PPAC-YEAST
7	382.5	16.6	467	1	PPA3-YEAST
8	355.5	15.4	468	1	PPAD-YEAST
9	352.5	15.3	479	1	PHYB-ASPAW
10	346.5	15.0	479	1	PHYB-ASPAW
11	338	14.7	468	1	PPAL-PICPA
12	334	14.5	469	1	PPA5-KLULA
13	326	14.1	453	1	PPAL-SCHPO
14	300	13.0	463	1	PPA2-SCHPO
15	134	5.8	755	1	PPAX-CAEEL
16	120.5	5.2	423	1	PPAL-RAT
17	112.5	4.9	421	1	PPAL-MOUSE
18	107.5	4.7	602	1	PEHX-ERWCH
19	105.5	4.6	423	1	PPAL-HUMAN
20	103.5	4.5	381	1	PPAP-RAT
21	100.5	4.4	693	1	LYSA-YEAST
22	98	4.2	844	1	YD25-SCHPO
23	97	4.2	1350	1	VG72-HSV1
24	95.5	4.1	386	1	PPAP-HUMAN
25	95.5	4.1	433	1	DHOM-SYNY3
26	95	4.1	721	1	NICA-CAEEL
27	95	4.1	3587	1	TYCB-BACBR
28	94.5	4.1	609	1	COPA-PSESM
29	94	4.1	1527	1	MRP3-HUMAN
30	93.5	4.1	396	1	ARSL-AQUAE
31	92	4.0	413	1	AGP-ECOLI
32	91.5	4.0	467	1	ATPX-BACFI
33	91.5	4.0	526	1	CLOS-CLOHI

RESULT 1

ID	PHYA-ASPAW	STANDARD	PRT	467 AA
AC	P34753;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE			
DE	3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE			
DE	PHOSPHOHYDROLASE A).			
DE	PHYA OR PHY.			
OS	Aspergillus awamori.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.			
OX	NCBI_TaxID=105351;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ALK0243;			
RX	MEDLINE=94040796; PubMed=8224894;			
RA	Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A.,			
RA	Miettinen-Oinonen A., Nevalainen H., Rambosek J.A.;			
RT	"The cloning and sequencing of the genes encoding phytase (phy) and			
RT	pH 2.5-optimium acid phosphatase (aph) from Aspergillus niger var.			
RL	awamori."			
CC	-!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE			
CC	FROM PHYTATE			
CC	-!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =			
CC	D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.			
CC	-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
EMBL	L02421; AAA16898.1; ..			
PIR	JN0889; JN0889.			
HSSP	P34752; LIHP.			
DR	InterPro: IPR000560; ..			
DR	Pfam: PF00328; acid_phosphat; 1.			
DR	PROSITE: PS00761; HIS_ACID_PHOSPHAT_1; 1.			
DR	PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.			
KW	Hydrolase; Glycoprotein; Signal.			
FT	SIGNAL 1 23			
FT	CHAIN 1 23			
FT	ACT_SITE 24 467			
FT	ACT_SITE 82 82			
FT	ACT_SITE 361 361			
FT	DISULFID 31 40			
FT	DISULFID 71 414			
FT	DISULFID 215 465			
FT	DISULFID 264 282			
FT	DISULFID 436 444			

Q09451 caenorhabdi
P32473 saccharomyc
O34092 staphylococ
P23984 infectious
Q02603 leuconostoc
P54987 mus musculu
P38132 saccharomyc
Q12923 homo sapien
P22871 erwinia her
O88563 rattus norv
O25655 helicobacte
P19584 thermoanaer

ALIGNMENTS

FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 467 AA; 51075 MW; 118E828A5D7EC661 CRC64;

Query Match 75.6%; Score 1745; DB 1; Length 467;
 Best Local Similarity 74.4%; Pred. No. 6.3e-135;
 Matches 326; Conservative 43; Mismatches 69; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTGTALGPRGNHSCDTVDGGYQCPEISHLWQYSPFFSLADE 60
 DB 1 MGVSAVLLPLYLAVTSLAVPASRNQSTCDTVDGGYQCFSETSHLWQYAPFFSLANE 60

QY 61 SAISDPVPGCRVTVQVLSRHGARYPTSSKYSALIEIAIQKNATAFKGYAFLKTYN 120
 DB 61 SAISDPVPGCRVTVQVLSRHGARYPTESKGYKYSALIEIQNVTTFDGKYAFLKTYN 120

QY 121 YTLGADLLTPFGEQWVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFTGFOSA 180
 DB 121 YSLGADLLTPFGEQVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFTGFQST 180

QY 181 KLADGANPHQASPVINIIPEAGYNTLDHGLCTAFEESELDGDDVBNFATVPAPPIR 240
 DB 181 KLKDPRAQPGQSSPKIDVIVSEASSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

QY 241 ARLEAHLPGVNTLDEVDVNLMDCFDVARVTSATQSLSPCDLTHDEWTDYDYLQSLG 300
 DB 241 QRLNDLSGVTITLDEVTYVLMDCSFDTISTSTVDTKLSPFCDLTHDEWTDYDYLQSLK 300

QY 301 KYGVGAGNPLGACGQVGNVLIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADF 360
 DB 301 KYGVGAGNPLGACGQVGNVLIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADF 360

QY 361 HDMTMSIFFALGLYNGTKPLSTTSVESTETDGYAASVTVPFAARAYVEMQCAKEP 420
 DB 361 HDNGIISILFALGLYNGTKPLSTTIVENTITQDGFSSATVTFASRLYVEMQCAKEP 420

QY 421 LVRVLVNDVRVPLHGGCV 438
 DB 421 LVRVLVNDVRVPLHGGCV 438

RESULT 2
 PHYA_ASNG STANDARD; PRT; 467 AA.

AC F34752;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAKISPHOSPHATE
 DE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL-HEXAKISPHOSPHATE
 DE PHOSPHOHYDROLASE A).
 GN PHYA.
 OS Aspergillus niger.
 OC Eukaryota; Fungi.
 OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OC NCBI_TaxID=5061;
 RN [1]
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
 RX MEDLINE=9325284; PubMed=8387447;
 RA van Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M.,
 RA Gouka R.J., Suykerbuyk M.E.G., Luiten R.G.M., van Paridon P.A.,
 RA Selten G.C.M., Veenstra A.E., van Gorcom R.F.M.,
 RA van den Hondel C.A.M.J.J.;

RT "Cloning, characterization and overexpression of the phytase-encoding
 RT gene (phyA) of *Aspergillus niger*.";
 RL Gene 127:87-94(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP Mullaney E.J.;
 RA Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN SEQUENCE OF 24-464.
 RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
 RX MEDLINE=93249451; PubMed=8387289;
 RA Ullah A.H.J., Dischinger H.C. Jr.;
 RT "Aspergillus ficuum phytase: complete primary structure elucidation
 RT by chemical sequencing.";
 RL Biochem. Biophys. Res. Commun. 192:747-753(1993).
 RN [4]
 RN SEQUENCE OF 71-93.
 RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
 RX MEDLINE=91298982; PubMed=1648914;
 RA Ullah A.H.J., Cummins B.J., Dischinger H.C. Jr.;
 RT "Cyclohexanedione modification of arginine at the active site of
 RT Aspergillus ficuum phytase.";
 RL Biochem. Biophys. Res. Commun. 178:45-53(1991).
 RN [5]
 RN CHARACTERIZATION, AND PARTIAL SEQUENCE.
 RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
 RX MEDLINE=89160685; PubMed=2852807;
 RA Ullah A.H.J.;
 RT "Aspergillus ficuum phytase: partial primary structure, substrate
 RT selectivity, and kinetic characterization.";
 RL Prep. Biochem. 18:459-471(1988).
 RN [6]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RC STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
 RX MEDLINE=97307250; PubMed=9164457;
 RA Kostrewa D., Gruninger-Leitch F., D'Arcy A., Broger C., Mitchell D.,
 RA van Loon A.P.;
 RT "Crystal structure of phytase from *Aspergillus ficuum* at 2.5-A
 RT resolution.";
 RL Nat. Struct. Biol. 4:185-190(1997).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTASE.
 CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
 CC D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
 CC -1- BIOTECHNOLOGY: IS USED AS A FOOD AND FEED ADDITIVE. IT CAN
 CC FACILITATE THE DEGRADATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS
 CC USED AS FOOD FOR MONOGASTRIC ANIMALS. SOLD BY NOVO NORDISK UNDER
 CC THE NAME PHYTASE NOVO.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; Z16414; CAA78904.1; -;
 CC EMBL; M94550; AAA32705.1; -;
 CC PIR; JN0482; JN0482.
 CC PIR; JN0023; JN0023.
 CC PIR; JN0656; JN0656.
 CC PDB; 1IHP; 18-MAR-98.
 CC InterPro; IPR000560; -;
 CC Pfam; PF00328; acid_phosphat; 1.
 CC PROSITE; PS00616; HIS-ACID-PHOSPHAT_1; 1.
 CC PROSITE; PS00778; HIS-ACID-PHOSPHAT_2; 1.
 CC Hydrolase; Glycoprotein; Signal; 3D-structure.
 CC SIGNAL 1 23
 CC CHAIN 24 467 3-PHYTASE A.
 CC ACT_SITE 82 82 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 CC ACT_SITE 361 361 PROTON DONOR (BY SIMILARITY).

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FT DISULFID 31 40
FT DISULFID 71 414
FT DISULFID 215 465
FT DISULFID 264 282
FT DISULFID 436 444
FT CARBOHYD 27 27
FT CARBOHYD 59 59
FT CARBOHYD 105 105
FT CARBOHYD 120 120
FT CARBOHYD 207 207
FT CARBOHYD 230 230
FT CARBOHYD 339 339
FT CARBOHYD 352 352
FT CARBOHYD 376 376
FT CARBOHYD 388 388
SQ SEQUENCE 467 AA; 51086 MW; 86FE8F3584341D6D CRC64;

Query Match 75.1%; Score 1733; DB 1; Length 467;
Best Local Similarity 74.2%; Pred. No. 6e-134;
Matches 325; Conservative 43; Mismatches 70; Indels 0; Gaps 0;

QY 1 MGCVFVLLSIATLFGSTGALPGNGSHSCDVTGGYQCFPEISHLMGWQSPFFSLADE 60
Db 1 MGVSALLPLLYLLSGVTSLGLAVPASRNOSCDTVDQGYQCFSESHLMGWQYAPFFSLANE 60

QY 61 SAISDPVPKGRVTFVQVLSRHGARYPTSSKSKYSALIEALOKNATAFKGYAFLKTYN 120
Db 61 SVISPEVPAGCRVTFVQVLSRHGARYPTSSKSKYSALIEALOKNATAFKGYAFLKTYN 120

QY 121 YTLGADDLTPGEGQOMVNSGKIFRYRYKALARKIVPFRASGSDRVASAEKTEGFQSA 180
Db 121 YSLGADDLTPGEGQOMVNSGKIFRYRYKALARKIVPFRASGSDRVASAEKTEGFQSA 180

QY 181 KIADPGANPHQASPVINVIPEGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLKDPAQPGGSSPKDVIIEAGSSNLTDPGCTVFEDSELADTVEANFTAVFAPPIR 240

QY 241 ARLEAHLPGVNLTDVVNLMDCMFPDFTVARTSDATOLSPFCDLFTDHEWIOYDYLQSLG 300
Db 241 QRLNDLSGVTLTDEVTYLMDCMFPDFTVARTSDATOLSPFCDLFTDHEWIOYDYLQSLK 300

QY 301 KYYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNNHTLDSNPATFPLNATLYADFS 360
Db 301 KYYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNNHTLDSNPATFPLNATLYADFS 360

QY 361 HDNTMVSITFFALGLYNGTKPLSTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420
Db 361 HDNGIISLTFALGLYNGTKPLSTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420

QY 421 LVRVLNDRVVPVPLHGGCV 438
Db 421 LVRVLNDRVVPVPLHGGCV 438

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RESULT 3
ID PHYB_EWEMI STANDARD; PRT; 463 AA.
AC 00093;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
DE 3-PHOSPHOHYDROLASE B) (3 PHYTASE B) (MYO-INOSITOL HEXAKISPHOSPHATE
DE PHOSPHOHYDROLASE B).
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=5072;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98007872; PubMed=9349716;
RA Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,

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RA van Loon A.P.;
RT "Cloning of the phytases from Emericella nidulans and the
RL thermophilic fungus Talaromyces thermophilus.";
RL Biochim. Biophys. Acta 1353:217-223(1997).
CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC FROM PHYTATE.
CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
CC D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL: U59803; AAB96871.1; -.
InterPro: IPR000560; -.
Pfam: PF00328; acid_phosphat; 1.
PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 463
FT ACT_SITE 80 80
FT ACT_SITE 81 81
FT ACT_SITE 357 357
FT CARBOHYD 26 26
FT CARBOHYD 41 41
FT CARBOHYD 103 103
FT CARBOHYD 118 118
FT CARBOHYD 203 203
FT CARBOHYD 226 226
FT CARBOHYD 331 331
FT CARBOHYD 335 335
FT CARBOHYD 372 372
SQ SEQUENCE 463 AA; 51786 MW; ECC5827D1E1C82A2 CRC64;

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Query Match 73.2%; Score 1689.5; DB 1; Length 463;
Best Local Similarity 72.6%; Pred. No. 2.1e-130;
Matches 318; Conservative 45; Mismatches 70; Indels 5; Gaps 3;

QY 1 MGCVFVLLSIATLFGSTGALPGNGSHSCDVTGGYQCFPEISHLMGWQSPFFSLADE 60
Db 1 MAFFTVALSLYLLSRVSAQA--PVQNHSCNTADGGYQCFNVSHVWGQYSPYFSIQE 58

QY 61 SAISDPVPKGRVTFVQVLSRHGARYPTSSKSKYSALIEATOKNATAFKGYAFLKTYN 120
Db 59 SAISEDVPHGCEVTFVQVLSRHGARYPTESKSKYSGLTAEIKNATSFQWGYAFLESYN 118

QY 121 YTLGADDLTPGEGQOMVNSGKIFRYRYKALARKIVPFRASGSDRVASAEKTEGFQSA 180
Db 119 YTLGADDLTPGEGQOMVNSGKIFRYRYKALARKIVPFRASGSDRVASAEKTEGFQSA 178

QY 181 KIADPGANPHQASPVINVIPEGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 179 QLHDHGSK--RATPVVNVIIPEIDGFNNTLDHISTCVSENDERADEIEANFTAVGPIR 236

QY 241 ARLEAHLPGVNLTDVVNLMDCMFPDFTVARTSDATOLSPFCDLFTDHEWIOYDYLQSLG 300
Db 237 KRLENDLPGIKLTNENVIYLMDCMFSFDTMAKTAHGTLSLPCAIIFTEKWLQYDYLQSL 296

QY 301 KYYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNNHTLDSNPATFPLNATLYADFS 360
Db 297 KYYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNNHTLDSNPATFPLNATLYADFS 356

QY 361 HDNTMVSITFFALGLYNGTKPLSTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420
Db 357 HDNSMISITFFAMGLYNGTKPLSTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 415

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U00029; AAB69729.1; -.
DR PIR; S48996; S48996.
DR HSSP; P34752; LIHP.
DR SGD; S0001258; PHO12.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
DR Hydrolase; Glycoprotein; Signal; Multigene family.
KW SIGNAL
FT CHAIN 1 17
FT ACT_SITE 75 75
FT ACT_SITE 337 337
FT CARBOHYD 97 97
FT CARBOHYD 162 162
FT CARBOHYD 192 192
FT CARBOHYD 250 250
FT CARBOHYD 315 315
FT CARBOHYD 356 356
FT CARBOHYD 390 390
FT CARBOHYD 439 439
FT CARBOHYD 445 445
FT CARBOHYD 461 461
FT CARBOHYD 461 461
SQ SEQUENCE 467 AA; 52699 MW; BEC606C0DF39B845B CRC64;

Query Match 16.8%; Score 387.5; DB 1; Length 467;
Best Local Similarity 26.4%; Pred. No. 4e-24;
Matches 115; Conservative 60; Mismatches 191; Indels 69; Gaps 13;

QY 24 PRGNHSCDTVGQCPPEISHLNGQYSPFSLADESAISPDVPGCRVTFVQVLSRHG 83
DB 21 PLGLSDIDKIGTQTEIFPFL-----GGSGPYYSFGDYGISHDLPESCCKQVQVGRHG 76
QY 84 ARPTSSKSKYSALIEATQKNATAFKGYAFK-----TNYNLT-----GADDL 128
DB 77 ERYPTVSKAKSINTWYKLSNYTGQFSGALSFLNDDEFFIRDTKNLEMETTLANSVNVL 136
QY 129 TPF-GEQGMVNSGKIPYRYKALAKIVDF-VRASGSDRVIASAKFEICGFSQAKLADPG 186
DB 137 NPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNRCHDTAQYFDG-----LGDK- 190
QY 187 ANPHQASPVINVL-----PEGAGVNTLDHGLCTAFSESLGDDVEANFTAVFAPPIRA 241
DB 191 -----FNISLQTSIAESAGANTLSAHSICPAWDD-DVNDLLKKYDKYLSGIK 240
QY 242 RLEAHLPGVNLTDDEYVNLMDMCPDVTARTSDATQLSPCDFTHDEWIDYDYLQSLGK 301
DB 241 RLNKENKGLNLTSSDANTFFAWCAVEINAR-----GYSDICNIFTKDELVRPSYQDLET 295
QY 302 YCYGAGNPLGPAOGVGVFNELIARLTHSPVDHFTSTNHTLDSNATPPLNATLYADFSE 361
DB 296 YYQTGPGYDVRSGANLNFNASVKLKESEVQDQ-----KWLSETH 337
QY 362 DNTMVSIFLALNGYTKPLSTTSVESIETDGYAASWTVPFAARAYVEMMQCEAKEPL 421
DB 338 DTDILNLTIGIIDDONNLTAHVPFMENT--FHRSWVVPQGVYTEKFC--SNDTY 393
QY 422 VRVLVNDVRVPLHGC 436
DB 394 VRYVINDAVVPIETC 408

RESULT 7
PPA3_YEAST
ID PPA3_YEAST STANDARD; PRT; 467 AA.
AC P24031;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CONSTITUTIVE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).

GN OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=85037940; PubMed=6093051;
RA Bajwa W., Mayhack B., Rudolph H., Schweingruber A.-M., Hinnen A.;
RT "Structural analysis of the two tandemly repeated acid phosphatase
RT genes in yeast.";
RL Nucleic Acids Res. 12:7721-7739(1984).
RN [2]
RX SEQUENCE FROM N.A.
RX STRAIN=S288C;
RX MEDLINE=95208357; PubMed=7900426;
RA Mannhaupt G., Stucka R., Ehme S., Vetter I., Feldmann H.;
RT "Analysis of a 70 kb region on the right arm of yeast chromosome II.";
RL Yeast 10:1363-1381(1994).
CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
CC ALCOHOL + ORTHOPHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01080; CAA25557.1; -.
DR EMBL; X78993; CAA55597.1; -.
DR EMBL; Z35961; CAA85045.1; -.
DR PIR; S44674; PABYCC.
DR HSSP; P34752; LIHP.
DR SGD; S0000296; PHO3.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
DR Hydrolase; Glycoprotein; Signal; Multigene family.
KW SIGNAL
FT CHAIN 1 17
FT ACT_SITE 75 75
FT ACT_SITE 337 337
FT CARBOHYD 97 97
FT CARBOHYD 103 103
FT CARBOHYD 162 162
FT CARBOHYD 192 192
FT CARBOHYD 250 250
FT CARBOHYD 315 315
FT CARBOHYD 356 356
FT CARBOHYD 390 390
FT CARBOHYD 439 439
FT CARBOHYD 445 445
FT CARBOHYD 456 456
FT CARBOHYD 461 461
FT CARBOHYD 461 461
FT CONFLICT 219 221
SQ SEQUENCE 467 AA; 52776 MW; 05FBB80DEB41B0FF CRC64;

Query Match 16.8%; Score 382.5; DB 1; Length 467;
Best Local Similarity 27.3%; Pred. No. 1e-23;
Matches 111; Conservative 59; Mismatches 179; Indels 57; Gaps 12;

QY 49 GOYSPFFSLADESAISPDVPGCRVTFVQVLSRHGARYPTSSKSKYSALIEATQKNATA 108
DB 42 GGAGPYFSPGPDYGISRDLPGCCCKQLQMLARHGERYPYPSKCATIMKTWYKLSNVTRQ 101
QY 109 PKGYAFK-L-TYNYTLGADD-----LTPF-GEQGMVNSGKIPYRYKALAK 152
DB 102 FNGSLFLNDDEYEFFIRDDDDLEMETTFANSNDVNLNPTGEMDAKRHAREFLAQYGYMFE 161

```

QY 153 KIVPF-VRASGSDRVIAAKFKFIEGFSOSAKLADPGANPHQASPVINVIIEGAGYNNITLD 211
 Db 162 NOTSFPIFAASSERVHTAQYFIDGL-----GDQFNISLOTVSEAMSAGA---NTLS 210
 QY 212 HG-LCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDDEVVNLMDCPDTVA 270
 Db 211 AGNACPGWDE-DAMDDILDYDITDYLDDIAKRLNKENKGLNLSKANTLFAWCAYELNA 269
 QY 271 RTSDATQLSPFCDLFTHDEWIOXDYLQSLGKYCYGAGNPLGPAQGVGFNELLIALRTHS 330
 Db 270 R-----GYSVDCDIFTEDELVRYSYGDLYSFYQDGPYDMISVGANLFENATLKLLKQS 324
 QY 331 PVQDHTSTNHLDSNPATFELNATLYADFSHDNTMWSIFFALGLYNGTKPLSTTSVESIE 390
 Db 325 ETOD-----LKVWLSFTHTDILNLTAGIIDDKNLTAETAYVPMFG 366
 QY 391 ETDGGAASWTVPFAARAYVEMMOCEARKEPLVRVLVNDVRVPLHGC 436
 Db 367 NT--FHKSWTVPQGARVYTEKFC--SNDTYVRYVINDAVVPIETC 408

RESULT 8

PPAD YEAST STANDARD; PRT; 468 AA.
 AC P52290;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PROBABLE ACID PHOSPHATASE YDL024C PRECURSOR (EC 3.1.3.2).
 GN YDL024C OR D2815.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Andre B., Vissers S., Urrestarazu L.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
 CC ALCOHOL + ORTHOPHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC [1]
 CC EMBL; 248432; CAA88335.1; -;
 DR EMBL; 274072; CAA98583.1; -;
 DR SGD; S0002182; YDL024C.
 DR InterPro; IPR000560; -;
 DR Pfam; PF00328; acid_phosphat; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Signal; Multigene family.
 FT SIGNAL 1 20
 FT CHAIN 21 468
 FT ACT_SITE 76 76
 FT ACT_SITE 338 338
 FT CARBOHYD 98 98
 FT CARBOHYD 163 163
 FT CARBOHYD 193 193
 FT CARBOHYD 202 202
 FT CARBOHYD 238 238
 FT CARBOHYD 251 251
 FT CARBOHYD 316 316
 FT CARBOHYD 357 357
 FT CARBOHYD 391 391

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 468 AA; 53076 MW; 1F07FF374DDF162C CRC64;

Query Match 15.4%; Score 355.5; DB 1; Length 468;
 Best Local Similarity 25.4%; Pred. No. 1.6e-21;
 Matches 108; Conservative 58; Mismatches 163; Indels 97; Gaps 12;

QY 49 GOYSFFFSLADRSATSPDPKGCRTVFQVLSRHGARTPTSSKSKYSALIEAIOKNATA 108
 Db 43 GSAPYFFSPANYGIPTDIPGECRLTQVMIGRHGERTPRSEAKDIFEVWYKISNYTGK 102
 QY 109 FRGKYAFKLT--YNYTL-----GADDLTPT-GEQMVNSGTFKRVRYKALAR 152
 Db 103 YEGSLSFLNNGYEFFIPDESLEMETTTONSIDVNLPTGEMNAKRHAREFLAKYKGLME 162
 QY 153 KIVPF-VRASGSDRVIAAKFKFIEGFSOSAKLADPGANPHQASPVINVIIEGAGYNNITLD 211
 Db 163 NCTNFPITNTSKRIYDTAQYFAEL-----GDGFNISLQ 197
 QY 212 HGLCTAFEESELG-----DDVEANFTAVFAPPIRARLEAHLPGVNL 253
 Db 198 -----TLSENSSGANTLAAKSCPNMNSNANDILMSYRDYLENISDLNDENKGLNLS 253
 QY 254 DEDVYNLMDCPFDVARTSDATQLSPFCDLFTHDEWIOXDYLQSLGKYCYGAGNPLGP 313
 Db 254 RDAALAFSWCAFEL-----NAKYSNCDIFSAALHYSYETDLTFSYONGPYKLIK 308
 QY 314 AOGVGFVN---ELIARLTHSPVQDHTSTNHTLDSNPATFELNATLYADFSHDNTMWSIFF 370
 Db 309 SIGANLENATVKLIQSAH-----LDQKWLISFTHTDILNLT 347
 QY 371 ALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCEARKEPLVRVLVNDVR 430
 Db 348 TAGLIDDTNLTNTNHVPPRDHS--YHRSWYIPOGARVYTEKFC--SNDTSVRYVNDVAV 403
 QY 431 VPLHGC 436
 Db 404 VPESC 409

RESULT 9

PHYB_ASPNG STANDARD; PRT; 479 AA.
 ID PHYB_ASPNG
 AC P34754; 1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE 3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
 DE 3-PHOSPHOHYDROLASE B) (3 PHYTASE B) (MYO-INOSITOL HEXAKISPHOSPHATE
 DE PHOSPHOHYDROLASE B).
 GN PHYB.
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-101; 133-141 AND 376-399.
 RX MEDLINE=93371452; PubMed=7916610;
 RA Ehrlich K.C., Montalbano B.G., Mullaney E.J., Dischinger H.C. Jr.,
 RA Ullah A.H.J.;
 RA "Identification and cloning of a second phytase gene (phyB) from
 RA Aspergillus niger (flicum).";
 RL Biochem. Biophys. Res. Commun. 195:53-57(1993).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
 CC D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC
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CC EMBL; L20567; AAA02934.1; --
 DR InterPro; IPR000560; --
 DR Pfam; PF00328; acid_phosphat; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 479
 FT ACT_SITE 81 81
 FT ACT_SITE 82 82
 FT ACT_SITE 337 337
 FT CARBOHYD 106 106
 FT CARBOHYD 191 191
 FT CARBOHYD 227 227
 FT CARBOHYD 250 250
 FT CARBOHYD 315 315
 FT CARBOHYD 425 425
 FT CARBOHYD 442 442
 FT CARBOHYD 458 458
 FT SEQUENCE 479 AA; 52611 MW; 395D4DA2B50DFC4 CRC64;

Query Match 15.3%; Score 352.5; DB 1; Length 479;
 Best Local Similarity 27.9%; Pred. No. 3e-21;
 Matches 117; Conservative 54; Mismatches 158; Indels 91; Gaps 16;

QY 49 GOYSPFFSLADESAISDPVPGKCRVTFVQVLSRHGARYPTSCKSKY-SALLIEATQKNAT 107
 DB 53 GPYSERVSY---GIARDPPTGCEVDQVIMVKRHGERYPSAGKSIEEALAKVYSINTT 108
 QY 108 AFKGYAFILKTYNTL-----GADDLT-PF-GEQMVNSGKIFRYRYKAL--ARKIVPF 157
 DB 109 EYKGLDLFLNDWTYYVNPCEYNAETSGPYAGLLDAYNHGNDYKARYGHLWNETVVPF 168
 QY 158 VRAGSDRVIASAEKFTIEGFSQAKLADPGANPHQASPVINVIPEGAGYNNLTDLHGLCTA 217
 DB 169 F-SSGYGRVETARKFGEGF-----FGYNSTNAALNII 201
 QY 218 FESELG-----DDVEANTAVFAPPRI---ARLEAHLPGVNLTDVNLMD 262
 DB 202 SESEVMGADSLTPTCDTNDNDQTTCDNLTYQLPQKYAAARLNSQPMNLTAADVYNLIV 261
 QY 263 MCPFDVARTSDATQSPFCDLFTHDWQYDYLQSLGKYGYGAGNPLGPAQGVGVNE 322
 DB 262 MASFELNAR-----PFSNWINAFTQDEWSFGVDELNYYCAGPKDKNAAGVAYANA 316
 QY 323 LIARLTHSPVDHTSTNHTLDSNPATPFLNATLYADFSHDNTMVSTFFALGLY--NGTKP 380
 DB 317 SLTLLNQG-----KEAGP-----LFFENFAHDTNITPLAALGVLPINEDLP 358
 QY 381 LSTSVESIEETGYAASVTWPFPAARAYVEMMCEA-----EKEPIVRLVNDRVVPLHGC 436
 DB 359 L-----DRVAFGNPYSGNITVPMGGHLTIERUSCOATLSDKGYTVRLVNLNAVLPFND 413

RESULT 10
 PHYB_ASFAW STANDARD; PRT; 479 AA.
 AC P34755;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
 DE 3-PHOSPHOHYDROLASE B) (PH 2.5 OPTIMUM ACID PHOSPHATASE).
 GN PHYB OR APH.
 OS Aspergillus awamori.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=105351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ALK0243;
 RX MEDLINE=94040796; PubMed=8224894;
 RA Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A.,
 RA Miettinen-Oinonen A., Nevalainen H., Rambosek J.A.;
 RT "The cloning and sequencing of the genes encoding phytase (phy) and
 RT pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
 RT awamori.";
 RL Gene 133:55-62(1993).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=99264417; PubMed=10329192;
 RA Kostrewa D., Wyss M., D'Arcy A., van Loon A.P.;
 RT "Crystal structure of Aspergillus niger pH 2.5 acid phosphatase at
 RT 2.4-A resolution.";
 RL J. Mol. Biol. 288:965-974(1999).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTASE.
 CC -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O =
 CC D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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EMBL; L02420; AAA16897.1; --
 DR PIR; JN0890; JN0890.
 DR PDB; 1QFX; 19-APR-00.
 DR InterPro; IPR000560; --
 DR Pfam; PF00328; acid_phosphat; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 479
 FT ACT_SITE 82 82
 FT ACT_SITE 337 337
 FT DISULFID 71 387
 FT DISULFID 128 472
 FT DISULFID 216 441
 FT DISULFID 225 298
 FT DISULFID 413 421
 FT CARBOHYD 191 191
 FT CARBOHYD 315 315
 FT CARBOHYD 458 458
 FT SEQUENCE 479 AA; 52678 MW; 4F8E0F3778CC3B08 CRC64;

Query Match 15.0%; Score 346.5; DB 1; Length 479;
 Best Local Similarity 27.4%; Pred. No. 9.2e-21;
 Matches 115; Conservative 54; Mismatches 160; Indels 91; Gaps 15;

QY 49 GOYSPFFSLADESAISDPVPGKCRVTFVQVLSRHGARYPTSCKSKY-SALLIEAQNAT 107
 DB 53 GPYSERVSY---GIARDPPTGCEVDQVIMVKRHGERYPSAGKIDEEALAKVYSINTT 108
 QY 108 AFKGYAFILKTYNTL-----GADDLT-PF-GEQMVNSGKIFRYRYKAL--ARKIVPF 157
 DB 109 EYKGLDLFLNDWTYYVNPCEYNAETSGPYAGLLDAYNHGNDYKARYGHLWNETVVPF 168
 QY 158 VRAGSDRVIASAEKFTIEGFSQAKLADPGANPHQASPVINVIPEGAGYNNLTDLHGLCTA 217
 DB 169 F-SSGYGRVETARKFGEGF-----FGYNSTNAALNII 201

```

QY 218 FEESLG-----DDVEANTAVFAPPPIR-----ARLEAHLPGVNLTDVVDVNLMD 262
Db 202 SESEVWAGDSLTPCTDNDQTTCDNLTYQLPOFKVAAAKLNQNGMNLNTASDVYNLWV 261
QY 263 MCFPDTVARTSDATQISPFCDLTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFVNE 322
Db 262 MASFELNAR-----PFSWNINAFQDEWVSFGVVDLNYCYCAGPGDKNAAGVAYANA 316
QY 323 LIARLTHSPVQDHTSYNHTLDSNPATFPLNATLYADFSDHNTWVSIFALGLY--NGTRP 380
Db 317 SLTLNQPKP-----AGSLFFNFAHDTNITPTLAAALGVLLPNEDEL 358
QY 381 LSTTSVESIETDGYAASWTVPFAARAYVEMOCEA-----EKEPLVRVLVNDVRVPLHGC 436
Db 359 L-----DRVAFGNPYSIGNIVPMGHLTLERLSCQATALSDEGTYVRLVNEAVLPFND 413

RESULT 11
PPAL_PICPA
ID PPAL_PICPA STANDARD; PRT; 468 AA.
AC P52291;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ACID PHOSPHATASE PHO1 PRECURSOR (EC 3.1.3.2).
GN PHO1.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4922;
RN SEQUENCE FROM N.A.
RX MEDLINE=96001238; PubMed=7557473;
RA Payne W.E., Gannon P.M., Kaiser C.A.;
RT "An inducible acid phosphatase from the yeast pichia pastoris:
RT characterization of the gene and its product.";
RL Gene 163:19-26(1995).
CC -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O -> AN
CC ALCOHOL + ORTHOPHOSPHATE.
CC -!- INDUCTION: BY PHOSPHATE STARVATION.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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CC -----
DR EMBL; U28658; AAA85503.1; .
DR HSSP; P34752; 1IHP.
DR InterPro; IPR000560; .
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase; Glycoprotein; Signal; Multigene family.
FT SIGNAL
FT CHAIN 1 22 POTENTIAL.
FT CHAIN 23 468 ACID PHOSPHATASE PHO1.
FT ACT_SITE 84 84 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 345 345 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 468 AA; 52690 MW; AE555B8E27718C2C CRC64;

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Query Match

Best Local Similarity 14.7%; Score 338; DB 1; Length 468;

Pred. No. 4.4e-20;

```

Matches 120; Conservative 75; Mismatches 180; Indels 90; Gaps 21;
QY 6 VLLSIATL---FGSTSGTALGRGNSHSCDVTVDGQYQCPEISHLWGYSPF--FSLADE 60
Db 10 IILALATLQSVFAVELQHLVGVNDRPYQRT--DDQYNILRHGLGL-GPYIGYNGWIAAE 67
QY 61 SAISPDVPGKGRVTQVLSRHGARYPTSSKSKYSALIE-AIOKNATAFKGYAFLKTY 119
Db 68 SEI-----ESCTIDQAHLLMRHGERYPSTNVGKQLEALYQKLLDADVRVPTGPLSEFFDY 122
QY 120 NYTLG---ADDLTPFGGQMVNSGKIF---YRYKAL-----ARKIVFVRSASGDR 165
Db 123 DYFVSDAAWYEQETTKGYISGLNTAFDGTTLRERYDHLINTSEGGKL--SVWAGSOER 180
QY 166 VTAAEKFTIEGFQSAKLADPGANPHQASPVINVAIPE---GAGYNNTLHDGLCT-----A 217
Db 181 VVDTAKYFAQGMKSNYTD-----MVEVVALEEKSQGLNSLTARTSCPNYNHSI 230
QY 218 FEESLGDDV---EANTAVAFAPPIRARLEAHLPGVNLTDVVDVNLMDMCPDFTVARTSD 274
Db 231 YKDGDFPNDAIAREAD-----RLNTLSFGFNITADDIPTIALYCGFELNVGRGE- 278
QY 275 ATQLSPFCDLFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIARLTHSPVQD 334
Db 279 ---SSFCDLVSREALLYTAYLRDLGHWYVNGNPNLGTIGYVYAN----- 321
QY 335 HTSNHTLDSNPATFPLNATLYADFSDHNTWVSIFALGLYNGTK-PLSTTSVESIETD 393
Db 322 --ATROLLENTEAD-PRDYPLYFSFSDTDLQVFTSLGFLNVTDLPL-----DQIQFQT 373
QY 394 GYAASWTVPFAARAYVEMOCC--EAEKEPLVRVLVNDVRVPLHGC 436
Db 374 SFKSTEIVPMGARLLTERLCTVGEKKYVYRTILNDVAVPLSDC 418

RESULT 12
PPA5_KLULA
ID PPA5_KLULA STANDARD; PRT; 469 AA.
AC P52289;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
GN PHO5.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN SEQUENCE FROM N.A.
RP STRAIN=CBS 2359/152;
RA Ferminan E.;
RL Thesis (1995), University of Salamanca, Spain.
CC -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O -> AN
CC ALCOHOL + ORTHOPHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- INDUCTION: REPRESSED BY INORGANIC PHOSPHATE (BY SIMILARITY).
CC -!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z33995; CAA83964.1; .
DR InterPro; IPR000560; .
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.

```


Db 310 LANSL--RSVENNTQ-----QVFFAFTHDANIIPVETALGFDTNTPN 351
 QY 383 TTSVESIEETDGAASWTPFAARAVEMMQCEAEKPLRVLVNDRVVPVPHGCG 437
 Db 352 PLPTSQVSHSMKASEFVPFAGNLITELFQCEDSKY-YVRHLVNEVPFLSDCG 405

RESULT 14

PPA2_SCHPO STANDARD; PRT; 463 AA.
 AC Q01682;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE THIAMINE-REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
 GN PHO4 OR SPB428.03C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-30.
 RX MEDLINE=91064763; Pubmed=2249257;
 RA Yang J., Schweingruber M.E.;
 RT "The structural gene coding for thiamin-repressible acid phosphatase
 in Schizosaccharomyces pombe";
 RL Curr. Genet. 18:269-272(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M., Rajandream M.A., Barrell B.G., Baker S., Mungall K.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY DEPHOSPHORYLATE THIAMINE PHOSPHATES.
 CC -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
 CC ALCOHOL + ORTHOPHOSPHATE.
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- INDUCTION: REPPRESSED BY THIAMINE.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).

CC EMBL; X56939; CAA40258.1; -
 CC DR EMBL; AL034382; CAA22278.1; -
 CC DR PIR; S14119; S14119.
 CC DR InterPro; IPR000560; -
 CC DR Pfam; PF00328; acid.phosphat; 1.
 CC DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 CC DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 CC KW Hydrolyase; Glycoprotein; Cell wall; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 463 THIAMINE-REPRESSIBLE ACID PHOSPHATASE.
 FT ACT_SITE 69 69 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 340 340 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 328 328 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 439 439 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 463 AA; 52118 MW; F48EAF8B6B234A CRC64;

Query Match 13.0%; Score 300; DB 1; Length 463;
 Best Local Similarity 25.4%; Pred. No. 5.5e-17;
 Matches 104; Conservative 66; Mismatches 181; Indels 58; Gaps 14;

OY 51 YSPFSLADESAISPDVPGCRVTFVQVLSRHGARYPTSS-----KSKKYSAIE----- 100
 Db 43 HEPYF-----NGPTTSFPESCAIKQVHLLQHRGSRNPTGDDTATDVSSAQYIDIFQNKLL 97
 QY 101 --AIQKNATAFKGYAFLKTYNTL--GADLLTPFGEOQMVGSGIKFYRRYKALARKIV 155
 Db 98 NGSIPVNFSEYPENPLYFVKHWPVKAENADQLSSSGRIEFLDGRQVFRFYELFDTDV 157
 QY 156 PFVRSASGSDRVIAAEKPIEGFQSAKLADPGANPHQASPVINVIPE--GAGYNTNLDHG 213
 Db 158 YDIATAQERVVDSAEWFSYGM-----FDDMQNKTNF-----IVLPEDDSAGANSLAMY 208
 QY 214 LCTAFESSELGDD--VEANFTA---VEAPPRIARLEAHL--PCVNLTDEDVNVLMDCBFD 268
 Db 209 SCPVEDNNIDENTEAAHTSWRVFLKPIANRLNKYFDSGYNLTVSDVRSLYICYEI 268
 QY 269 VARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGVNELIARLT 328
 Db 269 ALRDN-----SDFCSLFTSPSEFLNFYDSDLDYAYWGSPASEWASTLGGAYVNNLANNL- 322
 QY 329 HSPVQDHTSNTHTLDSNPATFPPLNATLYADFSHNTWYSIFFALGLYNGTKPLSTTSVES 388
 Db 323 -----RKGVNNASDRK-----VFLAFTHDSQIIPVEAALGFPPDITPEHPPLPTDK 367
 QY 389 IETDGYAASWTVDFFAARVAYVEMMQCEAEKPLRVLVNDRVVPVPHGCG 437
 Db 368 NIFTYSLKTSFVFPFAGNLITELFLC--SDNKYYVRHLVNNQVPLTDCG 415

RESULT 15

PPAX_CABEL STANDARD; PRT; 755 AA.
 AC Q09549; Q17843;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PUTATIVE ACID PHOSPHATASE F26C11.1 (EC 3.1.3.2).
 GN F26C11.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Matthews P., Lloyd C.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
 CC ALCOHOL + ORTHOPHOSPHATE.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).

CC EMBL; 247072; CAA87370.1; -
 CC DR EMBL; 254342; CAA87370.1; JOINED.
 CC DR EMBL; 254342; CAA91156.1; -
 CC DR EMBL; 247072; CAA91156.1; JOINED.
 CC DR Wormpep; F26C11.1; CE05732.
 CC InterPro; IPR000560; -
 CC Pfam; PF00328; acid.phosphat; 1.
 CC DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 CC DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 CC KW Hypothetical protein; Hydrolase.

Thu Oct 18 11:34:37 2001

```
FT ACT_SITE 356 356 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT ACT_SITE 399 399 BY SIMILARITY.
FT ACT_SITE 636 636 PROTON DONOR (BY SIMILARITY).
FT DISULFID 702 708 BY SIMILARITY.
SQ SEQUENCE 755 AA; 87783 MW; E7F3050115A235EB CRC64;

Query Match 5.88; Score 134; DB 1; Length 755;
Best Local Similarity 21.98; Pred. No. 0.0038;
Matches 91; Conservative 56; Mismatches 123; Indels 146; Gaps 23;

QY 57 LADESAISPDVPKGRVTFVQVLSRHGAR-----YPTSSSKKYSALIEAIQKNATAFK 110
DB 332 LAIEKSFSEV-DNNKLEFVQTIWRHGRSALGLFPISEK----- 371
QY 111 GKYAFKTYNYTLGA---DDLTPGEOQMVNSGKIFYRRY-----KALARKIVPFV 158
DB 372 -----NMTFGGGLGELTPMGSMENNLGTIFRRRYVEDQOFLSHRYAAKEI--YI 420
QY 159 RASGSDRVIASAEKFTIEGFQSAKLADPGANPHOASPVINVIPEGAGYNNFLD----- 211
DB 421 RSTNLNRTIISAMSLYG-----MPPPGA-----WNI---QGVDPNDVDWQOGETF 464
QY 212 -----HGL-----CTAFEE-----SELGDDVEANFTAVFAPPIRARLEAHLPGVN 251
DB 465 IPVHVDGIDQCAVAQLCNCRRFQELQEKWAEI-DEVKNATVAMIA--LNRVAAAF---YN 518
QY 252 LTDEDVNLMDMCPDPTVARTSDA--TQLSPFCD-LFTHDEWIQYDYLSGLKYYG---- 304
DB 519 VTDQP-----EKNRYTDANKCORNFNDTMYOQLPWYNEDLYNEAORTYAPFKR 568
QY 305 ---YGAGNP-----LGPAQGVGFVNELIARLTHSPVODHTSTNHTLD-SNPA 347
DB 569 FTEGFGNPKPSIVDIDIPQEVSTLQGGPLLNEIFERGREKIRCVADAENCSIDYLPKPL 628
QY 348 TPPLAATLYADFSDNTMWSIFFALGYNGTKPLSTTSVESIEETDGYAAKWTVPF 403
DB 629 KF-----YAYSSHQDLVYALLVTLGI-----TDVVKTVDGWPDTRSSSLITIEY 670
```

Search completed: October 16, 2001, 17:57:24
Job time: 562 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 16, 2001, 17:49:14 ; Search time 124.2 Seconds
(without alignments)
213.795 Million cell updates/sec

Title: US-09-488-265-26_COPY_1_438

Perfect score: 2307

Sequence: 1 MGVPVLLSLTLFGSTSGT.....EPLVRLVNDVRVPLHCCGV 438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
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17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2307	100.0	467	21	AA20524
2	2307	100.0	467	21	AA20524
3	2285	99.0	467	20	AA20524
4	2285	99.0	467	21	AA20527
5	2285	99.0	467	21	AA20527
6	2279	98.8	467	21	AA20533
7	2273	98.5	467	21	AA20533
8	2196	95.2	467	21	AA20531
9	2190	94.9	467	21	AA20532
10	2185	94.7	467	20	AA20532
11	2185	94.7	467	21	AA20526

12	2185	94.7	467	21	AA20526	Mutant phytase-1,
13	2181	94.5	441	21	AA20523	Consensus phytase
14	2154	93.4	467	20	AA20530	Fungal phytase pro
15	2154	93.4	467	21	AA20535	Consensus phytase
16	2154	93.4	467	21	AA20535	Phytase-1, a conse
17	2148	93.1	467	20	AA20538	Fungal consensus p
18	2147	93.1	467	20	AA20538	Fungal consensus p
19	2147	93.1	467	20	AA20538	Fungal consensus p
20	2144	92.9	467	20	AA20538	Ascomycete consens
21	2139	92.7	467	20	AA20538	Fungal consensus p
22	2138	92.7	467	20	AA20538	Fungal consensus p
23	2128	92.2	467	21	AA20530	Consensus phytase
24	2128	92.2	467	21	AA20530	Consensus phytase
25	2047	88.7	467	20	AA20530	Consensus phytase
26	2047	88.7	467	21	AA20530	Phytase-7, a deriv
27	2044	88.6	467	21	AA20530	Consensus phytase
28	2028	87.9	441	21	AA20530	Consensus phytase
29	1965	85.2	437	21	AA20525	Phytase-11, a cons
30	1965	85.2	437	21	AA20525	Consensus phytase
31	1916	83.1	431	21	AA20535	Initial consensus
32	1916	83.1	431	21	AA20535	Mutant Aspergillus
33	1916	83.1	467	21	AA20535	Consensus phytase
34	1903	82.5	424	21	AA20536	Consensus phytase
35	1903	82.5	424	21	AA20536	Initial consensus
36	1896	82.2	467	20	AA20528	Aspergillus fumiga
37	1896	82.2	467	21	AA20528	Mutant Aspergillus
38	1896	82.2	467	21	AA20528	Aspergillus fumiga
39	1770	76.7	465	19	AA20528	Mutant Aspergillus
40	1770	76.7	465	20	AA20528	Aspergillus fumiga
41	1760.5	76.3	440	21	AA20528	Aspergillus fumiga
42	1757.5	76.2	440	21	AA20528	Aspergillus fumiga
43	1757.5	76.2	440	21	AA20528	Aspergillus fumiga
44	1752.5	76.0	440	21	AA20528	Aspergillus fumiga
45	1752.5	76.0	440	21	AA20528	Aspergillus fumiga

ALIGNMENTS

RESULT 1	
AA20524	
ID	AA20524 standard; Protein; 467 AA.
AC	AA20524;
XX	
XX	
DT	05-DEC-2000 (first entry)
XX	
DE	Consensus phytase 10 SEQ ID NO:26.
XX	
KW	Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW	temperature stability; pH profile; temperature profile; reaction rate;
KW	specific activity; substrate specificity; substrate cleavage pattern;
KW	substrate binding; position specificity; phytate degradation rate;
KW	food; feed; phytate; manure.
XX	
OS	Synthetic.
XX	
PN	WO200043503-A1.
XX	
PD	27-JUL-2000.
XX	
PF	21-JAN-2000; 2000WO-DK00025.
XX	
PR	22-JAN-1999; 99DK-000092.
PR	21-SEP-1999; 99DK-0001340.
XX	
PA	(NOVO) NOVO NORDISK AS.
XX	
PI	Lehmann M;
XX	
DR	WPI; 2000-491161/43.
DR	N-PSDB; AAA73232.
XX	

PT Novel phytases with improved properties such as temperature stability,
PT pH stability and substrate specificity, for use in pharmaceuticals and
XX compound foods and feeds -
PS Claim 1; Fig 5a-c; 240pp; English.
XX
CC The present invention describes improved phytases, preferably with
CC increased thermostability, and methods for producing them. The methods
CC can be used for producing phytases with improved properties e.g.
CC temperature stability, pH stability, pH profile, temperature profile,
CC specific activity, substrate specificity, substrate cleavage pattern,
CC substrate binding, position specificity, the velocity and level of
CC release of phosphate from corn, reaction rate, phytate degradation rate,
CC and end level of released phosphate. The phytases can be used to produce
CC pharmaceutical compositions or compound food or feeds. The feed can be
CC used to reduce levels of phytate in animal manure, by converting it
CC into lower inositol phosphates and/or inositol and inorganic phosphate.
CC The present sequence represents a phytase sequence from the present
CC invention.
XX
XX Sequence 467 AA:
XX
XX Query Match 100.0%; Score 2307; DB 21; Length 467;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-23;
XX Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTGALPGRNHSCDVTGQYCFPEISHLWQYSPFFSLADE 60
DB 1 mgvfvlslatlfgstgaltgrnshscdtvqgycfpeishlwqyspffslade 60

QY 61 SATSPDVPKCRVTFVQVLSRHGARYPTSSKSKYSALIEAOKNATAPKGYAFILKTYN 120
DB 61 saispdvpkcrvtfvqvlshrgharyptsskkskysalieaoknatarkgyafilktyn 120

QY 121 YTLGADLTLPFGQVMNSGKRYRYKALARKIVPFRASGSDRVIASEAERFIEGFQSA 180
DB 121 ytlgaddltlpfgqvmnsgkryrykalkarkivpfrasgsdrviasaekfiegfsa 180

QY 181 KLADPGANPHQASPVINVIIPGAGYNNLTDLGLCTAFSESELGDDVEANFVAPPPIR 240
DB 181 kladpganphqaspviniipgagynntldlglctafeeseldgddveanfvaappir 240

QY 241 ARLEAHLPGVNLTDVNNLMDMCPDVTARTSDATQLSPFCDLTFHDEWIOYDIQLSLG 300
DB 241 arleahlpgvnltdvnnlmdmcpdvtartsdatlspfcldtfhdewiodyiqlslg 300

QY 301 KYGYGAGNPLGPAQGVGFVNELIARLTHSPVODHTSTNHTLDSNPATPLNATLYADFS 360
DB 301 kygygagnplgpaqgvfveliarlthspvohdhtstnhtldsnpatplnatlyadfs 360

QY 361 HDNTWVSIFPAGLYNGTKPLSTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420
DB 361 hdnwvsifpalyngtkplstsvesieetdgyaaswtvpfaarayvemmoceakep 420

QY 421 LVRVLNDRVVPVHLGCGV 438
DB 421 lrvlndrvvpvhlhcgvg 438

RESULT 2
ID AAY69566
XX AAY69566 standard; protein; 467 AA.
AC AAY69566;
XX
DT 19-APR-2000 (first entry)
XX
DE Phytase-10, a consensus phytase.
XX
KW Phytase: myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
KW thermostable; animal feed; monogastric animal; phytate phosphorus;
KW phosphate availability; consensus; phytase-10.

XX Aspergillus terreus 9A1.
OS Aspergillus terreus cbs16.46.
OS Aspergillus niger str. awamori.
OS Aspergillus fumigatus ATCC13073.
OS Aspergillus fumigatus ATCC32722.
OS Aspergillus fumigatus ATCC58128.
OS Aspergillus fumigatus ATCC26906.
OS Aspergillus fumigatus ATCC32239.
OS Emericella nidulans.
OS Talaromyces thermophilus ATCC20186.
OS Myceliophthora thermophila.
OS Paxillus involutus NN005693.
OS Trametes pubescens NN9343.
OS Agrocybe pediades NN009289.
OS Peniophora lycii NN006113.
OS Thermomyces lanuginosa.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX /note= "Phytase signal peptide from Aspergillus terreus
XX cbs16.46"
XX
XX Protein 27..467
XX /note= "Mature phytase-10 consensus"
XX
XX EP969089-A1.
XX
XX 05-JAN-2000.
XX
XX 23-JUN-1999; 99EP-0111949.
XX
XX 29-JUN-1998; 98EP-0111960.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Brugger R, Lehmann M, Wyss M;
XX
XX WPI: 2000-099429/09.
XX N-PSDB; AAZ59642.
XX
XX New stabilised enzyme formulation, useful for feed compositions for
XX monogastric animals -
XX
XX Example 4; Fig 17; 101pp; English.
XX
XX The invention relates to a novel stabilised dry or liquid enzyme
XX formulation, comprising phytase (myo-inositol hexakisphosphate
XX phosphohydrolase) and one or more stabilising agents including
XX xylitol or ribitol; polyethylene glycols with a molecular weight of 600
XX to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
XX glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
XX The stabilised phytase formulation is used in a method for preparing a
XX feed composition for monogastric animals (e.g., pigs, poultry) and
XX provides a monogastric animal with its dietary requirements of
XX phosphorus. Although a large amount of phosphate is present in animal
XX feed in the form of phytate phosphorus, monogastric animals are unable
XX to utilise this form of phosphate, resulting in the addition of extra
XX phosphate to the feed of such animals. Phytase enhances the nutritional
XX value of plant material without the need for adding additional phosphate
XX to the feed. The level of phosphate pollution in the environment is
XX reduced by adding phytase to animal feed, as the animal can make use of
XX the inorganic phosphate liberated from phytate phosphorus using the
XX enzyme. The phytase formulation of the invention has an improved
XX thermostability and can therefore remain stable during long-term storage
XX and can withstand feed processing methods such as extrusion, expansion
XX and pelleting. The present sequence represents a consensus phytase
XX designated phytase-10, which was derived from the mature phytase
XX sequences from a variety of fungi (AAY69544-Y69546, AAY69548-Y69556,
XX AAY69564) and the Basidiomycetes phytase consensus AAY69563 and
XX additionally contains the Aspergillus terreus cbs16.46 signal peptide at
XX the N-terminus.

```

XX SQ Sequence 467 AA;
Query Match 100.0%; Score 2307; DB 21; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.4e-223;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGVEVLLSTATLFGSTGALGRGNHSCDTVDGQYQCFPEISHLWGOYSPFFSLADE 60
Db 1 mgvfvllsialtfgstgatalgrgnhscdtvdggyqcfpeishlwqyspffslade 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKYSALIEAIQKNATAPKGYAFILKTYN 120
Db 61 saispdvpkgcrvtfvqlsrhgaryptsskkskysalialieaiaqknatafkgyafikty 120
QY 121 YTLGADDLTFPGEQMVNSGIFRYRYKALARKIVPFRASGSDRVIASAEKFIQFQSA 180
Db 121 ytlgaddltfpgeqmvnsgikfryrykalaraki vprfvrsgsdrviasaeekfiqfqs 180
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 kladpganphqaspviniiepegagynntldhglctafeeseelgddveanftavfappir 240
QY 241 ARLEAHLPGVNLTDVVDVNLMDMCPFDVTARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db 241 arleahlpvnltdedvvnldmcpfdvtartsdatsqlspfcldlthdewiqdyqlslg 300
QY 301 KYGYGAGNPLGPAQGVGVNLIARLTHSPVDHTSTNHTLDSNPATFPLNATLYADFS 360
Db 301 kygygagnplgpagvggvnliarlthspvqdhstnhtldsnpatfplnatlyadfs 360
QY 361 HDNTMVSIFPFGALGXNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAKEP 420
Db 361 hdntmvsiffalglyngtkplsttsvesieetdgyaaswtvpfaarayvemmqceakep 420
QY 421 LVRVLVNDRVPLHGCYV 438
Db 421 lvrvlvndrvplhgcgv 438
RESULT 3
AAAY43170
ID AAAY43170 standard; Protein; 467 AA.
AC AAAY43170;
DT 06-JAN-2000 (first entry)
DE Consensus phytase-10-thermo(3)-Q50T-K91A protein sequence.
XX Phytase; animal feed preparation; thermostable phytase; transgenic plant;
KW consensus sequence.
OS Synthetic.
XX WO9948380-A1.
XX 30-SEP-1999.
XX 22-MAR-1999; 99WO-DK00154.
XX 23-MAR-1998; 98DK-0000407.
XX 19-JUN-1998; 98DK-0000806.
XX 18-SEP-1998; 98DK-0001176.
XX 22-JAN-1999; 99DK-0000091.
XX 22-JAN-1999; 99DK-0000093.
XX (NOVO ) NOVO-NORDISK AS.
XX Petersen S;
XX WPI; 1999-591030/50.

```

```

DR N-PSDB; AAZ31521.
XX Preparing animal feed using a thermostable phytase -
PS Example 3; Fig 10; 7lpp; English.
XX This sequence represents the consensus phytase-10-thermo(3)-Q50T-K91A.
CC The invention relates to a process for preparing animal feed by
CC agglomerating feed ingredients with a thermostable phytase, which is
CC added before or during agglomeration. The thermostable phytase is useful
CC for expression in transgenic plants. These plants are useful in the
CC preparation of animal feed itself. The thermostable phytase allows animal
CC feed to be produced more efficiently, in addition to improved
CC phytase-expressing transgenic plants. These plants provide a feed
CC ingredient and a feed additive (phytase) simultaneously.
XX SQ Sequence 467 AA;
Query Match 99.0%; Score 2285; DB 20; Length 467;
Best Local Similarity 98.9%; Pred. No. 2.4e-221;
Matches 433; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 MGVEVLLSTATLFGSTGALGRGNHSCDTVDGQYQCFPEISHLWGOYSPFFSLADE 60
Db 1 mgvfvllsialtfgstgatalgrgnhscdtvdggyqcfpeishlwgtyspffslade 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKYSALIEAIQKNATAPKGYAFILKTYN 120
Db 61 saispdvpkgcrvtfvqlsrhgaryptssaskaysalialieaiaqknatafkgyafikty 120
QY 121 YTLGADDLTFPGEQMVNSGIFRYRYKALARKIVPFRASGSDRVIASAEKFIQFQSA 180
Db 121 ytlgaddltfpgeqmvnsgikfryrykalaraki vprfvrsgsdrviasaeekfiqfqs 180
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 kladpganphqaspviniiepegagynntldhglctafeeseelgddveanftavfappir 240
QY 241 ARLEAHLPGVNLTDVVDVNLMDMCPFDVTARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db 241 arleahlpvnltdedvvnldmcpfdvtartsdatsqlspfcldlthdewiqdyqlslg 300
QY 301 KYGYGAGNPLGPAQGVGVNLIARLTHSPVDHTSTNHTLDSNPATFPLNATLYADFS 360
Db 301 kygygagnplgpagvggvnliarlthspvqdhstnhtldsnpatfplnatlyadfs 360
QY 361 HDNTMVSIFPFGALGXNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAKEP 420
Db 361 hdntmvsiffalglyngtkplsttsvesieetdgyaaswtvpfaarayvemmqceakep 420
QY 421 LVRVLVNDRVPLHGCYV 438
Db 421 lvrvlvndrvplhgcgv 438
RESULT 4
AAAB20527
ID AAAB20527 standard; Protein; 467 AA.
XX AAAB20527;
XX AC AAAB20527;
XX 05-DEC-2000 (first entry)
XX Consensus phytase 10 thermo 3 q50t, k91a protein SEQ ID NO:31.
KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW temperature stability; pH profile; temperature profile; reaction rate;
KW specific activity; substrate specificity; substrate cleavage pattern;
KW substrate binding; position specificity; phytate degradation rate;
KW food; feed; phytate; manure.
XX Synthetic.
OS

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XX WO200043503-A1.
 XX 27-JUL-2000.
 XX 21-JAN-2000; 2000WO-DK00025.
 XX 22-JAN-1999; 99DK-0000092.
 XX 21-SEP-1999; 99DK-0001340.
 XX (NOVO) NOVO NORDISK AS.
 XX Lehmann M;
 XX WPI; 2000-491161/43.
 XX N-PSDB; AAA73234.
 XX Novel phytases with improved properties such as temperature stability,
 XX pH stability and substrate specificity, for use in pharmaceuticals and
 XX compound foods and feeds -
 XX Claim 4; Fig 8a-c; 240pp; English.
 XX The present invention describes improved phytases, preferably with
 XX increased thermostability, and methods for producing them. The methods
 XX can be used for producing phytases with improved properties e.g.
 XX temperature stability, pH stability, pH profile, temperature profile,
 XX specific activity, substrate specificity, substrate cleavage pattern,
 XX substrate binding, position specificity, the velocity and level of
 XX release of phosphate from corn, reaction rate, phytate degradation rate,
 XX and end level of released phosphate. The phytases can be used to produce
 XX pharmaceutical compositions or compound food or feeds. The feed can be
 XX used to reduce levels of phytate in animal manure, by converting it
 XX into lower inositol phosphates and/or inositol and inorganic phosphate.
 XX The present sequence represents a phytase sequence from the present
 XX invention.
 XX Sequence 467 AA;
 SQ
 Query Match 99.0%; Score 2285; DB 21; Length 467;
 Best Local Similarity 98.9%; Pred. No. 2.4e-221;
 Matches 433; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MGVFVLLSLATLFGSTGALPGRNHSCDTVDGCGYCFPEISHLWGQYSPFFSLADE 60
 DB 1 mgvfvlslatlfsgtsgalprgnshscdtvdggyqcfpeishlwgytspffslade 60
 QY 61 SAISPDPVPGCRVTFQVLSRHGARYPTSSKKYSALIEATOKNATAPKGYAFKTYN 120
 DB 61 saispdpvgcrvtfqvlshrhgaryptsskksalsalieatknatafkgayafkty 120
 QY 121 YTGADDLTFPGQWNSGKIFRYRYKALARKIVFVRASGSDRVIAAEKFEQFQA 180
 DB 121 ytgaddltfpgqwnsgkifryrykalkarkivfvrasgsdrviaaekefegfqa 180
 QY 181 KLADPGANPHQASPVNVIPEAGYNNLTDLHGLCTAFESLGDVEANFTAVFAPPIR 240
 DB 181 kladpganphqaspvniipeagynntldhglctafeeslgdveanftavfappir 240
 QY 241 ARLEAHLPGVNLDEDDVNLMDMCPDFTVARTSDATQLSFFCDLFTHDWQYDYLQSLG 300
 DB 241 arleahlpvgvnldeddvnlmdmcpdftvartsdatlqspfcldfthdewiqdyqlslg 300
 QY 301 KYGYGAGNPLGPAQGVFNELIARLTSPVODHTSTNHTLDSNATPLNATLVADFS 360
 DB 301 kygygagnplgpaqgvfneliarltspvqdhstnhtlidsnpatplnatlyadfs 360
 QY 361 HDNTMVSIFPAGLYNGTKPLSTTSVESIETPDGYAASVTVPFAARAYVEMQCEAKEP 420
 DB 361 hdntmvsifalgngtkplsttsvesieetdgyaswtvpfaarayvemmqceakep 420
 QY 421 LVRVLNDRVPLHGCV 438

Db 421 lvrvlndrvplhgcv 438
 RESULT 5
 AAY69569
 ID AAY69569 standard; Protein; 467 AA.
 XX
 AC AAY69569;
 XX
 DT 19-APR-2000 (first entry)
 XX
 DE Mutant phytase-10, phytase-10-thermo[3]-Q50T-K91A.
 XX
 KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
 KW thermostable; animal feed; monogastric animal; phytate phosphorus;
 KW phosphate availability; consensus; mutant; mutain.
 XX
 OS Aspergillus terreus 9A1.
 OS Aspergillus terreus cbs16.46.
 OS Aspergillus niger var. awamori.
 OS Aspergillus niger str. NRRL3135.
 OS Aspergillus fumigatus ATCC13073.
 OS Aspergillus fumigatus ATCC32722.
 OS Aspergillus fumigatus ATCC58128.
 OS Aspergillus fumigatus ATCC26906.
 OS Aspergillus fumigatus ATCC32239.
 OS Emerlicella nidulans.
 OS Talaromyces thermophilus ATCC20186.
 OS Myceliophthora thermophila.
 OS Paxillus involutus NN005693.
 OS Trametes pubescens NN9343.
 OS Agrocybe pediades NN009289.
 OS Peniophora lycii NN006113.
 OS Thermomyces lanuginosa.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..26
 FT /note= "Phytase signal peptide from Aspergillus terreus
 FT cbs16.46"
 FT Protein 27..467
 FT /note= "Mature phytase-10-thermo[3]-Q50T-K91A"
 XX
 PN EP969089-A1.
 XX
 PD 05-JAN-2000.
 XX
 PF 23-JUN-1999; 99EP-0111949.
 XX
 PR 29-JUN-1998; 98EP-0111960.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Brugger R, Lehmann M, Wyss M;
 XX
 DR WPI; 2000-099429/09.
 XX
 PT New stabilised enzyme formulation, useful for feed compositions for
 PT monogastric animals -
 XX
 PS Example 5; Fig 19; 101pp; English.
 XX
 CC The invention relates to a novel stabilised dry or liquid enzyme
 CC formulation, comprising phytase (myo-inositol hexakisphosphate
 CC phosphohydrolase) and one or more stabilising agents including
 CC xyloitol or ribitol; polyethylene glycols with a molecular weight of 600
 CC to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
 CC glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
 CC The stabilised phytase formulation is used in a method for preparing a
 CC feed composition for monogastric animals (e.g., pigs, poultry) and
 CC provides a monogastric animal with its dietary requirements of
 CC phosphorus. Although a large amount of phosphate is present in animal

CC feed in the form of phytate phosphorus, monogastric animals are unable
 CC to utilise this form of phosphate, resulting in the addition of extra
 CC phosphate to the feed of such animals. Phytase enhances the nutritional
 CC value of plant material without the need for adding additional phosphate
 CC to the feed. The level of phosphate pollution in the environment is
 CC reduced by adding phytase to animal feed, as the animal can make use of
 CC the inorganic phosphate liberated from phytate phosphorus using the
 CC enzyme. The phytase formulation of the invention has an improved
 CC thermostability and can therefore remain stable during long-term storage
 CC and can withstand feed processing methods such as extrusion, expansion
 CC and pelleting. The present sequence represents a mutant phytase-10
 CC consensus sequence, phytase-10-thermo[3]-Q50T-K91A, which has a
 CC temperature optimum and melting point 4 degrees Celsius higher than that
 CC of phytase-10 (AAV69566). Its specific activity with phytate as a
 CC substrate is also strongly increased.

XX Sequence 467 AA;

Query Match 99.0%; Score 2285; DB 21; Length 467;
 Best Local Similarity 98.9%; Pred. No. 2.4e-221;
 Matches 433; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGTVVLLSTATLFGSTGALGRGNHSCDVTGQYQCFPEISHLWGOYSPFFSLADE 60
 DB 1 mgvfvllsialtfgstgaltgrgnshscdvtggyqcfpeishlwgtyspffslade 60
 QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKYSALIEAIQKNATAFKGYAFKLYN 120
 DB 61 saispdvpkgrvtfvqvlshrhgaryptssaskaysalialqknatafkgyafklytn 120
 QY 121 YTLGADDLTPFGQOVMNSGKIFRYRYKALARKIYPFVRASGSDRVIASAEKFIQGFOSA 180
 DB 121 ytlgaddltpfgeqgmnsqikfyrrykalarkivpfiragsdrviasaeekfiqgfosa 180
 QY 181 KLADPGANPHQASPVINVIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
 DB 181 kladpganphqaspvinvipegagynntldhglctafeeseldgddveanftavfappir 240
 QY 241 ARLEAHLPGVNLTDDEVNLMDCPDTVARTSDATQLSPPCDLTFHDEWIDYDYLQSLG 300
 DB 241 arleahlpvnltdedvnlmdcpdvtartsdatsqlspcdlftdhewidydyqlslg 300
 QY 301 KYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
 DB 301 kygygagmplpaqgvgfvneliarlthspvqdhstnthtlidsnpatfplnatlyadfs 360
 QY 361 HDNTMWSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAKEP 420
 DB 361 hdnmtwsiffalglyngtkplsttsvesieetdgyaswtvfaarayvemmqceakep 420
 QY 421 LVRVLVNDRVVPLHGGCV 438
 DB 421 lvrvlvndrvvplhgcgv 438

RESULT 6
 AAB20533
 ID AAB20533 standard; Protein; 467 AA.
 XX
 AC AAB20533;
 XX
 DT 05-DEC-2000 (first entry)
 XX
 DE Consensus phytase 10 thermo 5 Q50T protein SEQ ID NO:95.
 XX

KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.
 OS Synthetic.

XX WO200043503-A1.
 XX 27-JUL-2000.
 XX 21-JAN-2000; 2000WO-DK00025.
 XX 22-JAN-1999; 99DK-0000092.
 XX 21-SEP-1999; 99DK-0001340.
 XX (NOVO) NOVO NORDISK AS.
 XX Lehmann M;
 XX WPI; 2000-491161/43.
 XX N-PSDB; AAA73292.

Novel phytases with improved properties such as temperature stability,
 pH stability and substrate specificity, for use in pharmaceuticals and
 compound foods and feeds -

Disclosure; Fig 24a-c; 240pp; English.

The present invention describes improved phytases, preferably with
 increased thermostability, and methods for producing them. The methods
 can be used for producing phytases with improved properties e.g.
 temperature stability, pH stability, pH profile, temperature profile,
 specific activity, substrate specificity, substrate cleavage pattern,
 substrate binding, position specificity, the velocity and level of
 release of phosphate from corn, reaction rate, phytate degradation rate,
 and end level of released phosphate. The phytases can be used to produce
 pharmaceutical compositions or compound food or feeds. The feed can be
 used to reduce levels of phytate in animal manure, by converting it
 into lower inositol phosphates and/or inositol and inorganic phosphate.
 The present sequence represents a phytase sequence from the present
 invention.

XX Sequence 467 AA;

Query Match 98.8%; Score 2279; DB 21; Length 467;
 Best Local Similarity 98.6%; Pred. No. 9.5e-221;
 Matches 432; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGTVVLLSTATLFGSTGALGRGNHSCDVTGQYQCFPEISHLWGOYSPFFSLADE 60
 DB 1 mgvfvllsialtfgstgaltgrgnshscdvtggyqcfpeishlwgtyspffslade 60
 QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKYSALIEAIQKNATAFKGYAFKLYN 120
 DB 61 saispdvpkgrvtfvqvlshrhgaryptssaskaysalialqknatafkgyafklytn 120
 QY 121 YTLGADDLTPFGQOVMNSGKIFRYRYKALARKIYPFVRASGSDRVIASAEKFIQGFOSA 180
 DB 121 ytlgaddltpfgeqgmnsqikfyrrykalarkivpfiragsdrviasaeekfiqgfosa 180
 QY 181 KLADPGANPHQASPVINVIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
 DB 181 kladpganphqaspvinvipegagynntldhglctafeeseldgddveanftavfappir 240
 QY 241 ARLEAHLPGVNLTDDEVNLMDCPDTVARTSDATQLSPPCDLTFHDEWIDYDYLQSLG 300
 DB 241 arleahlpvnltdedvnlmdcpdvtartsdatsqlspcdlftdhewidydyqlslg 300
 QY 301 KYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
 DB 301 kygygagmplpaqgvgfvneliarlthspvqdhstnthtlidsnpatfplnatlyadfs 360
 QY 361 HDNTMWSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAKEP 420
 DB 361 hdnmtwsiffalglyngtkplsttsvesieetdgyaswtvfaarayvemmqceakep 420
 QY 421 LVRVLVNDRVVPLHGGCV 438

Db 421 lvrvlndrvvplhgca 438
|||||

RESULT 7
AAB20534
ID AAB20534 standard; Protein; 467 AA.

XX AC AAB20534;

XX DT 05-DEC-2000 (first entry)

XX DE Consensus phytase 10 thermo 5 Q50T K91A protein SEQ ID NO:97.

XX KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
XX KW temperature stability; pH profile; temperature profile; reaction rate;
XX KW specific activity; substrate specificity; substrate cleavage pattern;
XX KW substrate binding; position specificity; phytate degradation rate;
XX KW food; feed; phytate; manure.

XX OS Synthetic.

XX PN WO200043503-A1.

XX PD 27-JUL-2000.

XX PF 21-JAN-2000; 2000WO-DK00025.

XX PR 22-JAN-1999; 99DK-0000092.

XX PR 21-SEP-1999; 99DK-0001340.

XX PA (NOVO) NOVO NORDISK AS.

XX PI Lehmann M;

XX DR WPI; 2000-491161/43.

XX DR N-PSDB; AAA73293.

XX PT Novel phytases with improved properties such as temperature stability,
XX PT pH stability and substrate specificity, for use in pharmaceuticals and
XX PT compound foods and feeds -

XX PS Disclosure; Fig 25a-c; 240pp; English.

XX CC The present invention describes improved phytases, preferably with
XX CC increased thermostability, and methods for producing them. The methods
XX CC can be used for producing phytases with improved properties e.g.
XX CC temperature stability, pH stability, pH profile, temperature profile,
XX CC specific activity, substrate specificity, substrate cleavage pattern,
XX CC substrate binding, position specificity, the velocity and level of
XX CC release of phosphate from corn, reaction rate, phytate degradation rate,
XX CC and end level of released phosphate. The phytases can be used to produce
XX CC pharmaceutical compositions or compound food or feeds. The feed can be
XX CC used to reduce levels of phytate in animal manure, by converting it
XX CC into lower inositol phosphates and/or inositol and inorganic phosphate.
XX CC The present sequence represents a phytase sequence from the present
XX CC invention.

XX SQ Sequence 467 AA;

Query Match 98.5%; Score 2273; DB 21; Length 467;

Best Local Similarity 98.4%; Pred. NO. 3.8e-220;

Matches 431; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSCTALGPRGNSHSCDVGQYQCPETISHLWCQYSPFESLAD 60

Db 1 mgyfvvllsiatlfgstgctalgprgnsctdvggycfpelsnlwgtysprfslad 60

QY 61 SAISDPVPRGCRVTFVQVLSRHGARYPTSSSKYSALIEATQKNATAFKGYAFKTYN 120

Db 61 saispdpvprgcrvtfvqlsrhgaryptssaskysalialqknatafkgyafkty 120

QY 121 YTLGADDLTPFGQOMVNSGIKFRYKALARKIVPFVRASGSDRVIASAEKFIQFQSA 180
|||||
Db 121 ytlgaddltpfgeqmvnsgikfrrykalkarkivpfirasgsdrviasaekfiqfqa 180
QY 181 KLADPGANPHQASPVINVIPEGAGYNNVLDHGLCTAFESSELGDDVEANFTAVFAPP 240
|||||
Db 181 kladpganphqaspvinvipegagynntldhglctafeestlgddveanftavfapp 240
QY 241 ARLEAHLPGVNLTDDEVNLMDCPFDVTARTSDATQLSPFCDLFTHDWIOYDYLSLG 300
|||||
Db 241 arleahlpgvnltdedvnlmdcmcpfdvtartsdacqlspfcldfhdewigydyqlslg 300
QY 301 KYGYGAGNPLGPAQGVGFVNLIELIARLTHSPVQDHTSTNHTLDSNPATPLNATLYADFS 360
|||||
Db 301 kygygagnpplgpaqgvgfvnliarlthspvqdhstnhtldsnpatplnatlyadfs 360
QY 361 HDNMTWSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAKEP 420
|||||
Db 361 hdnmtwsiffalglyngtkplsttsvesieetdgyaswtvpfaarayvemmqceakep 420
QY 421 LVRVLYNDRVVPPLHGCGV 438
|||||
Db 421 lvrvlndrvvplhgca 438

RESULT 8

AAB20531

ID AAB20531 standard; Protein; 467 AA.

XX AC AAB20531;

XX DT 05-DEC-2000 (first entry)

XX DE Consensus phytase 3 thermo 11 Q50T protein SEQ ID NO:91.

XX KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
XX KW temperature stability; pH profile; temperature profile; reaction rate;
XX KW specific activity; substrate specificity; substrate cleavage pattern;
XX KW substrate binding; position specificity; phytate degradation rate;
XX KW food; feed; phytate; manure.

XX OS Synthetic.

XX PN WO200043503-A1.

XX PD 27-JUL-2000.

XX PF 21-JAN-2000; 2000WO-DK00025.

XX PR 22-JAN-1999; 99DK-0000092.

XX PR 21-SEP-1999; 99DK-0001340.

XX PA (NOVO) NOVO NORDISK AS.

XX PI Lehmann M;

XX DR WPI; 2000-491161/43.

XX DR N-PSDB; AAA73290.

XX PT Novel phytases with improved properties such as temperature stability,
XX PT pH stability and substrate specificity, for use in pharmaceuticals and
XX PT compound foods and feeds -

XX PS Disclosure; Fig 22a-c; 240pp; English.

XX CC The present invention describes improved phytases, preferably with
XX CC increased thermostability, and methods for producing them. The methods
XX CC can be used for producing phytases with improved properties e.g.
XX CC temperature stability, pH stability, pH profile, temperature profile,
XX CC specific activity, substrate specificity, substrate cleavage pattern,
XX CC substrate binding, position specificity, the velocity and level of
XX CC release of phosphate from corn, reaction rate, phytate degradation rate,
XX CC and end level of released phosphate. The phytases can be used to produce

CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.
 CC The present sequence represents a phytase sequence from the present
 CC invention.

XX SQ Sequence 467 AA;

Query Match 95.2%; Score 2196; DB 21; Length 467;
 Best Local Similarity 94.5%; Pred. No. 2.2e-212;
 Matches 415; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MGVEVLLSTATLFGSTGALGRGNSHSCDVTGQYQCFPEISHLWGOYSPFFSLADE 60
 Db 1 mgvfvllsatiifgtsatlgprgnschscdvtggyqcfpeishlwgytspysfslade 60
 QY 61 SAISPDVPKGRVTFVOVLSRGARVPTSSKYSKYSALIEAOKNATAFKGYAFKLTYN 120
 Db 61 saispdvpkgrvtfvqlsrhgarvptsskskaysallieaigknatafkgyafikltn 120
 QY 121 YTLGADDLTPFGEQOMVNSGIFRYKALARKIVPFVRASGSDRVIASAEKIEGFQSA 180
 Db 121 ytlgaddltpfgenqmvnsgikfrrykalarkivpfirassgdrviasaekiefqfqa 180
 QY 181 KLADPGANPHQASPVINVIIEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPT 240
 Db 181 kladpgsqhqpaspvlnviiepgsgynntldhglctafedstlgddveanftalfapair 240
 QY 241 ARLEAHLPGVNLTDVNNLMDCPDFTVARTSDATQLSPPCDLFTHDEWIQYDYLQSLG 300
 Db 241 arleahlpgvnltdedvnylmdcpfdftvartsdatselspfcalfthdewiqdyylqslg 300
 QY 301 KYGYGAGNPLGPAQGVGFVNLIELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
 Db 301 kygygagnpplgpaqgvgfaneliarlthspvqgdhtstnhtldsnpatfplnatlyadfs 360
 QY 361 HDNTMWSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420
 Db 361 hdntmisiffalglyngtkplsttsvesieetdgyaswtvpfaarayvemmqcqaekp 420
 QY 421 LVRVLVNDRVPLHGGCV 438
 Db 421 lvrvlvndrvvplhgcav 438

RESULT 9

AAB20532
 ID AAB20532 standard; Protein; 467 AA.

AC AAB20532;

DT 05-DEC-2000 (first entry)

XX Consensus phytase 3 thermo 11 Q50T K91A protein SEQ ID NO:93.

DE Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.

OS Synthetic.

XX WO200043503-A1.

PN 27-JUL-2000.

XX 21-JAN-2000; 2000WO-DK000025.

XX 22-JAN-1999; 99DK-0000092.

PR 21-SEP-1999; 99DK-0001340.

XX

PA (NOVO) NOVO NORDISK AS.

XX Lehmann M;

XX WPI; 2000-491161/43.

DR N-PSDB; AAA73291.

XX Novel phytases with improved properties such as temperature stability,
 PT pH stability and substrate specificity, for use in pharmaceuticals and
 PT compound foods and feeds -

XX Disclosure; Fig 23a-c; 240pp; English.

XX The present invention describes improved phytases, preferably with
 CC increased thermostability, and methods for producing them. The methods
 CC can be used for producing phytases with improved properties e.g.
 CC temperature stability, pH stability, pH profile, temperature profile,
 CC specific activity, substrate specificity, substrate cleavage pattern,
 CC substrate binding, position specificity, the velocity and level of
 CC release of phosphate from corn, reaction rate, phytate degradation rate,
 CC and end level of released phosphate. The phytases can be used to produce
 CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.
 CC The present sequence represents a phytase sequence from the present
 CC invention.

XX SQ Sequence 467 AA;

Query Match 94.9%; Score 2190; DB 21; Length 467;
 Best Local Similarity 94.5%; Pred. No. 8.8e-212;
 Matches 414; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MGVEVLLSTATLFGSTGALGRGNSHSCDVTGQYQCFPEISHLWGOYSPFFSLADE 60
 Db 1 mgvfvllsatiifgtsatlgprgnschscdvtggyqcfpeishlwgytspysfslade 60
 QY 61 SAISPDVPKGRVTFVOVLSRGARVPTSSKYSKYSALIEAOKNATAFKGYAFKLTYN 120
 Db 61 saispdvpkgrvtfvqlsrhgarvptsskskaysallieaigknatafkgyafikltn 120
 QY 121 YTLGADDLTPFGEQOMVNSGIFRYKALARKIVPFVRASGSDRVIASAEKIEGFQSA 180
 Db 121 ytlgaddltpfgenqmvnsgikfrrykalarkivpfirassgdrviasaekiefqfqa 180
 QY 181 KLADPGANPHQASPVINVIIEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPT 240
 Db 181 kladpgsqhqpaspvlnviiepgsgynntldhglctafedstlgddveanftalfapair 240
 QY 241 ARLEAHLPGVNLTDVNNLMDCPDFTVARTSDATQLSPPCDLFTHDEWIQYDYLQSLG 300
 Db 241 arleahlpgvnltdedvnylmdcpfdftvartsdatselspfcalfthdewiqdyylqslg 300
 QY 301 KYGYGAGNPLGPAQGVGFVNLIELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
 Db 301 kygygagnpplgpaqgvgfaneliarlthspvqgdhtstnhtldsnpatfplnatlyadfs 360
 QY 361 HDNTMWSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420
 Db 361 hdntmisiffalglyngtkplsttsvesieetdgyaswtvpfaarayvemmqcqaekp 420
 QY 421 LVRVLVNDRVPLHGGCV 438
 Db 421 lvrvlvndrvvplhgcav 438

RESULT 10

AAY43169

ID AAY43169 standard; Protein; 467 AA.

XX AAY43169;

XX

DT 06-JAN-2000 (first entry)
 XX Consensus phytase-1-thermo(8)-Q50T-K91A protein sequence.
 XX Phytase; animal feed preparation; thermostable phytase; transgenic plant;
 KW consensus sequence.
 XX Synthetic.
 PN WO9949380-A1.
 XX 30-SEP-1999.
 XX 22-MAR-1999; 99WO-DK00154.
 XX 23-MAR-1998; 98DK-0000407.
 PR 19-JUN-1998; 98DK-0000806.
 PR 18-SEP-1998; 98DK-0001176.
 PR 22-JAN-1999; 99DK-0000091.
 PR 22-JAN-1999; 99DK-0000093.
 XX (NOVO) NOVO-NORDISK AS.
 PA Petersen S;
 XX WPI: 1999-591030/50.
 DR N-PSDB; AAZ31520.
 XX Preparing animal feed using a thermostable phytase -
 PT Example 3; Fig 9; 7lpp; English.
 XX This sequence represents the consensus phytase-1-thermo(8)-Q50T-K91A.
 CC The invention relates to a process for preparing animal feed by
 CC agglomerating feed ingredients with a thermostable phytase, which is
 CC added before or during agglomeration. The thermostable phytase is useful
 CC for expression in transgenic plants. These plants are useful in the
 CC preparation of animal feed itself. The thermostable phytase allows animal
 CC feed to be produced more efficiently, in addition to improved
 CC phytase-expressing transgenic plants. These plants provide a feed
 CC ingredient and a feed additive (phytase) simultaneously.
 XX Sequence 467 AA;

Query Match 94.7%; Score 2185; DB 20; Length 467;
 Best Local Similarity 94.3%; Pred. No. 2.8e-211;
 Matches 413; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTGQYQCPEISHLWGOYSPFFSLADE 60
 DB 1 mgvfvlslatlfgstsgtalprgnshscdvtggyqcfpeishlwgtyspyfslade 60
 QY 61 SAISDPVPGCRVTFQVLSRHGARYPTSSKSKYKSAIEIAIKNATAFKGYAFLKTYN 120
 DB 61 saispdpdcrcvtftvqlsrhgarpytssaskysaieialqknatafkgyaflkty 120
 QY 121 YTLGADDLTPFGEQWNSGKFKYRYKALARKIVPVRASGSDRVITASAEKFTIEGQSA 180
 DB 121 ytlgaddltpfgeqwnsgkfkryrykalkarkivpvrasgsdrvitasaeakftiegfsa 180
 QY 181 KIADPGANPHQASPVINIIPEGAGYNNLTDLGLCTAFEESELGDDVEANFTAVFAPPIR 240
 DB 181 kiadpgsqhgaspvinlipegsgynnltdhgtctafeselselgddveanftalfapair 240
 QY 241 ARLEAHLPGVNLTDENVNLMDCPFDFVARTSDATQLSPCDLTFHDEWTOYDYLQSLG 300
 DB 241 arleahlpgvnltdenvylmndcpcfdfvartsdatsdateisfcalthdewiqdyqlsg 300
 QY 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNNHTLDSNPATFPLNATLYADFS 360
 DB 301 kyygyaggnplgpaqgvfaneliarlthspvqdhstnnhtldsnpatfplnatlyadfs 360

QY 361 HDNTMVSIFFFALGLYNGTKPLSTTSVESIEETDGYAASWTVFFAARAYVEMMQCAKEP 420
 DB 361 hdnmtvisiffalgllyngtkplsttsvesieetdgyaswtvfaarayvemmqcakep 420
 QY 421 LVRVLVNDVRVPLHGCV 438
 DB 421 lvrvlvndrvrplhgcv 438

RESULT 11
 AAB20526
 ID AAB20526 standard; Protein; 467 AA.
 XX AC AAB20526;
 XX 05-DEC-2000 (first entry)
 XX Consensus phytase 1 thermo 8 q50t, k91a protein SEQ ID NO:29.
 DE Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 XX Temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.
 XX Synthetic.
 OS WO2000043503-A1.
 PN 27-JUL-2000.
 XX 21-JAN-2000; 2000WO-DK00025.
 XX 22-JAN-1999; 99DK-0000092.
 PR 21-SEP-1999; 99DK-0001340.
 XX (NOVO) NOVO NORDISK AS.
 PA Lehmann M;
 PI WPI: 2000-491161/43.
 DR N-PSDB; AAA73233.

Novel phytases with improved properties such as temperature stability,
 pH stability and substrate specificity, for use in pharmaceuticals and
 compound foods and feeds -
 Claim 5; Fig 7a-c; 240pp; English.
 The present invention describes improved phytases, preferably with
 increased thermostability, and methods for producing them. The methods
 can be used for producing phytases with improved properties e.g.
 temperature stability, pH stability, pH profile, temperature profile,
 specific activity, substrate specificity, substrate cleavage pattern,
 substrate binding, position specificity, the velocity and level of
 release of phosphate from corn, reaction rate, phytate degradation rate,
 and level of released phosphate. The phytases can be used to produce
 pharmaceutical compositions or compound food or feeds. The feed can be
 used to reduce levels of phytate in animal manure, by converting it
 into lower inositol phosphates and/or inositol and inorganic phosphate.
 The present sequence represents a phytase sequence from the present
 invention.

Sequence 467 AA;

Query Match 94.7%; Score 2185; DB 21; Length 467;

Best Local Similarity 94.3%; Pred. No. 2.8e-211;

Matches 413; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTGQYQCPEISHLWGOYSPFFSLADE 60
 DB 1 mgvfvlslatlfgstsgtalprgnshscdvtggyqcfpeishlwgtyspyfslade 60

```

QY 61 SAISPDVPGKCRVTFVOVLSRHGARYPTSSKSKYSALIEAIQKNATAFKGYAFLKTYN 120
DB 61 saispdvpddcrvtfvqlsrhrgaryptssaskaysalialqknatafkgyafllktyN 120
QY 121 YTLGADDLTPFGQOMVNSGKIFRYRYKALARKIVPFVRASGSDRVIASAEKFIQFQSA 180
DB 121 ytlgaddltpfgengmqvnsqkifryrykalarKivpfirasgsdrviasaekfieqfqsA 180
QY 181 KLADPGANPHQASPVINVIIPGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPTR 240
DB 181 kladpgsqhgaspvinviipegsgynntldhgtctafedseiseldgddveanftalfapair 240
QY 241 ARLEAHLPGVNLTDDEVDVNLMDPCPDTVARTSDATQLSPFCDLTFHDEWIOYDYLSQSLG 300
DB 241 arleahlpgvntldedvvylnmdcpfdvtartsdatselpfcalfhdewiqdydylsqslg 300
QY 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 kygygagnpplgpaqvgfaneliarlthspvqdhstnhtldsnpatfplnatlyadfs 360
QY 361 HDNTMWSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAKEP 420
DB 361 hdntmisiffalglngtkplsttsvesieetdgyaswtvpfaarayvemmqcqaekp 420
QY 421 LVRVLNDRVVPVPLHGCGV 438
DB 421 lvrvlndrvvpplhgcaV 438

RESULT 12
AAV69568
ID AAV69568 standard; protein; 467 AA.
XX AC AAV69568;
XX DT 19-APR-2000 (first entry)
XX DE Mutant phytase-1, phytase-1-thermo[8]-Q50T-K91A.
XX KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
KW thermostable; animal feed; monogastric animal; phytate phosphorus;
KW phosphate availability; consensus; mutant; mutein.
XX OS Aspergillus terreus 9A1.
XX OS Aspergillus terreus cbs16.46.
XX OS Aspergillus niger var. awamori.
XX OS Aspergillus niger T213.
XX OS Aspergillus niger str. NRRL3135.
XX OS Aspergillus fumigatus ATCC13073.
XX OS Aspergillus fumigatus ATCC32722.
XX OS Aspergillus fumigatus ATCC58128.
XX OS Aspergillus fumigatus ATCC26906.
XX OS Aspergillus fumigatus ATCC32239.
XX OS Emericella nidulans.
XX OS Talaromyces thermophilus ATCC20186.
XX OS Myceliophthora thermophila.
XX OS Synthetic.
XX FH Key
XX FT Location/Qualifiers
XX FT 1..26
XX FT /note= "Phytase signal peptide from Aspergillus terreus
XX FT cbs16.46"
XX FT
XX FT Protein
XX FT 27..467
XX FT /note= "Mature phytase-1-thermo[8]-Q50T-K91A"
XX
XX EP969089-A1.
XX
XX PD 05-JAN-2000.
XX
XX PF 23-JUN-1999; 99EP-0111949.
XX
XX PR 29-JUN-1998; 98EP-0111960.

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XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PI Brugger R, Lehmann M, Wyss M;
XX
XX WPI; 2000-099429/09.
DR N-PSDB; AAZ59715.
XX
PT New stabilized enzyme formulation, useful for feed compositions for
PT monogastric animals -
PS
PS Example 5; Fig 19; 101pp; English.
XX
XX The invention relates to a novel stabilised dry or liquid enzyme
XX formulation, comprising phytase (myo-inositol hexakisphosphate
XX phosphohydrolase) and one or more stabilising agents including
XX xylitol or ribitol; polyethylene glycols with a molecular weight of 600
XX to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
XX glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
XX The stabilised phytase formulation is used in a method for preparing a
XX feed composition for monogastric animals (e.g., pigs, poultry) and
XX provides a monogastric animal with its dietary requirements of
XX phosphorus. Although a large amount of phosphate is present in animal
XX feed in the form of phytate phosphorus, monogastric animals are unable
XX to utilise this form of phosphate, resulting in the addition of extra
XX phosphate to the feed of such animals. Phytase enhances the nutritional
XX value of plant material without the need for adding additional phosphate
XX to the feed. The level of phosphate pollution in the environment is
XX reduced by adding phytase to animal feed, as the animal can make use of
XX the inorganic phosphate liberated from phytate phosphorus using the
XX enzyme. The phytase formulation of the invention has an improved
XX thermostability and can therefore remain stable during long-term storage
XX and can withstand feed processing methods such as extrusion, expansion
XX and pelleting. The present sequence represents a mutant phytase-1
XX consensus sequence, phytase-1-thermo[8]-Q50T-K91A, which has a
XX temperature optimum and melting point 7 degrees Celsius higher than that
XX of phytase-1 (AAV69558).
XX
XX Sequence 467 AA;

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Query Match 94.7%; Score 2185; DB 21; Length 467;
Best Local Similarity 94.3%; Pred. No. 2.8e-211;
Matches 413; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLPGSTSGTALGPRGNHSCDVTVDGGYQCPPEISHLWGQYSPFFSLADE 60
DB 1 mgvfvlisiatlfgstsgtalgprgnshscdvtvggvcfpeishlwgtyspyfslade 60
QY 61 SAISPDVPGKCRVTFVOVLSRHGARYPTSSKSKYSALIEAIQKNATAFKGYAFLKTYN 120
DB 61 saispdvpddcrvtfvqlsrhrgaryptssaskaysalialqknatafkgyafllktyN 120
QY 121 YTLGADDLTPFGQOMVNSGKIFRYRYKALARKIVPFVRASGSDRVIASAEKFIQFQSA 180
DB 121 ytlgaddltpfgengmqvnsqkifryrykalarKivpfirasgsdrviasaekfieqfqsA 180
QY 181 KLADPGANPHQASPVINVIIPGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPTR 240
DB 181 kladpgsqhgaspvinviipegsgynntldhgtctafedseiseldgddveanftalfapair 240
QY 241 ARLEAHLPGVNLTDDEVDVNLMDPCPDTVARTSDATQLSPFCDLTFHDEWIOYDYLSQSLG 300
DB 241 arleahlpgvntldedvvylnmdcpfdvtartsdatselpfcalfhdewiqdydylsqslg 300
QY 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 kygygagnpplgpaqvgfaneliarlthspvqdhstnhtldsnpatfplnatlyadfs 360
QY 361 HDNTMWSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAKEP 420
DB 361 hdntmisiffalglngtkplsttsvesieetdgyaswtvpfaarayvemmqcqaekp 420

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QY 421 LVRVLNDRVPLHCGGV 438
 Db 421 lvrvlndrvrplhgcav 438

RESULT 13

AAB20523
 ID AAB20523 standard; Protein; 441 AA.

XX AAB20523;

DT 05-DEC-2000 (first entry)

XX Consensus phytase 10 (Fcp10) SEQ ID NO:24.

XX Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
 KW temperature stability; pH profile; temperature profile; reaction rate;
 KW specific activity; substrate specificity; substrate cleavage pattern;
 KW substrate binding; position specificity; phytate degradation rate;
 KW food; feed; phytate; manure.

XX Synthetic.

XX WO200043503-A1.

XX 27-JUL-2000.

PF 21-JAN-2000; 2000WO-DK00025.

PR 22-JAN-1999; 99DK-0000092.

PR 21-SEP-1999; 99DK-0001340.

XX (NOVO) NOVO NORDISK AS.

PI Lehmann M;

XX WPI; 2000-491161/43.

XX Novel phytases with improved properties such as temperature stability,
 PT pH stability and substrate specificity, for use in pharmaceuticals and
 PT compound foods and feeds -

PS Example 2; Fig 4a-d; 240pp; English.

XX The present invention describes improved phytases, preferably with
 CC increased thermostability, and methods for producing them. The methods
 CC can be used for producing phytases with improved properties e.g.
 CC temperature stability, pH stability, pH profile, temperature profile,
 CC specific activity, substrate specificity, substrate cleavage pattern,
 CC substrate binding, position specificity, the velocity and level of
 CC release of phosphate from corn, reaction rate, phytate degradation rate,
 CC and end level of released phosphate. The phytases can be used to produce
 CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.
 CC The present sequence represents a phytase sequence from the present
 CC invention.

XX Sequence 441 AA;

Query Match 94.5%; Score 2181; DB 21; Length 441;
 Best Local Similarity 100.0%; Pred. No. 6.5e-211;
 Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 NSHSCDVTGQYQCFPEISHLWGQYSPFFSLADESATSPDVPKGRVTFVQVLSRHGARY 86

Db 1 nshscdvtggyqcfpeishlwgyspfisladesaisspdkgrvtfvqvlshrghary 60

QY 87 PTSSKSKYSALIEAOKNAFAKGYAFKTYNTYTGADDLTPFGQOVMNSGKRYRR 146

Db 61 ptsskksyaliealqknaafkgyafktyntygaddltpfgeqvmnsgikryrr 120

QY 147 YKALARKIVFVRASGSDRVIAAEKFIIEGFSQAKLADPGANPHQASPVINVIIEGAGY 206
 Db 121 ykalarakiyfvrasgsdrviaseakfiiegfsakladpganphqaspvinviliegagy 180
 QY 207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPRIARLEAHLPGVNLTDDEVNLMDCPF 266
 Db 181 nntldhglctafeeselgddveanftavfappriarleahlpvgnltdevvnlmdmcpf 240
 QY 267 DTIVARTSDATQLSPPFCDLFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIAR 326
 Db 241 dtivartsdatqslspfcldlthdewiqydlqslgkygygagnpigpagvgvfnvneliar 300
 QY 327 LTHSPVQDHTSTNNHTLDSNPATFPPLNATLYADFSDHNTMVSIFFAFGLYNGTKPLSTTSV 386
 Db 301 lthspvqdgthstnhtlidsnpatfplnatlyadfsdntmvsiffalglyngtkplsttsv 360
 QY 387 ESTEEDTGAASWTVPFAARAYVEMMQCEAEKEPLVRVLNDRVPLHCGGV 438
 Db 361 esleetdgyaaswtvpfaarayvemmqceakeplvrvlndrvrplhgcgv 412

RESULT 14

AAW93380
 ID AAW93380 standard; Protein; 467 AA.

XX AAW93380;

DT 11-JUN-1999 (first entry)

XX Fungal phytase protein consensus DNA.

XX Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food;
 KW feed additive; variant; mutein; feed; pharmaceutical.

OS Fungi.

OS Synthetic.

XX EP897985-A2.

PD 24-FEB-1999.

XX 15-JUL-1998; 98EP-0113176.

XX 24-JUL-1997; 97EP-0112688.

XX (HOFF) HOFFMANN LA ROCHE AG F.

PI Lehmann M;

XX WPI; 1999-134647/12.

DR N-PSDB; AAX23022.

XX Preparation of a consensus protein, especially a phytase - using
 PT programs to compare evolutionary similarity of sequences

PS Claim 8; Fig 2; 30pp; English.

XX This invention describes a novel process for the preparation of a
 CC consensus protein. The specific example given in the specification is
 CC that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses
 CC phytase to valuable feed additives, with a fully defined amino acid
 CC sequence given in the specification, or variant or mutein. The method is
 CC useful for improving protein properties by altering their sequence. The
 CC consensus protein and mutein are useful in food, feed or pharmaceutical
 CC compositions. This sequence represents the consensus phytase protein used
 CC in the method of the invention.

XX Sequence 467 AA;

Query Match 93.4%; Score 2154; DB 20; Length 467;

Best Local Similarity 92.9%; Pred. No. 3.7e-208;

Matches 407; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

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QY 1 MGFWVLLSIATLFGSTGATLGRGNSHCDTVDGQCFCPEISHLWGQSPFSLADE 60
Db 1 mgfwvllsiatlfgstgatalgrgnshcdtvdggyqcfpeishlwgygspysfslade 60
QY 61 SAISPDVPGRCRVTFQVLSRHGARYPTSSKSKYSALIEAIQKNATAPKGYAFLKTYN 120
Db 61 saispdvpgdcrvtfqvlsrhgaryptsskkskysalsalieaiqknatafkgyafikty 120
QY 121 YTLGADDLTPFGQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQFQSA 180
Db 121 ytlgaddltpfgqomvnsqkifryrykalkarkivpvrasgsdrviasaeekfiqfqs 180
QY 181 KLADPGANPHQASPVINVIPEGAGYNNLTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 kladpgsqhqsapvidviipegsgyntltdhgtctafedseigddveanftalfapair 240
QY 241 ARLEAHLPGVNLTDDEVNLMDCPFDVTARTSDATQLSPPCDFTHDEWIQDYLSLG 300
Db 241 arleadlpgvntldedvynlmdcpfdvtartsdatselppcalftdhedwrydylyslg 300
QY 301 KYGYGAGNPLGPAQGVFVNLIELARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db 301 kygygagnpplgpaqgvgnlielarlthspvqdhstntnhtldsnpatfplnatlyadfs 360
QY 361 HDNTMVSIFPAGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAKEP 420
Db 361 hdntmsiffalglyngtaplsttsvesieetdgyaswtvpfgarayvemmqcqaekp 420
QY 421 LVRVLVNDRVVPLHGCGV 438
Db 421 lvrvlvndrvvplhgcv 438

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RESULT 15
AAB20515
ID AAB20515 standard; Protein; 467 AA.
XX
AC AAB20515;
XX
DT 05-DEC-2000 (first entry)
XX
DE Consensus phytase SEQ ID NO:16.
XX
KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW temperature stability; pH profile; temperature profile; reaction rate;
KW specific activity; substrate specificity; substrate cleavage pattern;
KW substrate binding; position specificity; phytate degradation rate;
KW food; feed; phytate; manure.
XX
OS Synthetic.
XX
XX WO200043503-A1.
XX
XX PD 27-JUL-2000.
XX
XX PF 21-JAN-2000; 2000WO-DK00025.
XX
XX PR 22-JAN-1999; 99DK-0000092.
XX
XX PR 21-SEP-1999; 99DK-0001340.
XX
XX PA (NOVO ) NOVO NORDISK AS.
XX
XX PI Lehmann M;
XX
XX DR WPI; 2000-491161/43.
XX
XX DR N-PSDB; AAA73231.
XX
XX PT Novel phytases with improved properties such as temperature stability,
XX PT pH stability and substrate specificity, for use in pharmaceuticals and
XX PT compound foods and feeds -
XX
XX PS Example 9; Fig 2a-c; 240pp; English.

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XX The present invention describes improved phytases, preferably with
CC increased thermostability, and methods for producing them. The methods
CC can be used for producing phytases with improved properties e.g.
CC temperature stability, pH stability, pH profile, temperature profile,
CC specific activity, substrate specificity, substrate cleavage pattern,
CC substrate binding, position specificity, the velocity and level of
CC release of phosphate from corn, reaction rate, phytate degradation rate,
CC and end level of released phosphate. The phytases can be used to produce
CC pharmaceutical compositions or compound food or feeds. The feed can be
CC used to reduce levels of phytate in animal manure, by converting it
CC into lower inositol phosphates and/or inositol and inorganic phosphate.
CC The present sequence represents a phytase sequence from the present
CC invention..
XX
SQ Sequence 467 AA;
Query Match 93.4%; Score 2154; DB 21; Length 467;
Best Local Similarity 92.9%; Pred. No. 3.7e-208;
Matches 407; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
QY 1 MGFWVLLSIATLFGSTGATLGRGNSHCDTVDGQCFCPEISHLWGQSPFSLADE 60
Db 1 mgfwvllsiatlfgstgatalgrgnshcdtvdggyqcfpeishlwgygspysfslade 60
QY 61 SAISPDVPGRCRVTFQVLSRHGARYPTSSKSKYSALIEAIQKNATAPKGYAFLKTYN 120
Db 61 saispdvpgdcrvtfqvlsrhgaryptsskkskysalsalieaiqknatafkgyafikty 120
QY 121 YTLGADDLTPFGQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQFQSA 180
Db 121 ytlgaddltpfgqomvnsqkifryrykalkarkivpvrasgsdrviasaeekfiqfqs 180
QY 181 KLADPGANPHQASPVINVIPEGAGYNNLTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 kladpgsqhqsapvidviipegsgyntltdhgtctafedseigddveanftalfapair 240
QY 241 ARLEAHLPGVNLTDDEVNLMDCPFDVTARTSDATQLSPPCDFTHDEWIQDYLSLG 300
Db 241 arleadlpgvntldedvynlmdcpfdvtartsdatselppcalftdhedwrydylyslg 300
QY 301 KYGYGAGNPLGPAQGVFVNLIELARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db 301 kygygagnpplgpaqgvgnlielarlthspvqdhstntnhtldsnpatfplnatlyadfs 360
QY 361 HDNTMVSIFPAGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAKEP 420
Db 361 hdntmsiffalglyngtaplsttsvesieetdgyaswtvpfgarayvemmqcqaekp 420
QY 421 LVRVLVNDRVVPLHGCGV 438
Db 421 lvrvlvndrvvplhgcv 438

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Search completed: October 16, 2001, 17:49:16
Job time: 20965 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: October 16, 2001, 17:56:19 ; Search time 197.94 Seconds
(without alignments)
292.763 Million cell updates/sec
Title: US-09-488-265-26_COPY_1_438
Perfect score: 2307
Sequence: 1 MGVEVLLSLATLFGSTSGT.....EPLVRLVNDVRVPLHCGGV 438
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL16.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_unclassified.*
 - 13: sp_vertebrate.*
 - 14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1770	76.7	465	3 O00092	O00092 aspergillus
2	1731	75.0	467	3 Q9UWZ7	Q9UWZ7 aspergillus
3	1726	74.8	467	3 Q93838	Q93838 aspergillus
4	1712	74.2	467	3 Q9HEQ0	Q9HEQ0 aspergillus
5	1681	72.9	466	3 O00100	O00100 aspergillus
6	1629	70.6	466	3 O00085	O00085 aspergillus
7	1580	68.5	466	3 O00096	O00096 talaromyces
8	1263.5	54.8	487	3 O00107	O00107 thielavia h
9	337	14.6	469	3 Q9Y846	Q9Y846 kluyveromyc
10	325.5	14.1	442	3 Q74677	Q74677 pichia angu
11	299	13.0	463	3 O60172	O60172 schizosacch
12	204	8.8	451	11 Q35217	Q35217 rattus norv
13	196	8.5	481	11 Q922L6	Q922L6 mus musculu
14	195	8.5	487	4 Q9UNW1	Q9UNW1 homo sapien
15	194	8.4	487	4 Q9UGA3	Q9UGA3 homo sapien
16	192	8.3	487	4 Q9VW72	Q9VW72 drosophila
17	191	8.3	460	5 Q96421	Q96421 drosophila
18	182.5	7.9	467	5 Q96421	Q96421 drosophila
19	179	7.8	449	13 Q92170	Q92170 gallus gall

20	169.5	7.3	453	5 O96420	O96420 drosophila
21	168.5	7.3	453	5 O9W438	O9W438 drosophila
22	167.5	7.3	198	3 Q9UTX1	Q9UTX1 schizosacch
23	147.5	6.4	468	10 O04509	O04509 arabidopsis
24	144	6.2	274	11 Q9JJD5	Q9JJD5 mus musculu
25	130	5.6	449	5 Q19076	Q19076 caenorhabdi
26	119.5	5.2	513	2 Q46334	Q46334 comamonas t
27	119	5.2	380	5 Q22525	Q22525 caenorhabdi
28	116	5.0	374	11 Q9JMG5	Q9JMG5 mus musculu
29	115	5.0	381	11 Q90XG5	Q90XG5 mus musculu
30	108.5	4.7	513	2 Q24719	Q24719 comamonas t
31	108	4.7	827	2 Q47871	Q47871 eubacterium
32	106.5	4.6	730	5 Q20826	Q20826 caenorhabdi
33	105.5	4.6	381	11 Q9QXH7	Q9QXH7 mus musculu
34	105	4.6	354	5 Q19709	Q19709 caenorhabdi
35	104	4.5	499	3 P87212	P87212 polyporacea
36	102.5	4.4	1013	14 Q9TILX9	Q9TILX9 retroperito
37	101.5	4.4	602	2 Q9KSA0	Q9KSA0 erwinia chr
38	101	4.4	516	5 Q25327	Q25327 leishmania
39	100.5	4.4	1225	5 Q20330	Q20330 caenorhabdi
40	100	4.3	438	5 Q9VAD0	Q9VAD0 drosophila
41	100	4.3	452	5 Q19175	Q19175 caenorhabdi
42	100	4.3	683	5 Q00838	Q00838 leishmania
43	100	4.3	707	5 Q00839	Q00839 leishmania
44	99.5	4.3	763	2 Q9R6Y7	Q9R6Y7 anabaena sp
45	98.5	4.3	642	1 O26446	O26446 methanobact

ALIGNMENTS

RESULT 1
O00092
ID O00092 PRELIMINARY; PRT; 465 AA.
AC O00092;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DE 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
DE 3-PHTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-
DE PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
DE PHOSPHOHYDROLASE A).
GN PHVA.
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-37.
RC STRAIN=ATCC 34625;
RX MEDLINE=97288063; PubMed=9143104;
RA Pasamontes L., Haiker M., Wyss M., Tessier M., van Loon A.P.G.M.;
RT "Gene cloning, purification, and characterization of a heat-stable
RT Phytase from the fungus Aspergillus fumigatus.";
RL Appl. Environ. Microbiol. 63:1696-1700(1997).
CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC FROM PHYTATE.
CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
CC INSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MISCELLANEOUS: SHOWS HIGH ACTIVITY WITH 4-NITROPHENYL PHOSPHATE AT
CC A PH RANGE OF 3 TO 5 AND WITH PHYTIC ACID AT A PH RANGE OF 2.5 TO
CC 7.5. IT IS ABLE TO WITHSTAND TEMPERATURES UP TO 100 DEGREES
CC CELSIUS OVER A PERIOD OF 20 MIN, WITH A LOSS OF ONLY 10% OF THE
CC INITIAL ENZYMACTIC ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC EMBL; U59804; AAB96872.1; -;
DR HSP; P34752; 1IHP.
DR InterPro; IPR000560; -;
DR Pfam; PF00328; acid.phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00776; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 26

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FT CHAIN 27 465 3-PHYTASE A.
FT ACT_SITE 81 81 REQUIRED FOR BINDING SUBSTRATE (BY
FT ACT_SITE 82 82 SIMILARITY).
FT ACT_SITE 359 359 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT DISULFID 30 39 PROTON DONOR (BY SIMILARITY).
FT DISULFID 70 412 BY SIMILARITY.
FT DISULFID 213 463 BY SIMILARITY.
FT DISULFID 262 280 BY SIMILARITY.
FT DISULFID 434 442 BY SIMILARITY.
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 465 AA; 50836 MW; 86FC1D9058C9B2C9 CRC64;

Query Match 76.7%; Score 1770; DB 3; Length 465;
Best Local Similarity 76.9%; Pred. No. 4.4e-137;
Matches 337; Conservative 33; Mismatches 66; Indels 2; Gaps 2;

QY 1 MGVFVLLSTATLFGSTGALGRGNSHSCDVTGQYOCFPEISHLWGOYSPFFSLADE 60
DB 1 MVTLLLSAAYLLSRVSAAPSSAG-SKSCDVTDLGQYOCSPATSHLWGOYSPFFSLEDE 59
61 SAISPDVPKGCRTVFOVLSRHGARYPTSSKKYSALIEAIQKNATAFKGYAFUKTYN 120
60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKKYSKYLKLTVAIQANATDFKGFALUKTYN 119
121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQEGFQA 180
120 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQEGFQA 179
181 KLADPGANPHQASPVINVIPEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
180 KLADPGAT-NRAAPATSVIPESETFNNTLDHGCTKFEASQLGDEVAANFTALFAPDIR 238
241 ARLEAHLPGVNLTDDEVDVNLMDMCPDFTVARTSDATQLSPPCDLFTHDEWIQYDYLQSLG 300
239 ARAEKHLPGVNLTDDEVDVNLMDMCPDFTVARTSDATQLSPPCDLFTHDEWIQYDYLQSLG 298
301 KYCYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFES 360
299 KYCYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFES 358
361 HDNTWVSIFTFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420
359 HDNSMVSIFTFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCKSEKEP 418
421 LVRVLVNDRVVPLHGCGV 438
419 LVRALINDRVVPLHGCDV 436

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RESULT 2
Q90U27 PRELIMINARY; PRT; 467 AA.
AC Q90U27
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE MYO-INOSITOL HEXAPHOSPHATE PHOSPHOHYDROLASE PRECURSOR (EC 3.1.3.8).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Hongning W., Qi W., Jing X.;
RT "PCR, cloning and characterization of the phytase (phyA) gene of

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RT Aspergillus niger (China Strain).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218813; AAF25481.1; -.
DR HSSP; P34752; 1IHP.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Signal; Lyase; Hydrolase.
FT SIGNAL 1 19 POTENTIAL.
SQ SEQUENCE 467 AA; 51029 MW; F4300A8F165EBF92 CRC64;

Query Match 75.0%; Score 1731; DB 3; Length 467;
Best Local Similarity 74.0%; Pred. No. 7.1e-134;
Matches 324; Conservative 45; Mismatches 69; Indels 0; Gaps 0;

QY 1 MGVFVLLSTATLFGSTGALGRGNSHSCDVTGQYOCFPEISHLWGOYSPFFSLADE 60
DB 1 MGVSALLPLYLGSVTSGLAVPASRNQCTDIVDQGYQCFSETSHLWGOYAPFFSLANE 60
61 SAISPDVPKGCRTVFOVLSRHGARYPTSSKKYSALIEAIQKNATAFKGYAFUKTYN 120
61 SAISPDVPAGCRVTFQAQVLSRHGARYPTDSKKYSALIEIQKNATTFDGKYAFUKTYN 120
121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQEGFQA 180
121 YSLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPVRASGSDRVIASAEKFIQEGFQA 180
181 KLADPGANPHQASPVINVIPEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
181 KLADPGAGGSSPKRIDVIVISEASSNNTLDPGTCTVFEDSELADAVEANFTAVFAPPIR 240
241 ARLEAHLPGVNLTDDEVDVNLMDMCPDFTVARTSDATQLSPPCDLFTHDEWIQYDYLQSLG 300
241 QLENDLSGVSILTEVTYLMDCSFDTISTSTVDTKLSPPCDLFTHDEWIQYDYLQSLG 300
301 KYCYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFES 360
301 KYCYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFES 360
361 HDNTWVSIFTFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420
361 HDNGIISILFALGLYNGTKPLSTTVQNTITQDGFSSAWTVPFAARAYVEMMOCEAKEP 420
421 LVRVLVNDRVVPLHGCGV 438
421 LVRVLVNDRVVPLHGCPV 438

RESULT 3
O93838 PRELIMINARY; PRT; 467 AA.
AC O93838
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE PHYTASE.
GN PHYA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
RT "Phytase having high-affinity for phytic acid."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB022700; CAB19824.1; -.
DR HSSP; P34752; 1IHP.
DR InterPro; IPR000560; -.
DR Pfam; PF00328; acid_phosphat; 1.

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DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.
 SQ SEQUENCE 467 AA; 51028 MW; 7A38AD543EDC265C CRC64;

Query Match 74.8%; Score 1726; DB 3; Length 467;
 Best Local Similarity 73.1%; Pred. No. 1.8e-133;
 Matches 320; Conservative 49; Mismatches 69; Indels 0; Gaps 0;

QY 1 MGVSFVLLSIATLFGSTGALPGRNHSCDTPDGGYQCFPEISHLWGQYSPFFSLADE 60
 DB 1 MGVSFVLLSIATLFGSTGALPGRNHSCDTPDGGYQCFPEISHLWGQYSPFFSLADE 60
 QY 61 SAISPDVPGKCRVTFVQVLSRHGARYPTSSKSKYSALIEAIOKNATAFKGYAFKLTYN 120
 DB 61 SAISPDVPGKCRVTFVQVLSRHGARYPTSSKSKYSALIEAIOKNATAFKGYAFKLTYN 120
 QY 121 YTLGADDLTPFGEQOQVNSGKIFRYRYKALARKIVFVRASGSDRVIASAEKFEQFOSA 180
 DB 121 YTLGADDLTPFGEQOQVNSGKIFRYRYKALARKIVFVRASGSDRVIASAEKFEQFOSA 180
 QY 181 KLADPGANPHQASPVINVIPEGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
 DB 181 KLADPGANPHQASPVINVIPEGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
 QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPDFTVARTSDATQLSPCDFLTHDEWIQDYQLSLG 300
 DB 241 ARLEAHLPGVNLTDDEVVNLMDMCPDFTVARTSDATQLSPCDFLTHDEWIQDYQLSLG 300
 QY 301 KYYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADF 360
 DB 301 KYYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADF 360
 QY 361 HDNTMVSIFFGALGNGTKPLSTTSVESIETDGYAASWTPFAARAYVEMMOCEAKEP 420
 DB 361 HDNTMVSIFFGALGNGTKPLSTTSVESIETDGYAASWTPFAARAYVEMMOCEAKEP 420
 QY 421 LVRVLNDRVVPVHLGGCV 438
 DB 421 LVRVLNDRVVPVHLGGCV 438

RESULT 4

Q9HEO0 PRELIMINARY; PRT; 467 AA.
 AC Q9HEO0;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE PHYTASE.
 OS Aspergillus ficuum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 RN NCBI_TaxID=5058;
 RP SEQUENCE FROM N.A.
 RA Zhang L., Ap L., Wang Y., Yuan X.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY013315; AAG40885.1; -;
 SQ SEQUENCE 467 AA; 51012 MW; 3F69AD543C0B565B CRC64;

Query Match 74.2%; Score 1712; DB 3; Length 467;
 Best Local Similarity 72.8%; Pred. No. 2.6e-132;
 Matches 319; Conservative 49; Mismatches 70; Indels 0; Gaps 0;

QY 1 MGVSFVLLSIATLFGSTGALPGRNHSCDTPDGGYQCFPEISHLWGQYSPFFSLADE 60
 DB 1 MGVSFVLLSIATLFGSTGALPGRNHSCDTPDGGYQCFPEISHLWGQYSPFFSLADE 60
 QY 61 SAISPDVPGKCRVTFVQVLSRHGARYPTSSKSKYSALIEAIOKNATAFKGYAFKLTYN 120
 DB 61 SAISPDVPGKCRVTFVQVLSRHGARYPTSSKSKYSALIEAIOKNATAFKGYAFKLTYN 120

QY 121 YTLGADDLTPFGEQOQVNSGKIFRYRYKALARKIVFVRASGSDRVIASAEKFEQFOSA 180
 DB 121 YTLGADDLTPFGEQOQVNSGKIFRYRYKALARKIVFVRASGSDRVIASAEKFEQFOSA 180
 QY 181 KLADPGANPHQASPVINVIPEGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
 DB 181 KLADPGANPHQASPVINVIPEGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
 QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPDFTVARTSDATQLSPCDFLTHDEWIQDYQLSLG 300
 DB 241 ARLEAHLPGVNLTDDEVVNLMDMCPDFTVARTSDATQLSPCDFLTHDEWIQDYQLSLG 300
 QY 301 KYYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADF 360
 DB 301 KYYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADF 360
 QY 361 HDNTMVSIFFGALGNGTKPLSTTSVESIETDGYAASWTPFAARAYVEMMOCEAKEP 420
 DB 361 HDNTMVSIFFGALGNGTKPLSTTSVESIETDGYAASWTPFAARAYVEMMOCEAKEP 420
 QY 421 LVRVLNDRVVPVHLGGCV 438
 DB 421 LVRVLNDRVVPVHLGGCV 438

RESULT 5

Q00100 PRELIMINARY; PRT; 466 AA.
 AC Q00100;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DE 3-PHYTASE PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-
 DE PHOSPHOHYDROLASE) (3 PHYTASE) (MYO-INOSITOL HEXAKISPHOSPHATE
 DE PHOSPHOHYDROLASE).
 OS Aspergillus terreus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 RN NCBI_TaxID=33178;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS 116.46;
 RA Pasamontes L., Haiker M., Henriquez Huecas M., Hug D., Mitchell D.B.,
 RA Broger C., van Loon A.P.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O -> D-MYO-
 CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL; U60412; AAB58465.1; -;
 DR HSP; P34752; IHP.
 DR InterPro; IPR000560; -;
 DR Pfam; PF00328; acid_phosphat; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 466 3-PHYTASE.
 FT ACT_SITE 82 82 REQUIRED FOR BINDING SUBSTRATE (BY
 FT ACT_SITE 83 83 SIMILARITY).
 FT ACT_SITE 361 361 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT DISULFID 31 40 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 71 414 BY SIMILARITY.
 FT DISULFID 215 465 BY SIMILARITY.
 FT DISULFID 264 282 BY SIMILARITY.
 FT DISULFID 436 444 BY SIMILARITY.
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).

[illegible]

AC 000096;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-
 DE PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
 GN PHYA.
 OS Talaromyces thermophilus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Talaromyces.
 OX NCBI_TaxID=28565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 20186;
 RA MEDLINE=98007872; PubMed=9349716;
 RA Pasanontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
 RA van Loon A.P.G.M.;
 RT "Cloning of the phytases from *Emmericella nidulans* and the thermophilic
 RT fungus *Talaromyces thermophilus*.";
 RL Biochim. Biophys. Acta 1353:217-223(1997).
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
 CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
 CC -!- MISCELLANEOUS: HAS POTENTIAL AS FOOD AND FEED ADDITIVE. IT CAN
 CC FACILITATE THE DEGRADATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS
 CC USED AS FOOD FOR MONOGASTRIC ANIMALS.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL: U59802; AAB96873.1; -.
 DR HSSP: P34752; LIHP.
 DR InterPro: IPR000560; -.
 DR Pfam: PF00328; acid_phosphat_1;
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1;
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 14 POTENTIAL.
 FT CHAIN 15 466 3-PHYTASE A.
 FT ACT_SITE 79 79 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 357 357 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 28 37 BY SIMILARITY.
 FT DISULFID 68 410 BY SIMILARITY.
 FT DISULFID 212 461 BY SIMILARITY.
 FT DISULFID 261 278 BY SIMILARITY.
 FT DISULFID 432 440 BY SIMILARITY.
 FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 466 AA; 51450 MW; FC4575B521A5C929 CRC64;

Query Match 68.5%; Score 1580; DB 3; Length 466;
 Best Local Similarity 68.4%; Pred. No. 1.8e-121;
 Matches 301; Conservative 44; Mismatches 87; Indels 8; Gaps 3;
 QY 1 MGCVFVLLS--IATLFGSTGALPGRNHSCDVTGQYCFEISHLWQYSPFFSLA 58
 DB 1 MSLLLLVSLGGLVALYVSRN-----PHVDSHCNTVEGQYCFEISHWQYSPFFSLA 55
 QY 59 DESAISPDPKGRVTFVOVLSRHGARYPTSSKKYSALIEATOKNATAPKGYAFKLT 118
 DB 56 DQSEISPDPONCKITFVOLLRSRGARYPTSSKLTSLRSQIRKQATATKGYAFKLT 115
 QY 119 NYNTLGADLLPFGQQMVNSGKIFRYRKALKARKIVPFVFRASGSDRVIAAEKFIQFQ 178
 DB 116 YRYQLGANDLPFGENQIQIGIKFYNHYSKLARNVFPVRCSDRVIAAGRLFIEGFQ 175
 QY 179 SAKLADPCANPHQSPVNIIPGAGYNNNTLDHGLCTAFEESELGDDVEANFTAVFAPP 238
 DB 176 SAKVLDPHSDKHDAPPTINVIIEGPGSYNNNTLDGCPVFEDSSGGHDAQEKFAKQAPA 235

QY 239 IRARLEAHLPGVNLTDDEYVNLMDMCPDFTVARTSDATOLSPFCDLTFHDEWQIYDQLS 298
 DB 236 ILEKIKDHLPGVDLAVSDVPYLMDLCPETLARNHTDI-LSPFCALSTQEQWQAYDYQSS 294
 QY 299 LGKYGYGAGNPLGPAQGVGFVNELIARLTHSPVDHTSTNHTLDSNPATPLNATLYAD 358
 DB 295 LGKYGGNGGGNPLGPAQGVGFVNELIARLTHSPVDHTSTNHTLDSNPATPLNATLYAD 354
 QY 359 FSHDNTMVSIFALGLYNGTRPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEK 418
 DB 355 FSHDNTMTSIFAALGLYNGTAKLSTTEIKSIEETDGYAASWTVPFGGRAYTEMQCDSDS 414
 QY 419 EPLVRLVNDRVVPLHGCV 438
 DB 415 EPLVRLVNDRVVPLHGCEV 434

RESULT 8
 000107 PRELIMINARY; PRT: 487 AA.
 ID 000107;
 AC 000107;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE 3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-
 DE PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
 GN PHYA.
 OS Thielavia heterothallica.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Chaetomiaceae; Thielavia.
 OX NCBI_TaxID=78579;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9717792; PubMed=9025298;
 RA Mitchell D.B., Vogel K., Weimann B.J., Pasanontes L.,
 RA van Loon A.P.G.M.;
 RT "The phytase subfamily of histidine acid phosphatases: isolation of
 RT genes for two novel phytases from the fungi *Aspergillus terreus* and
 RT *Myceliophthora thermophila*.";
 RL Microbiology 143:245-252(1997).
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
 CC FROM PHYTATE.
 CC -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
 CC INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- MISCELLANEOUS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF
 CC 3.5 TO 8.5, WITH MAXIMAL ACTIVITY BETWEEN PH 5.5 AND 6.0. ALSO
 CC ACCEPT 4-NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA
 CC SHIFTED TO MORE ACIDIC PH VALUES.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL: U59806; AAB52508.1; -.
 DR HSSP: P34752; LIHP.
 DR InterPro: IPR000560; -.
 DR Pfam: PF00328; acid_phosphat_1;
 DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1;
 DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
 KW Hydrolase; Glycoprotein; Signal.
 FT SIGNAL 1 75 POTENTIAL.
 FT CHAIN 7 487 3-PHYTASE A.
 FT DOMAIN 267 270 POLY-SER.
 FT DOMAIN 423 433 POLY-GLY.
 FT ACT_SITE 75 75 REQUIRED FOR BINDING SUBSTRATE (BY
 FT SIMILARITY).
 FT ACT_SITE 76 76 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE 368 368 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 26 35 BY SIMILARITY.
 FT DISULFID 64 421 BY SIMILARITY.
 FT DISULFID 208 485 BY SIMILARITY.
 FT DISULFID 260 289 BY SIMILARITY.
 FT DISULFID 456 464 BY SIMILARITY.
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 487 AA; 52537 MW; 97D10EDC83D051DB CRC64;

Query Match 54.8%; Score 1263.5; DB 3; Length 487;
Best Local Similarity 54.6%; Pred. No. 1.8e-95;
Matches 255; Conservative 52; Mismatches 117; Indels 43; Gaps 6;

QY 1 MGVEVVL---LSTATLFGSTGALPGRNHSCDVTGQYCFPEISHLMGQYSPFFSL 57
DB 4 LGWVWVWGLAASL-----QSESRPCDTPDLGFCQGTATSHFWGQYSPYFSV 52

QY 58 ADESAISDPVPGKCRVTFVQVLSRHGARYPTSSKKYSALIEAIQKNATAFKGYAFLK 117
DB 53 PSE--LDASIPDDCEVTFQAQLSRHGARYPTSSKKYSALIEAIQKNATAFKGYAFLK 110

QY 118 TYNYTLGADDLPGFQOQVNSGIRFYRYKALARKIVPFVRAAGSDRVASAEKFIQGF 177
DB 111 TYDTTLGADDLPGFQOQVNSGIRFYRYKALARKIVPFVRAAGSDRVASAEKFIQGF 170

QY 178 QSAKLADPGANPHQASPVINVIPEGAGYNNLTDLHGLCTAFEE---SELGDDVEANFTAV 234
DB 171 HSALLADRGSTVRPTLPYDMVVIPTAGANNLTHNDLCTAFEEGPGYSTIGDDAQDTYLS 230

QY 235 FAPPIRLEAHLPGVNLDEVDVNLMDMCPDFTVARTS-----DATQLSPDCD 283
DB 231 FAGPITARNANLPGANLTDADTVMLDLCFETVAUSSSDPATADAGGNGRPLSPPCR 290

QY 284 LFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVFNVELIARLTHSPVQDHTSTNHTLD 343
DB 291 LFSESEWRAVDYLOSKYKYGCGNPLGTPQGVFNVELIARLTHSPVQDHTSTNHTLD 350

QY 344 SNPATPLNATLYADFSHONTMVSIFPALLGLYNGTKPLSTTSVESTTEEDGTAASWTFV 403
DB 351 GDRPTPLGRPLYADFSHONTMVSIFPALLGLYNGTKPLSTTSVESTTEEDGTAASWTFV 410

QY 404 AARAYVEMQC-----EAEKPLVRLVNDVRVPLHGC 437
DB 411 AARIYVENMRKSGGGGGGEGGEGRQKDEWVRVRLVNDVRVPLHGC 457

RESULT 9
QY9846 PRELIMINARY; PRT; 469 AA.

AC QY9846
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACID PHOSPHATASE (EC 3.1.3.2).
GN PHO3.
OS Kluyveromyces lactis (Yeast).
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2360/7;
RA San Vicente A., Ferminan E., Dominguez A.;
RT "Isolation and characterization of KIPHO3 a gene encoding a
RT constitutive acid phosphatase from Kluyveromyces lactis."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RR EMBL: AJ007502; CAB46490.1;
DR HSSP; P34755; IQFX
DR InterPro; IPR000560;
DR Pfam; PF00328; acid.phosphat; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW Hydrolase.
FT CHAIN
SQ SEQUENCE 17 469 ACID PHOSPHATASE.
Query Match 17.4%; Score 325.5; DB 3; Length 442;
Best Local Similarity 26.3%; Pred. No. 1.6e-18;
Matches 104; Conservative 59; Mismatches 150; Indels 83; Gaps 16;

Query Match 14.6%; Score 337; DB 3; Length 469;
Best Local Similarity 25.5%; Pred. No. 2e-19;
Matches 118; Conservative 64; Mismatches 196; Indels 84; Gaps 16;

QY 7 LLSTATLFGSTGALPGRNHSCDVTGQYCF-----PEISHLMGQYSPFFSLA 58
DB 1 MLSTLLSLLSGTHAAPISK-----DNGTVCYALNSSTTDESFPPLNGOGPHYDYP 53

QY 59 DESAISDPVPGKCRVTFVQVLSRHGARYPTSSKKYSALIEAIQKNATAFKGYAFLK 118
DB 54 QSGIPEVDPQCTVEHVQMLARHGERYPPTASKGLWALWDLKKEFGQYNGPMVEFND 113

QY 119 YNY-----TLGADDLT-----PF-GEQMVNSGIRFYRYKALARKIVPFVRAAGSD 164
DB 114 YEFFVSNTKYFDQLTSTNDVPSNPYAGAKTAQHLGKYIAYNYGDLFSDSNP-VFTSSG 172

QY 165 RVIASAEKFIQGFQASAKLADPGANPHQASPVINV-----IIPEG--AGYNNLTDLHGLCTA 217
DB 173 RVHOTAKYVWSLEEE-----LDIOLDLQIIQENETSGANSLTPADSCWT 217

QY 218 FEESLGDVDEANFTAVFAPPIRLEAHLPGVNLT---DEDVNLMDMCPDFTVARTSDA 275
DB 218 Y-NGDLGDEYENATLPLTDIKNRWKKNSNLNLTLEHDDIELLDVWCAFEINVKGSSA 276

QY 276 TQLSPFCDLFTHEWIOYDYLQSLGKYGYGAGNPLGPAQGVFNVELIARLTHSPVQDH 335
DB 277 V-----CDLPERNDLVAYSYYANNFVRGAGNPMNPICGLVNNASYNLLTQADELDN 331

QY 336 TSTNHTLDSNPATPLNATLYADFSHONTMVSIFPALLGLY-NGTKPLSTTSVESTTEEDG 394
DB 332 -----KWLVSFSDHTDIOQFTSALGLDNG---VTEYSLDQVDFQNI 370

QY 395 YAASTVTPFAARAYVEMQC-----EAEKPLVRLVNDVRVPLHGC 436
DB 371 QQLSWTTPGGRIFTEKLC--GNASYRYIINDVIIIPVPGC 410

RESULT 10
QY4677 PRELIMINARY; PRT; 442 AA.

AC QY4677
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE REPRESSIBLE ACID PHOSPHATASE (EC 3.1.3.2).
GN PHO1.
OS Pichia angusta (Yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4905;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC34438;
RX MEDLINE=98386672; PubMed=9720203;
RA Phongdara A., Merckelbach A., Keup P., Gellissen G., Hollenberg C.P.;
RT "Cloning and characterization of the gene encoding a repressible acid
RT phosphatase (PHO1) from the methylotrophic yeast Hansenula
RT polymorpha."
RL Appl. Microbiol. Biotechnol. 50:77-84(1998).
RR EMBL: AF051161; AAC62537.1;
DR HSSP; P34755; IQFX
DR InterPro; IPR000560;
DR Pfam; PF00328; acid.phosphat; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 442 AA; 49370 MW; 7087D91A85B05C31 CRC64;

Query Match 14.1%; Score 325.5; DB 3; Length 442;
Best Local Similarity 26.3%; Pred. No. 1.6e-18;
Matches 104; Conservative 59; Mismatches 150; Indels 83; Gaps 16;

QY 66 DVPKGRVTFVQVLSRHGARYPTSSKKYSALIEAIQKNATAFKGYAFLKTYNTLG 124

Db 55 DTPPHCEIQALFMRHGERFPTKSSQKQYKFKYDKLKRANITDYKGLAFIEDLEYFVP 114
 QY 125 ADDLTTPGEOQVNSGI-----YRYKAL--ARKIVPVRASGSDRVIASAEKFI 174
 Db 115 DSNYELETTRGYSGLLNFAKFGYRLRYDSLVDTSSVLPFAAAS--EDRVVDTRASFG 173
 QY 175 EGFQSAKLADPGANPHQASPVINVI-----IPEGAGYNNITLDHGLC-----TAFESEELGDD 226
 Db 174 RGFFGPDYA-----TSCSIQVNETDTSGKANALITKDN--CPTYNSSYDYSFGDE 223
 QY 227 V-----EAFNTAVAPPTRARLEAHLPGVNTDDEVNLMDCPFDVARTSDATQLSPPFGD 283
 Db 224 IFOREAD-----RLNELSPGFINITADIIITMGTYCAYETNVKGH-----SSFGD 267
 QY 284 LFTHDWDIYQVLYSLQSLGKYGYGAGNPLGPAQGVGFVNELIARLTHSPVODHTSTNHTLD 343
 Db 268 ALSREAFIALQVNDVTKFYQPGVNMGAAGVYAN----- 305
 QY 344 SNPATPL---NATLYADFSDHTMVSIFPFGALGLYNGTKPLSTTSVESIEETDGYAASWT 400
 Db 306 ---ATAKLQEDCKLWFSFSDNDLLNYITALGLITDTE-----LGTEVDVFRSKTSEL 358
 QY 401 VPPAARAYVEMMQCEAEKEPIVRLVNDVRVPLHGC 436
 Db 359 VPOGARLIIEKLNC--SDTSFVRTIINDKVPVPGC 392

RESULT 11

O60172 ID 060172 PRELIMINARY; PRT; 463 AA.
 AC O60172;
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE PROBABLE ACID PHOSPHATASE (EC 3.1.3.2).
 GN SPC2147.03C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M., Rajandream M.A., Barrell B.G., Xiang Z., Aves S.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
 CC ALCOHOL + ORTHOPHOSPHATE.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL; AL023286; CAAL18863.1; -.
 DR HSSP; P34755; 10FX.
 DR InterPro; IPR000560; -.
 DR Pfam; PF00328; acid_phosphat_1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase; Glycoprotein.
 FT ACT_SITE; 69 69 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
 FT ACT_SITE; 340 340 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 324 324 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 439 439 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 463 AA; 52758 MW; 6C41AF422C6D624A CRC64;

Query Match 13.08; Score 299; DB 3; Length 463;
 Best Local Similarity 24.7%; Pred. No. 2.6e-16;
 Matches 101; Conservative 68; Mismatches 182; Indels 58; Gaps 12;

QY 51 YSPFSLADEAISPDVPKGRVTFQVLSRHGARYPTS--SKSKKYS-----L 98

Db 43 HEPYFDGLDSA-----FPETCEIQVHLLQRHGRSNRPTGDTATDVYSSQYLNNFQEKLL 97
 QY 99 IEAIQKNATAFKGYAFLTKTYNTL---GADDLTPFGEOQVNSGIRFYRYKALARKIV 155
 Db 98 NGSPVNSYSPENPLCFIKQWTPVIDAENADQLSRGRLFLDLGRQLYRYKLFDSYV 157
 QY 156 PFRVSRASGRVIAAEKFIIEGFSQSAKLADPGANPHQASPVINVIPEG--AGYNNITLDHG 213
 Db 158 YDINTAEQERVVESAKWFTYGLFGDKMYE-----KTNFILLSEGKAAGANSLSYN 208
 QY 214 LCTAFEESEL---GDDVEANFTAVFAPPTRARLEAHL--PCVNLTDDEVNLMDCPFD 268
 Db 209 ACPVKDNFNKKNATDAHAVRNIFTEPIVNRKLAKYFDSYKLTINDVRSFLFICEYEI 268
 QY 269 VARTSDATQLSPPFGDLFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFVNELIARLT 328
 Db 269 AIKDH-----SDFCSITPSEFLNFEYDSLDQAYGGPVSEWASTLGGAYINNLA 322
 QY 329 HSPVODHTSTNHTLDSNPATFPPLNATLYADFSDHTMVSIFPFGALGLYNGTKPLSTTSVES 388
 Db 323 -----RNVTPNPFDRK-----VELAFTHDSNIIPVEAALGFFPDITPQNPLPTDK 367
 QY 389 IEETDGYAASWTVPFAARAYVEMMQCEAEKEPIVRLVNDVRVPLHGC 437
 Db 368 NIYTSOKTSFVFPAGNLITELFFC--SDSKYYVYRHLVNOQVYPLIDCG 415

RESULT 12
 O35217 ID 035217 PRELIMINARY; PRT; 451 AA.
 AC O35217;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-AUG-1999 (Tremblrel. 11, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE HEPATIC MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE (EC 3.1.3.-)
 DE (MIPP).
 GN MIPPI.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE OF 11-451 FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RC TISSUE=LIVER;
 RX MEDLINE=98028656; PubMed=9359836;
 RA Craxton A., Caffrey J.J., Burkhardt W., Safrany S.T., Shears S.B.;
 RT "Molecular cloning and expression of a rat hepatic multiple inositol
 RT polyphosphate phosphatase.";
 RL Biochem. J. 328:75-81(1997).
 RN [2]
 RP CATALYTIC ACTIVITY.
 RX MEDLINE=91358435; PubMed=1653239;
 RA Nogimori K., Hughes P.J., Glennon M.C., Hodgson M.E., Putney J.W. Jr.,
 RA Shears S.B.;
 RT "Purification of an inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase
 RT activity from rat liver and the evaluation of its substrate
 RT specificity.";
 RL J. Biol. Chem. 266:16499-16506(1991).
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INOSITOL 1,3,4,5-
 CC TETRAKISPHOSPHATE TO INOSITOL 1,4,5-TRIPHOSPHATE AND INOSITOL
 CC 1,3,4,5,6-PENTAKISPHOSPHATE TO INOSITOL 1,4,5,6-TETRAKISPHOSPHATE
 CC AND THEN TO INOSITOL 1,4,5-TRIPHOSPHATE. DEPHOSPHORYLATES
 CC INOSITOL HEXAKISPHOSPHATE WITHOUT SPECIFICITY TOWARDS A PARTICULAR
 CC PHOSPHATE GROUP.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY AND LIVER.
 CC -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
 DR EMBL; AF012714; AAC3453.1; -.
 DR InterPro; IPR000560; -.
 DR InterPro; IPR000886; -.
 DR Pfam; PF00328; acid_phosphat; 2.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.

Query Match		8.5%;	Score 195;	DB 4;	Length 487;
Best Local Similarity		21.7%;	Pred. No. 9.6e-08;		
Matches		90;	Conservative 69;	Mismatches 170;	Indels 86; Gaps 17;
QY	65 PDVPGK-CRVTFVQVLSRHGARYPTSSKSKYSALIEAIOKNATAFKGKYAFKTYNYTL	123			
Db	71 PELLEGCTPVQVALIRHGTTRYPTVKQIRKLRLHGLLQPRGSRDGGASS---TGSRDL	127			
QY	124 GA-----DDLTPEGEQMVNSGIGKIFRYRYKAL-ARKIVPFVR--ASGSDRV	166			
Db	128 GAALRDWPLWYADWMDGQVLEGRQDMRHLVALRLASLFPALFSRENYGRRLITSSKHRC	187			
QY	167 IASAEKFIIEGFSQAKLADPGANPHQAS-----PVINVIPEGAGYNTLDHGLCTAFEE	220			
Db	188 MDSSAAFLQGLW--QHYHPLGPPDVADMEFGPPTVNDKL-----MRFFDH--CEKFL-	236			
QY	221 SELGDDVEANFTAVFAPPFIRARLEAHLPG-----HVEAFKTPGEMQNLKKAATLQVPVNDLNADLIQVAF	262			
Db	237 -----TEVEKNATALY-----HVEAFKTPGEMQNLKKAATLQVPVNDLNADLIQVAF	286			
QY	263 MCPEDTAVTSDATQLSPFCDLTFHDEWIQDYIQLSLGKYYGYGAGNPLGPAQGVGVNE	322			
Db	287 TCSFDLAIKGVK-----SPWCDVFDIDDAKVEYLNDLKQYWKRGYGYTINSRSCTLFQD	342			
QY	323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMYSIFFALGLYNGTKPLS	382			
Db	343 IFQHLDKAVEQKORSQ-----PISSPVILQFGHAETLLPLSLMGYFKDKEPLT	391			
QY	383 TTSVESIEETDGYAASWTVPFAARAYVEMMOCEAEKEP-----LVRVLVNDRVVPL	433			
Db	392 AYNYKK-QMHRKFRSGLIVPYASNLIFVLYHCENAKTPKEQFRVQMLLNKVLPL	445			
RESULT 15					
ID	Q9UNW1	PRELIMINARY;	PRT;	487 AA.	
AC	Q9UNW1;				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DT	01-JUN-2000 (TrEMBLrel. 14, Last annotation update)				
DE	MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99120488; PubMed=9923613;				
RA	Caffrey J.J., Hidaka K., Matsuda M., Hirata M., Shears S.B.;				
RT	"The human and rat forms of multiple inositol polyphosphate				
RT	phosphatase: functional homology with a histidine acid phosphatase up-				
RT	regulated during endochondral ossification.";				
RL	FEBS Lett. 442:99-104(1999).				
DR	EMBL; AF084943; AAD09751.1;				
DR	InterPro; IPR000560;				
DR	InterPro; IPR000886;				
DR	Pfam; PF00328; acid_phosphat; 2.				
DR	PROSITE; PS00014; ER_TARGET; UNKNOWN_1.				
SQ	SEQUENCE 487 AA; 55051 MW; 89B8F347885B320A CRC64;				
Query Match					
Best Local Similarity		8.4%;	Score 194;	DB 4;	Length 487;
Matches		90;	Conservative 68;	Mismatches 171;	Indels 86; Gaps 17;
QY	65 PDVPGK-CRVTFVQVLSRHGARYPTSSKSKYSALIEAIOKNATAFKGKYAFKTYNYTL	123			
Db	71 PELLEGCTPVQVALIRHGTTRYPTVKQIRKLRLHGLLQPRGSRDGGASS---TGSRDL	127			
QY	124 GA-----DDLTPEGEQMVNSGIGKIFRYRYKAL-ARKIVPFVR--ASGSDRV	166			

Search completed: October 16, 2001, 17:56:20
Job time: 7524 sec

Db	128 GAALADWPLWYADWMDGQVLEGRQDMRQLALRLASLFPALFSRENYGRRLITSSKHRC	187
QY	167 IASAEKFIIEGFSQAKLADPGANPHQAS-----PVINVIPEGAGYNTLDHGLCTAFEE	220
Db	188 MDSSAFLQGLW--QHYHPLGPPDVADMEFGPPTVNDKL-----MRFFDH--CEKFL-	236
QY	221 SELGDDVEANFTAVFAPPFIRARLEAHLFG-----HVEAFKTPGEMQNLKKAATLQVPVNDLNADLIQVAF	286
Db	237 -----TEVEKNATALY-----HVEAFKTPGEMQNLKKAATLQVPVNDLNADLIQVAF	286
QY	263 MCPEDTAVTSDATQSLSPFCDLTFHDEWIQDYIQLSLGKYYGYGAGNPLGPAQGVGVNE	322
Db	287 TCSFDLAIKGVK-----SPWCDVFDIDDAKVEYLNDLKQYWKRGYGYTINSRSCTLFQD	342
QY	323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMYSIFFALGLYNGTKPLS	382
Db	343 IFQHLDKAVEQKORSQ-----PISSPVILQFGHAETLLPLSLMGYFKDKEPLT	391
QY	383 TTSVESIEETDGYAASWTVPFAARAYVEMMOCEAEKEP-----LVRVLVNDRVVPL	433
Db	392 AYNYKK-QMHRKFRSGLIVPYASNLIFVLYHCENAKTPKEQFRVQMLLNKVLPL	445

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OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 15:46:02 ; Search time 12806.7 Seconds
(without alignments)
1597.903 Million cell updates/sec

Title: US-09-488-265-25_COPY_90_1412
Perfect score: 1323
Sequence: 1 aattctcactctgtgacac.....actgggaagaattttcgt 1323

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba1.*
2: gb_ba2.*
3: gb_ba3.*
4: gb_in1.*
5: gb_in2.*
6: gb_in3.*
7: gb_om.*
8: gb_ov.*
9: gb_pat1.*
10: gb_pat2.*
11: gb_ph.*
12: gb_pl1.*
13: gb_pl2.*
14: gb_pl3.*
15: gb_pl4.*
16: em_ba1.*
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95: gb_rol2.*
96: gb_in4.*
97: gb_pr10.*
98: em_ba3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	787	59.5	1350	56	AF295325
3	613.6	46.4	1571	9	AX000634
4	613.6	46.4	1812	15	SF059804
5	606.4	45.8	1404	9	A19452
6	606.4	45.8	1404	10	I13430
7	606.4	45.8	1404	10	I33881
8	606.4	45.8	2000	13	ANPHYAG
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					AF295325 Synthetic
					AX000634 Sequence
					U59804 Aspergillus
					A19452 phytase cDN
					I13430 Sequence 33
					I33881 Sequence 19
					Z16414 A.niger phy

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9 606.4 45.8 2665 13 ASNPHYTASE
10 606.4 45.8 6756 9 A19451
11 606.4 45.8 6756 10 I13429
12 604.6 45.7 2363 9 AR018076
13 604.6 45.7 2363 9 AR051916
14 604.6 45.7 2379 9 AR053934
15 604.6 45.7 2379 13 ASNPHYTAS
16 601.4 45.5 1528 13 AF218813
17 595 45.0 1515 12 AB022700
18 593.4 44.9 1590 14 AY013315
19 590.6 44.6 1553 12 AB042805
20 580 43.8 1931 9 AX000630
21 580 43.8 1931 14 EN059803
22 561.6 42.4 1912 9 A46793
23 544.4 41.1 1845 9 AX000632
24 544.4 41.1 1845 15 TT059802
25 516 39.0 1567 9 AX000636
26 516 39.0 1770 14 ATU60412
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28 516 39.0 2327 14 ATU59805
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30 510 38.5 1584 10 AX085192
31 510 38.5 1922 10 AX085191
32 410.4 31.0 4898 10 AX085207
33 355.6 26.9 2200 9 AR031151
34 292.6 22.1 853 10 AX085213
35 278.6 21.1 860 10 AX085208
36 265.2 20.0 3995 9 A46785
37 265.2 20.0 3995 14 MTU59806
38 134.4 10.2 950 10 AX085210
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40 69.6 5.3 1404 14 SCU19789
41 64.8 4.9 5097 15 YSCH9177
42 64 4.8 1404 14 SCPH05A
43 64 4.8 1904 10 AX072908
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ALIGNMENTS

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RESULT 1
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DEFINITION Sequence 3 from Patent EP0897985.
ACCESSION AX021809
VERSION AX021809.1 GI:10045052
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 1426)
AUTHORS Lehmann, M.
TITLE Consensus phytases
JOURNAL Patent: EP 0897985-A 3 24-FEB-1999;
HOFFMANN LA ROCHE (CH)
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Best Local Similarity 96.1%; Pred. No. 0;
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Db 90 AATTCTCACTCTTGTGACACTGTGTGACGGTGGTGTACCAATGTTTCCAGAAATTTCTCAC 149

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Db 1410 GCT 1412

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AF295325 1350 bp mRNA SYN 18-OCT-2000
DEFINITION Synthetic construct phytase mRNA, complete cds.
ACCESSION AF295325
VERSION AF295325.1 GI:10732782
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1350)
AUTHORS Yang,L., Chen,Z., Bei,J., Liao,L. and Wang,X.
TITLE Synthetic sequence of phytase gene for expression in Pichia pastoris
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1350)
AUTHORS Chen,Z.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-2000) Animal Science Institute, Guangdong Academy of Agricultural Sciences, Guangzhou, Guangdong 510640, China
REFERENCE 3 (bases 1 to 1350)
AUTHORS Yang,L., Bei,J., Liao,L. and Wang,X.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-2000) Biopharmaceutical Center, Zhongshan University, Guangzhou, Guangdong 510275, China
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Best Local Similarity 74.9%; Pred. No. 9.8e-195;
Matches 985; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

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DEFINITION Aspergillus fumigatus phytase gene, complete cds.
ACCESSION U59804.1 GI:2108353
VERSION 1
KEYWORDS Aspergillus fumigatus.
SOURCE Aspergillus fumigatus.
ORGANISM Aspergillus fumigatus.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 1800)
AUTHORS Pasamontes,L., Haiker,M., Wyss,M., Tessier,M. and van Loon,A.P.
TITLE Gene cloning, purification, and characterization of a heat-stable
phytase from the fungus Aspergillus fumigatus
JOURNAL Appl. Environ. Microbiol. 63 (5), 1696-1700 (1997)
MEDLINE 97288063
REFERENCE 2 (bases 1 to 1812)
AUTHORS Pasamontes,L.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1996) Luis Pasamontes, VFCB, F. Hoffmann-La Roche
AG., Basel 4070, Switzerland
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RESULT 5
LOCUS A19452
DEFINITION phytase cDNA fragment.
ACCESSION A19452
VERSION A19452.1 GI:583195
KEYWORDS

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SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1404)
AUTHORS van Gorkom, R.F.M., van Hartingsveldt, W., van Paridon, P.A.,
Veenstra, A.E., Luiten, R.G.M. and Sellen, G.C.M.
TITLE Cloning and expression of microbial phytase
JOURNAL Patent: EP 0420358-A 41 03-APR-1991;
GIST-BROCADES N.V.
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BASE COUNT 293 a 436 c 344 g 331 t
ORIGIN

Query Match 45.8%; Score 606.4; DB 9; Length 1404;
Best Local Similarity 66.4%; Pred. No. 1.3e-147;
Matches 871; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

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LOCUS L13430 1404 bp DNA PAT 26-JUL-1995
DEFINITION Sequence 33 from patent US 5436156.
ACCESSION L13430
VERSION L13430.1 GI:910771
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Van Gorkom, R.F.M., Van Hartingsveldt, W., Van Paridon, P.A.,
Veenstra, A.E., Luiten, R.G.M. and Sellen, G.C.M.
TITLE Cloning and expression of phytase from aspergillus
JOURNAL Patent: US 5436156-A 33 25-JUL-1995;
FEATURES
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BASE COUNT 293 a 436 c 344 g 331 t

ORIGIN

Query Match 45.8%; Score 606.4; DB 10; Length 1404;
 Best Local Similarity 66.4%; Pred. No. 1.3e-147;
 Matches 871; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

QY 12 ttgtgacactgttgacggtgttaccagtgttccacagaaatttccacttggggtca 71
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LOCUS I33881 1404 bp DNA PAT 06-FEB-1997

DEFINITION Sequence 19 from patent US 5593963.

ACCESSION I33881

VERSION I33881.1 GI:1824672

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1404)

AUTHORS Van Ooijen,A.J.J., Rietveld,K., Hoekema,A., Pen,J., Sijmons,P.C. and Verwoerd,T.C.

TITLE Expression of phytae in plants

JOURNAL Patent: US 5593963-A 19 14-JAN-1997;

FEATURES

source

BASE COUNT 293 a 436 c 344 g 331 t

ORIGIN

Query Match 45.8%; Score 606.4; DB 10; Length 1404;
 Best Local Similarity 66.4%; Pred. No. 1.3e-147;
 Matches 871; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

QY 12 ttgtgacactgttgacggtgttaccagtgttccacagaaatttccacttggggtca 71

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QY	912	tccagttcaagaccacacttctactaacacacactttggactgttaacgaacttctcc	971
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VERSION	Z16414.1	GT:2392	
KEYWORDS	phyA gene.		
SOURCE	Aspergillus niger.		

ORGANISM	Aspergillus niger			
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.			
AUTHORS	1 (bases 1 to 2000) van Hartingsveldt, W., Van Zeijl, C.M.J., Harteveld, M.G., Gouka, R.J., Suykerbuyk, M.E.G., Luiten, R.G.M., Van Paridon, P.A., Selden, G.C.M., Veenstra, A.E., Van Gorcom, R.F.M. and Van Den Hondel, C.A.M.J.			
TITLE	Cloning, molecular characterization and overexpression of the phyA gene (phyA) of Aspergillus niger			
JOURNAL	Gene (1992) In press			
REFERENCE	2 (bases 1 to 2000)			
AUTHORS	van Hartingsveldt, W.			
TITLE	Direct Submission			
JOURNAL	Submitted (05-OCT-1992) Van Hartingsveldt W., TNO Medical Biological Laboratory, Lange Kleiweg 139, Rijswijk, the Netherlands			
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QY	372	ggctagaagaatgttccattcgttagaagcttctgtgtctgtacagagttattgtttctgc	431
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QY	672	taactgaactgaagaagaagttgttaactgaagacatgtgtccattcagacactgttgc	731
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Db	1121	CACGAGCACGTCGACACCAAGCTGTCCCTCTCTGTCACCTGTTACCCATGACGAATG	1180
QY	792	gattcaataagacactcttgcacatcttgggtaagtactacggtttacggtgctggttaaccc	851
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LOCUS			
DEFINITION	ASNPHYTASE 2665 bp DNA 27-APR-1993		
	Aspergillus niger myo-inositol hexaphosphate phosphohydrolyase gene, complete cds.		
ACCESSION	M94550		
VERSION	M94550.1 GI:1166520		
KEYWORDS	myo-inositol hexaphosphate phosphohydrolyase; phytase.		
SOURCE	Aspergillus niger (library: EMBL 3; NRRL 3135) DNA.		
ORGANISM	Aspergillus niger		
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Euryotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.		
REFERENCE	1 (bases 1 to 2665)		
AUTHORS	Mullaney,E.J., Gibson,D.M and Ullah,A.H.		
TITLE	Positive identification of a lambda gt11 clone containing a region of fungal phytase gene by immunoprobe and sequence verification		
JOURNAL	Appl. Microbiol. Biotechnol. 35, 611-614 (1991)		
MEDLINE	92000601		
REFERENCE	2 (bases 1 to 2665)		
AUTHORS	Mullaney,E.J.,		
TITLE	Sequence of the Aspergillus niger (flicum) phytase gene		
JOURNAL	Unpublished (1992)		
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intron	727. .828		
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BASE COUNT	633 a 808 c 574 g 650 t		
ORIGIN			

		Query Match	45.8%;	Score 606.4;	DB 13;	Length 2665;
		Best Local Similarity	66.4%;	Pred. No. 1.4e-147;		
		Matches 871;	Conservative 0;	Mismatches 441;	Indels 0;	Gaps
Qy	12	tgtgacacgttgagcgtggatgccaatgtttccacagaatttctcacctgtgggtcca	71			
Db	874	TTGCGATACGGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATCTTTGGGGTCA	933			
Qy	72	atactctccattctctctttggctgcagcaatctgtattttccacagcttcocaaagg	131			
Db	934	ATACGACCGGTTCTTCTCTTGCGAAACGAATCGGTTCATCTCCCTCGAGGTGCCCGCGG	993			

QY 132 ttgtagagttacttctggttcaagttttgtctagacacggtgtgttagatatacccaactcttc 191
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 QY 492 ccaagtttccagttattaaagttattattccagaaggtgtgtgtgtgtgtgtgtgtgtgt 551
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 QY 552 ggaacagttgtgtactgttttgaagattctgaagttgtgtgtgtgtgtgtgtgtgtgtgt 611
 Db 941 CGACCCAGGACCTGACGCTGTCTCGAGACAGCGAATTTGGCCGATACCGTTCGAAGCCAA 1000
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 DEFINITION Sequence 31 from patent US 5436156.
 ACCESSION I13429
 VERSION I13429.1 GI:910770
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 6756)
 AUTHORS Van Gorcom,R.F.M.; Van Hartingsveldt,W.; Van Paridon,P.A.;
 Veenstra,A.E.; Luiten,R.G.M. and Sellen,G.C.M.
 TITLE Cloning and expression of phytase from aspergillus
 JOURNAL Patent: US 5436156-A 31 25-JUL-1995;
 FEATURES Location/Qualifiers
 source 1..6756
 BASE COUNT 1615 a 1714 c 1715 t
 ORIGIN

Query Match 45.8%; Score 606.4; DB 10; Length 6756;
 Best Local Similarity 66.4%; Pred. No. 1.4e-147;
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QY 12 ttgtgacactgttgacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 71
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AR018076 2363 bp DNA PAT 05-DEC-1998
LOCUS
DEFINITION Sequence 7 from patent US 5780292.
ACCESSION AR018076
VERSION AR018076.1 GI:3973679
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2363)
Nevalainen,H.K.M., Paloheimo,M.T., Miettinen-Olinen,A.S.K.,
Torikelli,T.K., Cantrell,M., Piddington,C.S., Rambossek,J.A.,
Turunen,M.K. and Fagerstrom,R.B.
Production of phytate degrading enzymes in trichoderma
Patent: US 5780292-A 7 14-JUL-1998;
FEATURES
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BASE COUNT 559 a 732 c 510 g 562 t
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Query Match 45.7%; Score 604.6; DB 9; Length 2363;
Best Local Similarity 66.2%; Pred. No. 4e-147;
Matches 871; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

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1 (bases 1 to 2379)
 Nevalainen,H.K.M., Paloheimo,M.T., Fagerstrom,R.B.,
 Miettinen-Oinonen,A.S.K., Turunen,M.K., Rambosek,J.A.,
 Piddington,C.S., Houston,C.S. and Cantrell,M.A.
 Recombinant cells that express phytate degrading enzymes in desired
 ratios
 JOURNAL Patent: US 5834286-A 1 10-NOV-1998;
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 Query Match 45.7%; Score 604.6; DB 9; Length 2379;
 Best Local Similarity 66.2%; Pred. No. 4e-147;
 Matches 871; Conservative 0; Mismatches 444; Indels 0; Gaps 0;
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RESULT 15
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 LOCUS Aspergillus niger var awamori phytase gene, complete cds.
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 ACCESSION 102421.1 GI:166518
 VERSION 1
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 SOURCE Aspergillus niger (strain ALK0243, sub_species awamori) DNA.
 ORGANISM Aspergillus niger
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 REFERENCE 1 (sites)
 AUTHORS Piddington,C.S., Houston,C.S., Paloheimo,M., Cantrell,M.,
 Miettinen-Oinonen,A., Nevalainen,H. and Rambosek,J.
 TITLE The cloning and sequencing of the genes encoding phytase (phy) and
 pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
 JOURNAL awamori
 MEDLINE Gene 133 (1), 55-62 (1993)
 REFERENCE 2 (bases 1 to 2379)
 AUTHORS Carter,J.R., Franden,M.A., Aebersold,R.H. and McHenry,C.S.
 TITLE Molecular cloning, sequencing and overexpression of the gene
 encoding the psi subunit of E. coli DNA polymerase III holoenzyme
 JOURNAL Unpublished (1992)
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SUMMARIES

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ALIGNMENTS

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; Sequence 3, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
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RESULT 2

US-08-151-574-33
; Sequence 33, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seiden
; TITLE OF INVENTION: Cloning and Expression of Microbial
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; TOPOLOGY: linear
; STRANDEDNESS: double
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: *Aspergillus ficuum* (*Aspergillus niger*)
; STRAIN: NRRL 3135
; US-08-151-574-33

Query Match 44.3%; Score 620.2; DB 1; Length 1404;
Best Local Similarity 65.2%; Pred. No. 4.8e-173;
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 Db 1321 TTGGGAGATGATCCCGGATAGCTTTGTGAGGGGGTGTAGCTTTGCTAGATCTGGGGGT 1380
 QY 1381 aactgggaagaagtgttctgct 1401
 Db 1381 GATTGGCGGAGTGTCTTTGCT 1401

RESULT 3

US-08-146-424-19
 : Sequence 19, Application US/08146424
 : Patent No. 5593963
 : GENERAL INFORMATION:
 : APPLICANT: VAN OOLJEN, ALBERT J. J.
 : APPLICANT: RIETVELD, KRIJN
 : APPLICANT: HOEKEMA, ANDREAS
 : APPLICANT: PEN, JAN
 : APPLICANT: SIJMONS, PETER C.
 : APPLICANT: VERWOERD, TEUNIS C.
 : TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
 : NUMBER OF SEQUENCES: 31
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: MORRISON & FOERSTER
 : STREET: 755 Page Mill Road
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94304-1018
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/146,424
 : FILING DATE: 02-NOV-1993
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: KENNEDY, BILL
 : REGISTRATION NUMBER: 33,407
 : REFERENCE/DOCKET NUMBER: 44615-20011.24
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (415) 813-5600
 : TELEFAX: (415) 494-0792
 : INFORMATION FOR SEQ ID NO: 19:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1404 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 1..1401
 : FEATURE:
 : NAME/KEY: mat_peptide
 : LOCATION: 70
 : US-08-146-424-19

Query Match 44.3%; Score 620.2; DB 1; Length 1404;
 Best Local Similarity 65.2%; Pred. No. 4.8e-173;
 Matches 913; Conservative 0; Mismatches 488; Indels 0; Gaps 0;

QY 1 atggcggtgttgcgtgctactgtccatgcccacttgttgcgttccacatcccggtacc 60
 Db 1 ATGGCGGCTCTGCTGCTTCTACTCTTTGTATCTCTCTGAGTACCTCTCCGACTG 60
 QY 61 gcttgggtccctcgtggtaattctcactctgtgacactgttgacggttggttaccatgt 120

; LENGTH: 1404 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Aspergillus ficuum (Aspergillus niger)
 ; STRAIN: NRRL 3135
 ; US-08-419-448-33

Query Match 44.3%; Score 520.2; DB 2; Length 1404;
 Best Local Similarity 65.2%; Pred. No. 4.8e-173;
 Matches 913; Conservative 0; Mismatches 488; Indels 0; Gaps 0;

QY 1 atggcggttcgtgctgctacgtccattgcccactttgctggttcacacacccgttacc 60
 Db 1 atggcggttcgtgctgctacgtccattgcccactttgctggttcacacacccgttacc 60
 QY 61 gcttgggttcctcggtgtaattctcactcttctgtgacactgttgagcgttggttaacaaatgt 120
 Db 61 gcttgggttcctcggtgtaattctcactcttctgtgacactgttgagcgttggttaacaaatgt 120
 QY 121 ttccacagaattctcactgttggtggtcaataactctcctcattctctcttggctgacgaa 180
 Db 121 ttccacagaattctcactgttggtggtcaataactctcctcattctctcttggctgacgaa 180
 QY 181 tctgctattctccagacgttccaaagggttgtagagttactttgcttcaagttttgct 240
 Db 181 tctgctattctccagacgttccaaagggttgtagagttactttgcttcaagttttgct 240
 QY 241 agacacggtgctagataccacactctcttcttaagtctaagaagtaactctgcttgaatga 300
 Db 241 agacacggtgctagataccacactctcttcttaagtctaagaagtaactctgcttgaatga 300
 QY 301 gctattcaaaagacgtactcttctcaagggttaagtaagcgtttcttgaagacttacacac 360
 Db 301 gctattcaaaagacgtactcttctcaagggttaagtaagcgtttcttgaagacttacacac 360
 QY 361 tacactttgggtgctgacgacttgactccattcggtgacacacaaatggttaactctggt 420
 Db 361 tacactttgggtgctgacgacttgactccattcggtgacacacaaatggttaactctggt 420
 QY 421 attaatctacagaagatacagaagcttggctgataagaagattgttccattgcttagagct 480
 Db 421 attaatctacagaagatacagaagcttggctgataagaagattgttccattgcttagagct 480
 QY 481 tctggttctgacagagttattcttctgctgataagaagattgttccattgcttagagct 540
 Db 481 tctggttctgacagagttattcttctgctgataagaagattgttccattgcttagagct 540
 QY 541 aagttgggtgaccaggtgcttaacacacacacacacacacacacacacacacacacacacac 600
 Db 541 aagttgggtgaccaggtgcttaacacacacacacacacacacacacacacacacacacacac 600
 QY 601 ccagaagggtgctgttccacacacacacacacacacacacacacacacacacacacacacac 660
 Db 601 ccagaagggtgctgttccacacacacacacacacacacacacacacacacacacacacacac 660
 QY 720 tctgaattgggtgacgacgttgaagtaacttaactgctgctgctgctgctgctgctgctgctg 720
 Db 720 tctgaattgggtgacgacgttgaagtaacttaactgctgctgctgctgctgctgctgctgctg 720
 QY 721 gctagattggaactcactgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 780
 Db 721 gctagattggaactcactgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 780
 QY 781 atggacatgtgctcactcgcacactgttgcacactgttgcacactgttgcacactgttgcacac 840
 Db 781 atggacatgtgctcactcgcacactgttgcacactgttgcacactgttgcacactgttgcacac 840

QY 841 ttctgtgacttcttactcaccagcaaatgattcaatacagactaacttgcgaatcttgggt 900
 Db 841 ttctgtgacttcttactcaccagcaaatgattcaatacagactaacttgcgaatcttgggt 900
 QY 901 aagtaactacggttaacggtgctggttaacccattggttccagctcaaggtggttggctt 960
 Db 901 aagtaactacggttaacggtgctggttaacccattggttccagctcaaggtggttggctt 960
 QY 961 aacgaattgattgctagattgactcactcctcagttcaagaccacacttctactaacacac 1020
 Db 961 aacgaattgattgctagattgactcactcctcagttcaagaccacacttctactaacacac 1020
 QY 1021 actttgacttaacccagctacttcccattgaaacgctactttgttaacgctgacttct 1080
 Db 1021 actttgacttaacccagctacttcccattgaaacgctactttgttaacgctgacttct 1080
 QY 1081 cagcaacacactaggtttcttcttcttctgctggtttgttacaacggtactaacgca 1140
 Db 1081 cagcaacacactaggtttcttcttcttctgctggtttgttacaacggtactaacgca 1140
 QY 1141 ttcttactacttctgtgaattctattgaagaaactgacggttaacgctgcttcttggact 1200
 Db 1141 ttcttactacttctgtgaattctattgaagaaactgacggttaacgctgcttcttggact 1200
 QY 1201 gttccattgctgctagagcttactggttaaatgacatgcaatgaaagctgaaaggaacca 1260
 Db 1201 gttccattgctgctagagcttactggttaaatgacatgcaatgaaagctgaaaggaacca 1260
 QY 1261 ttggttagattggttaacgacagattgttccattgacggttgggtggtggtggtggtggt 1320
 Db 1261 ttggttagattggttaacgacagattgttccattgacggttgggtggtggtggtggtggt 1320
 QY 1321 ttggttagattggttaacgacagattgttccattgacggttgggtggtggtggtggtggt 1380
 Db 1321 ttggttagattggttaacgacagattgttccattgacggttgggtggtggtggtggtggt 1380
 QY 1381 aactgggaagaatgtttcgt 1401
 Db 1381 aactgggaagaatgtttcgt 1401

RESULT 6

US-07-923-724-7
 ; Sequence 7, Application US/07923724
 ; Patent No. 5780292
 ; GENERAL INFORMATION:
 ; APPLICANT: Nevalainen, Helena K.M.
 ; APPLICANT: Paloheimo, Marja T.
 ; APPLICANT: Miettinen-Oinonen, Arja S.K.
 ; APPLICANT: Torkkeli, Tuula K.
 ; APPLICANT: Cantrell, Michael
 ; APPLICANT: Piddington, Christopher S.
 ; APPLICANT: Rambosek, John A.
 ; APPLICANT: Turunen, Marja K.
 ; APPLICANT: Fagerstr m, Richard B.
 ; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/923,724
 ; FILING DATE: 31-JUL-1992

TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/609,426A
APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant E.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 1050.0080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: join(404..447, 550..1906)
US-08-609-426A-7

Query Match 44.0%; Score 616.2; DB 2; Length 2363;
Best Local Similarity 65.2%; Pred. NO. 9.le-172;
Matches 906; Conservative 0; Mismatches 483; Indels 0; Gaps 0;

QY 13 gtcgtgctactgtccattgcaactgttggttcacatccggtaccgcttggtgct 72
DB 518 GTGGGACTACTCGCTGACAACTGTGCGAGATCACCTCCGGACTGGCATCCCGCC 577
QY 73 cgtggttaattctcaactctgtgacactgtgacggtgttaccatgtttccagaaatt 132
DB 578 TCAGAAATCAATCCACTTGGCATAGGTCGATCAAGGGTATCAATGCTTCTCCGAGACT 637
QY 133 tctcaattggtgggtcaactactctcattctctcttcttcttcttcttcttcttcttct 192
DB 638 TCGCATCTTTGGGGTCAATACGCGCGTCTTCTCTCTGCGCAACGAATCGGCCATCTCC 697
QY 193 ccagacgtttccaaagggtgtgagctactcttcttcttcttcttcttcttcttcttcttct 252
DB 698 CCGTGTGTCGCCCGGGTTCGAGAGTCACTTTTCGCTCAGGTCTCTCCCGTCAATGGAGCG 757
QY 253 agatacccaacttcttctaaagctaaagactactctgttcttcttcttcttcttcttcttct 312
DB 758 CGGTATCCGACCGAGTCCCAAGGGCAAGAAATACTCCGCTCTCATTTGAGGAGATCCAGCAG 817

QY 313 aacgctactgctttcaagggttaagtacgctttcttctgaagacttaacaactaacttgggt 372
DB 818 AAGGTGACCACTTTGATGAAAAATATGCTTCTTCTGAAGACATACAACACTACAGTGGGT 877
QY 373 gctgacgacttgactccattcggtgaacaaacaaaggttaactctggtatttaagtctac 432
DB 878 GCAGATGACGTGACTCCCTTCGGAGAGCAGGAGCTAGTCAACTCCGGCATCAAGTTCATC 937
QY 433 agaagatacaaggctttggcttagaagattgttcattcgtttagagcttctgttctgac 492
DB 938 CAGCGATACGATCGCTCACAGGACATCATTCCTTCATCCGATCCTCTGGCTCCAGC 997
QY 493 agagttattgcttctgctgaagttcattgaaggtttccaatctgcttaagtgtgactgac 552
DB 998 CGGTGATCGCTCCGCGGAGAAATTCATTGAGGGCTTCCAGAGCACCACCAATGAAGAT 1057
QY 553 ccaggtgtaacccacacacaaagcttctccagttatttaacgtttatttccagaagtgct 612
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QY 613 ggttaacaacacactttggaccacggtttgttactgctttcogaagaatctgaattgggt 672
DB 1118 TCAATCAACAACACTCTCGACCCAGGCACCTGCACCTGTCTTTGAAGACACAGCAATGGGC 1177
QY 673 gacgagttgaagtaacttaactgctgttttctgctccacattattagactgagtgaa 732
DB 1178 GATACGGTCAAGCCAAATTTACCCGCACGTTGCGCCCCCTCCATTCGTCAACGCTCTGGAG 1237
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DB 1238 AAGACTGTCTGGGTGACTCTCACAGACACAGAGTGAACCTACTCATGGACATGTC 1297
QY 793 ccattgacactgttctagaacttctgacgctactcaattgtctccattctgtgactgt 852
DB 1298 TCCTTGACACCATCTCCACACGACCGTCGACACCAAGCTGTCCCTTCTGTGACCTG 1357
QY 853 tcaactcaagaagaattgatttaactgaactacttcaactcttctggtgaagtactacgt 912
DB 1358 TTCACCATGACGAATGGATCCACTACGACTACCTCCAGTCCCTGAAATAAATACTACGGC 1417
QY 913 tacggtgctgttaacccattgggtccagctccaagggtgttgggttcttcttaacgaattgatt 972
DB 1418 CATGGCCAGGTAAACCGCTCGCGCCGACCCAGCGCTCGGTACGCTAACGAGCTCATC 1477
QY 973 gctagattgactcaactctccagttcaagaacacacacttctacttaacacacttggactct 1032
DB 1478 GCCGCTCTACCCACTCGCCTGTCCACGATGACACACAGCTCCAAACCCACACCTTGGACTCG 1537
QY 1033 aacccagctacttccattgaacgctacttgtacgctgaacttctctcacgacacact 1092
DB 1538 AACCCAGCTACCTTCCGCTCAACTCTACTCTCTACGCGGACTTTTCCACGATAACGGC 1597
QY 1093 atggttctcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1152
DB 1598 ATCATCTCTATCTTCTTGTGTTGGGTCTGTACAACGGCACCTAAGCGCTGTCTACACG 1657
QY 1153 tctgttaacttctgaagaactgaaggttaagctgcttcttcttcttcttcttcttcttct 1212
DB 1658 ACCGTGAGAAATATCACCCAGACAGATGGGTCTCTGCTCTGCTGGAGGCTTCCGTTGCT 1717
QY 1213 gctagagcttacgttgaatgatgaatgtgaagctgaaaggaacacattggttagagt 1272
DB 1718 TCGCGTGTGACTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1777
QY 1273 ttggttaacgacagaggttcttcttcttcttcttcttcttcttcttcttcttcttctt 1332
DB 1778 TTGTTAATGATCGCTTGTGAGGGGTTTGAGCTTGTAGATCTGGGGGTGATTGGGGAGATG 1837
QY 1333 aagagagacacttctgaaggttcttcttcttcttcttcttcttcttcttcttcttctt 1392
DB 1838 ACCCGGATACCTTGTGAGGGGTTTGAGCTTGTAGATCTGGGGGTGATTGGGGGAG 1897
QY 1393 tgtttcgtct 1401

QY 1153 tctgttaaatcttaagaagaactgcaggttacgctcttcttgagctgttccattcgt 1212
Db 1674 ACCGTGGAGAAATACACCCACAGATGGGTTCGCTCTGCTGGACGGTTCGGTTGGCT 1733
QY 1213 gctagagcttacgttgaatgatcaatgtgaagctgaaaggaacccattggttagagtt 1272
Db 1734 TCGCGTCTGTACGTCGAGATGATCAGTGCAGCCAGCAGGAGCGCTGGTCCGTGTC 1793
QY 1273 ttggttaacacagagttgttccattgcacaggttggtgttgacaggttggttagatgt 1332
Db 1794 TTGGTTAATGATCGCGTGTGTCCTCCCTGCATGGGTGCCAATTGATGTGTTGGGAGATGT 1853
QY 1333 aagaagacgactctgtgaaggttcttcttcgctagatctggttaactgggaagaa 1392
Db 1854 ACCCGGATAGCTTGTGAGGGGTGAGCTTGTCTAGATCTGGGGTGATTGGGCGGAG 1913
QY 1393 tgttctcgt 1401
Db 1914 TGTTCGTCT 1922

RESULT

US-08-151-574-31
; Sequence 31, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phylase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOPHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135

; IMMEDIATE SOURCE:
; LIBRARY: lambda AF
; CLONE: pAF2-3, pAF2-6, pAF2-7
; FEATURE:
; NAME/KEY: exon
; LOCATION: 210..253
; FEATURE:
; NAME/KEY: intron
; LOCATION: 254..355
; FEATURE:
; NAME/KEY: exon
; LOCATION: 356..1715
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(210..253, 356..1715)
; OTHER INFORMATION: /codon_start= 210
; OTHER INFORMATION: /product= "Phytase"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 210..380
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 381..1712
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "inositol phosphate"
; OTHER INFORMATION: /phosphatase
; OTHER INFORMATION: /product= "Phytase"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; US-08-151-574-31

Query Match 44.0%; Score 616.2; DB 1; Length 6756;
Best Local Similarity 65.2%; Pred. No. 1.5e-171;
Matches 906; Conservative 0; Mismatches 483; Indels 0; Gaps 0;
QY 13 gtcgtgctactgtccattgccacctgttcggttcacacatcccggtacccgcttgggtcct 72
Db 324 GTGGGACTACTGATCGCTGACTATCTGTGCGAGAGTCACTCCGGACTGGCAGTCCCGGCC 383
QY 73 cgtgttaattctcactcttgtgacactgttgcaggtgtggttaccacatgtttccacagaatt 132
Db 384 TCGAGAAATCAATCCAGTTCCGATACGGTTCGATCAGGGGTATCAATGCTTCTCCGAGACT 443
QY 133 tctcaactgtggggtaactacttccattcttcttcttggctgacgaactctgctattct 192
Db 444 TCGCATCTTTGGGGTCAATACGACACCGCTTCTTCTCTGGCAAAACGAATCGGTCACTCC 503
QY 193 ccagacgttccaaaagggtgtgagagttacttctggttcaagtcttctctgacacacgtgct 252
Db 504 CCTGAGTGCCTCCCGGATGCAGAGTCACTTTCGCTCAGGTCTCTCCGCTCATGGAGCG 563
QY 253 agatacccaacttcttctaagtctaagaagtaactctgcttcttgaagctattcctaaag 312
Db 564 GGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCGCTCTCATTTGAGGAGATCCAGCAG 623
QY 313 aacgtactgtttcaagggttaagtaacgttcttcttgaagacttacaactacactttgggt 372
Db 624 AACCGCACCACTTTGACGGGAAATATGCTTCTCTGAAGACATACAACTACACTTGGGT 683
QY 373 gctgacactgtgactcattcgtggaacacaaatgttaactctggtattgaagtctctac 432
Db 684 GCATGACCTGACTCCCTTCGGAGAACAGGAGCTAGTCAACTCCGGCATCAAGTCTAC 743
QY 433 agaagatacagggttggcttagaagaattgttccattctttagagcttctggttctgac 492
Db 744 CAGCGGTACGAATCGCTCACAAGGAACATCGTTCATTCATCCGATCCTCTGGCTCCAGC 803
QY 493 agattattgtcttctgtaaaagtctcatigaaaggtttccaattctgctatgttggctgac 552
Db 804 CGCGTATCGCCTCCGGCAAGAAATTCATCGAGGCTTCCAGAGCCACCAAGCTGAAGAT 863
QY 553 ccaggtgctaacccacacacagcttctccagttattacgttattattccagaaggtgct 612

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Db 864 CCTCGTGCCAGCCGCGCAATCGTCGCCAAGATCGATGCTGCTATTTCCGAGGCCAGC 923
QY 613 ggttaacaaacactttggacacggtttgtgtaactgttttgaagaatctgaattgggt 672
Db 924 TCATCCAACAACACTCTGACCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 983
QY 673 gacgagcttgaagctaaactcactcgtgttttgcgtccacattattagacgtagattgaa 732
Db 984 GATACCGTCGAAGCCAAATTCACCGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1043
QY 733 gctcaattgccaggtgttaacttgactgacgaagcgtttgttaacttgatgacatggt 792
Db 1044 AAGCACTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1103
QY 793 ccattcgacactgttgtagaacttctgacgctactcaattgtctccattctgtgactgt 852
Db 1104 TCTTCGACACCATCTCCACAGCAGCCGTCGACACCAAGCTGTCCCTCTGCTGACCTG 1163
QY 853 ttaactcagcagaatggattcaactacgactacttgcacttcttgggttaagtactacggt 912
Db 1164 TTCACCCATGACGAATGGATCAACTACGACTTACCTCCAGTCTTGAAAGATTAATACCG 1223
QY 913 taagggtgtgtaaccattgggtccagctcaagggtgtgtgttgggttaacgaattgatt 972
Db 1224 CATGGTCAGGTAACCCGCTCGGCCCGCCAGGCGCTGCGCTACGCTAACGAGTCAATC 1283
QY 973 gctagattgactcactctccagttcaagaccacacttctactaaccacactttgactct 1032
Db 1284 GCCCGTCTGACCCATCGCCTGTCCACATGACACCAAGTTCACACCACTTTGGACTCG 1343
QY 1033 aaccagctacttcccaattgaacgctactttgtacgctgacttctctcagcagcaaac 1092
Db 1344 AGCCCGGTACCTTTCCGCTCAACTCTACTCTACGCGGACTTTTCGATGACACAGCG 1403
QY 1093 atggttctatttcttcgcttgggtgttgacacggtactaagcacttgcctactact 1152
Db 1404 ATCACTCTCAATCTCTTGTCTTGGTGTGTACACGCGCACTAAGCGGCTATCTACCA 1463
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Db 1704 TGTGTTGCT 1712

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RESULT 10

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; US-08-419-448-31
; Sequence 31, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorkom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Sellen
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52

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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,448
; FILING DATE: 10-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; IMMEDIATE SOURCE:
; LIBRARY: lambda AF
; CLONE: pAF2-3, pAF2-6, pAF2-7
; FEATURE:
; NAME/KEY: exon
; LOCATION: 210..253
; FEATURE:
; NAME/KEY: Intron
; LOCATION: 254..355
; FEATURE:
; NAME/KEY: exon
; LOCATION: 356..1715
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(210..253, 356..1715)
; OTHER INFORMATION: /codon_start=210
; OTHER INFORMATION: /product="Phytase"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 210..380
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 381..1712
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function="inositol phosphate
; OTHER INFORMATION: phosphatase"
; OTHER INFORMATION: /product="Phytase"
; OTHER INFORMATION: /evidence=EXPERIMENTAL
;
; US-08-419-448-31

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Query Match 44.0%; Score 616.2; DB 2; Length 6756;
Best Local Similarity 65.2%; Pred. No. 1.5e-171;
Matches 906; Conservative 0; Mismatches 483; Indels 0; Gaps 0;

QY 13 gtcgtgctactgtccattgccacattgttctggtttccacatccggtaccgcttggtct 72
Db 324 GTGGGACTACTGATCGCTGACTATCTGTGCAGAGTCACCTCCGGACTCCGCCGCC 383

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QY 73 cgtgtaattctcactctgttgacactgttgacggtgtttacaaatgtttccagaaatt 132
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 QY 133 tctcactgtgtgggttcaatactctccattctctcttctgtgtgacgaactgtctattct 192
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 QY 193 ccagactgtccaaaggggtgttagagttactctgttcaagttttgtctagacagcgtgct 252
 Db 504 CCGAGGTGCGCGCGGATGACAGAGTCAATTCGCTCAGGTCCCTCCCGTCATGGAAG 563
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 Db 564 CGGTATCGACCGACTCCAGGGCAAGAAATACCTCCGCTCTCATTTAGGAGATCCAGAG 623
 QY 313 aacgtactgttttcaaggggtaagtacgtctttcttgaagacttaacactacactttgggt 372
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 QY 373 gctgacactgaactccattcgtgtgaacaaatggttaactctgtgtattaaattctac 432
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 QY 1213 gctagagcttaagtgaatgatgaatgaagctgaaagaaacacattgtgttagagtt 1272
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 QY 1273 ttgtttaacgacagacttcttccattgacagcgtgtgtgttgacaaagtgtggtgtagatgt 1332
 Db 1584 TTGTTAATGATCGCTTCTCCGCTGCATGGTGTCCGCTTGTGATGCTTTGGGAGATGT 1643
 QY 1333 aagagagacgactctctgaaggtttgtcttctctgtagatctgtgtgtaactgggaagaa 1392
 Db 1644 ACCCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTGGCGGAG 1703
 QY 1393 tgtttcgtc 1401
 Db 1704 TGTTTGTCT 1712

RESULT 11
 US-09-155-855-5
 ; Sequence 5, Application US/09155855
 ; Patent No. 6139902
 ; GENERAL INFORMATION:
 ; APPLICANT: KONDO, Hidemasa
 ; APPLICANT: ANAZAWA, HiGeharu
 ; APPLICANT: KANEKO, Syunichi
 ; APPLICANT: NAGASHIMA, Tadashi
 ; APPLICANT: TANGE, Tatsuya
 ; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
 ; FILE REFERENCE: 81356/124
 ; CURRENT APPLICATION NUMBER: US/09/155,855
 ; CURRENT FILING DATE: 1998-10-05
 ; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
 ; EARLIER FILING DATE: 1997-04-04
 ; EARLIER APPLICATION NUMBER: JP 084314
 ; EARLIER FILING DATE: 1996-04-05
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 1515
 ; TYPE: DNA
 ; ORGANISM: Aspergillus niger
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: (1)..(45)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(45)
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: (157)..(183)
 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: (184)..(1512)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (157)..(1512)
 ; US-09-155-855-5

Query Match 42.7%; Score 597.6; DB 3; Length 1515;
 Best Local Similarity 64.9%; Pred. No. 2.e-166;
 Matches 885; Conservative 0; Mismatches 479; Indels 0; Gaps 0;
 QY 38 tgttcggttccacatccggtacccgcttgggtctcgtgtgtaattctcactctgtgaca 97
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RESULT 12
 US-09-155-855-4
 : Sequence 4, Application US/09155855
 : Patent No. 6139902
 : GENERAL INFORMATION:
 : APPLICANT: KONDO, Hidemasa
 : APPLICANT: ANAZAWA, Hideharu
 : APPLICANT: KANEKO, Syunichi
 : APPLICANT: NAGASHIMA, Tadashi
 : APPLICANT: TANGE, Tatsuya
 : TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
 : FILE REFERENCE: 81356/124
 : CURRENT APPLICATION NUMBER: US/09/155,855
 : CURRENT FILING DATE: 1998-10-05
 : EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
 : EARLIER FILING DATE: 1997-04-04
 : EARLIER APPLICATION NUMBER: JP 084314
 : EARLIER FILING DATE: 1996-04-05
 : NUMBER OF SEQ ID NOS: 7
 : SOFTWARE: Patent In Ver. 2.0
 : SEQ ID NO 4
 : LENGTH: 1332
 : TYPE: DNA
 : ORGANISM: Aspergillus niger
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (1)..(1332)
 US-09-155-855-4

Query Match 42.5%; Score 595.4; DB 3; Length 1332;
 Best Local Similarity 65.6%; Pred. No. 9.3e-166;
 Matches 869; Conservative 0; Mismatches 456; Indels 0; Gaps 0;

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Qy 1397 tgcgt 1401
Db 1325 tgcgt 1329

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RESULT 13
 US-08-819-825-1
 ; Sequence 1, Application US/08819825
 ; Patent No. 5866118
 ; GENERAL INFORMATION:

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; APPLICANT: Berka, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: NO. 58661180 No. 5866118disk of No. 5866118th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,825
; FILING DATE: 18-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4758.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-819-825-1

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Query Match      25.4%; Score 355.6; DB 2; Length 2200;
Best Local Similarity 57.7%; Pred. No. 4.3e-95;
Matches 759; Conservative 0; Mismatches 509; Indels 48; Gaps 5;

QY 127 gaaattctcaatttggtgggttcaatactctcattctctcttcttggctgaagaatctgct 186
Db 607 GACATTGCCCGCAGTGGGGCCAGTACTGCGCTTCTTCTCGCTGGCCGAGGTCTCTGAA 666
QY 187 atttctccagagcttccaaagggttgtagagttactcttcttcaagtttcttctagacac 246
Db 667 ATCTCGCTCGCGTGGCCCAAGGCTGTGCTGTGAGTTTGTGCAGGTGCTGTCCCGGCAC 726
QY 247 ggtgctagatacccaactcttcttaagtcttaagaagtagtcttcttgaagaagctatt 306
Db 727 GGAGCTCGGTATCTTACTGCTCACAAGAGTGAAGTCTACGCCGAGTTGCTTCAAAGATC 786
QY 307 caaagaacgctactgcttctcaagggttaagtagcgttcttctgaagaacttacaactacac 366
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QY 547 gctgaccccgagtgtaacccacacacagcttctccagttatttaacgttatttaccagaa 606
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RESULT 15

US-09-221-654-1
; Sequence 1, Application US/09221654
; Patent No. 6054306
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren
; APPLICANT: Bech, Lisbeth
; APPLICANT: Fuglsang, Claus
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Ostergaard, Peter
; TITLE OF INVENTION: Peniophora Phytase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6054306 No. 6054306th America, Inc.
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,654
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,358
FILING DATE: 12-DEC-1997
APPLICATION NUMBER: 0529/97
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5101,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-221-654-1

Query Match 9.4%; Score 131.4; DB 3; Length 1320;

Best Local Similarity 56.9%; Pred. No. 3.2e-29;

Matches 268; Conservative 0; Mismatches 191; Indels 12; Gaps 1;

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Qy 1083 cgacaacactatggttcttctatttctcgtttgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1133
Db 1002 TGATACACCATGGTGCCCATCTTTGGCGGCTCGGGCTCTTCAACGCCAC 1052

Search completed: October 16, 2001, 12:02:43

Job time: 357 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 17:47:06 ; Search time 7358.5 Seconds
(without alignments)
1799.748 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	117.8	8.4	837	226	AQ255459	mgxb0014M
3	113.8	8.1	581	104	AJ274007	AJ274007
4	88.6	6.3	753	225	AQ163004	AQ163004
5	79.6	5.7	699	225	AQ162040	mgxb0021D
6	79.4	5.7	769	227	AQ361474	mgxb0010F
7	73.8	5.3	810	225	AQ161556	mgxb0008I
8	72	5.1	669	221	AQ361495	mgxb0004K
9	45.2	3.2	1016	221	CNS04ESQ	AL287459 Tetraodon
10	43	3.1	545	224	AQ140737	AQ140737 HS-3124-A
11	42	3.0	468	151	BF637070	BF637070 NF049F02L
12	41.8	3.0	341	109	AV054552	AV054552 AV054552
13	41.8	3.0	481	225	AQ202816	AQ202816 RPC111-48
14	41.2	2.9	231	25	AV129427	AV129427
15	41.2	2.9	234	109	AV064132	AV064132
16	41.2	2.9	236	109	AV054718	AV054718
17	41.2	2.9	247	28	AV293643	AV293643
18	41.2	2.9	264	108	AV002759	AV002759
19	41.2	2.9	269	109	AV077122	AV077122
20	41.2	2.9	278	25	AV114552	AV114552
21	41.2	2.9	285	109	AV081956	AV081956
22	41.2	2.9	297	109	AV060181	AV060181
23	41.2	2.9	300	109	AV053884	AV053884
24	41.2	2.9	306	25	AV118366	AV118366
25	41.2	2.9	342	109	AV047696	AV047696
26	40.4	2.9	482	30	AV423243	AV423243
27	40.2	2.9	265	109	AV049962	AV049962
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31	39.6	2.8	266	109	AV091633	AV091633
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37	39.6	2.8	289	109	AV055109	AV055109
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39	39.6	2.8	291	25	AV151459	AV151459
40	39.6	2.8	296	109	AV058485	AV058485
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42	39.6	2.8	298	109	AV067677	AV067677
43	39.6	2.8	300	109	AV054136	AV054136
44	39.6	2.8	303	25	AV118481	AV118481
45	39.6	2.8	303	25	AV164971	AV164971

ALIGNMENTS

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 DEFINITION clone mgxb0019C01r, DNA sequence.
 ACCESSION AQ324539
 VERSION AQ324539.1 GI:4116391
 KEYWORDS GSS.
 SOURCE Magnaporthe grisea.
 ORGANISM Magnaporthe grisea.
 Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 1 (bases 1 to 802)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
 TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome

JOURNAL COMMENT

Unpublished (1998)
 Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4233
 Email: rdeane@clemson.edu
 Seq primer: GGAACACGCTATGACCATG
 Class: BAC ends
 High quality sequence stop: 408.

FEATURES

Location/Qualifiers
 1..802
 /organism="Magnaporthe grisea"
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 /clone="mgxb0019C01r"
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 /tissue_type="Protoplasts"
 /lab_host="E. coli DH10B"
 /note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
 Rice blast is one of the most devastating fungal diseases
 of rice world wide. It is a filamentous ascomycete with
 a haploid genome (n=7) of approximately 40 Mbp. Rice
 blast is an important model fungal pathogen for studying
 numerous aspects of the fungal-host interaction. In
 order to facilitate genome wide analysis, a BAC library
 containing 9216 clones with an average insert size of 130
 kbp was constructed. This library represents greater
 than 25X genome coverage. High density colony filters
 are available upon request."

BASE COUNT 166 a 218 c 209 g 208 t 1 others
 ORIGIN

Query Match 10.8%; Score 151; DB 227; Length 802;
 Best Local Similarity 55.2%; Pred. No. 4.4e-33;
 Matches 342; Conservative 0; Mismatches 266; Indels 12; Gaps 2;

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 Db 614 AGGTTGAAGCTCAGGCCAAGCAAGCGGTGCAGATCATGAGCTTCTGCCCGTTGAGAC 555
 QY 804 tttgttagaactctgacgactactcaattgttcattctgtgacttgcactcaaga 863
 Db 554 CGTGGCAGATCCNACGCCAC-----CCTGTGCGAGTTCTGCACGCTGTTACGCAACG 501
 QY 864 cgaatggattcaatacagactacttgcaatcttgggttaagtactacggttacgtgtgctgg 923
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 QY 924 taaccattgggttcagctcaagggtgtgttcttcgttaacgaattgattgctagattgac 983
 Db 440 CAACCCCTGGGCTCCAGCAAGGGGTGGGCTTCGTCAACAGAGCTCATCGGAGGCTGCT 381
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 QY 1218 agcttacctgtaaatgatcaatgtgaagctgaaaggaaccattggttagatttgg 1277

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Db 140 GATGTTTTCAGAAAATGACTTCGCCAGGCGCAGAACGAGGAGTTGTGAGAAATCCTGGT 81
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RESULT 2
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DEFINITION mgxb0014M15r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0014M15r, DNA sequence.
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VERSION AQ255459.1 GI:3779774
KEYWORDS GSS.
SOURCE Magnaporthe grisea.
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REFERENCE 1 (bases 1 to 837)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A., and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 60
High quality sequence stop: 277.

FEATURES
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/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
BASE COUNT 248 a 154 c 188 g 243 t 4 others
ORIGIN
8.4%; Score 117.8; DB 226; Length 837;
Best Local Similarity 56.2%; Pred. No. 2.4e-23;
Matches 221; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

Qy 737 acttgcaggttgaactgacgacgagcgttggtaacttgatggacatggtgccat 796
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Db 140 ATTTTCAAGGTGCTGGGTTTAACGGTTCAGACGCTGCTAAATCTTATGGGACTGTGCACCA 199
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Db 200 TGAACAAACGCGCAACTTTTGAACAACTTGGCAACTTTCACCGCTTTCGAATCTGTTTA 259
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Db 260 CGAAGCAGATTGGGTAAATATGTTTACTTGTCCAGCGTCAGAAAATGGTACAGATACG 319
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Db 320 GAAACGGTAATCCTTTGGGCCCACTATGCGGTGGATGGGTAAACGAACCTATTTCAC 379
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Db 380 GATTAAACCGAAGCCAGTCCAAAGATCAAAACCATGTCCTCAATACGACACTTGACATGAC 439
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Db 440 CGGAAACCTTACTCTCTACAAAGCAATTTATGCTGATTTTATCCATACGGACGATATTA 499
Qy 1097 ttctatttcttcgcttctgggtttgtacaag 1129
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Db 500 TAGGATTTACGCGCGTGGTGGCTATTTTAACG 532

RESULT 3
LOCUS AJ274007 581 bp mRNA EST 29-DEC-1999
DEFINITION AJ274007 Metarhizium anisopliae ARSEF 2575 Metarhizium anisopliae
CDNA clone Ma#1628, mRNA sequence.
ACCESSION AJ274007
VERSION AJ274007.1 GI:6433380
KEYWORDS EST.
SOURCE Metarhizium anisopliae.
ORGANISM Metarhizium anisopliae
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Metarhizium.
REFERENCE 1 (bases 1 to 581)
AUTHORS Screen, S.E., Mathur, P. and St. Leger, R.J.
TITLE EST analysis of the insect pathogenic fungus Metarhizium anisopliae
JOURNAL Unpublished (1999)
COMMENT Contact: Screen SE
Entomology
University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA.

FEATURES
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/organism="Metarhizium anisopliae"
/strain="ARSEF 2575"
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/clone="Ma#1628"
/note="Vector: Unizap; Metarhizium anisopliae was grown on
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BASE COUNT 138 a 153 c 146 g 144 t
ORIGIN

Query Match 8.1%; Score 113.8; DB 104; Length 581;
Best Local Similarity 58.5%; Pred. No. 3.1e-22;
Matches 237; Conservative 0; Mismatches 162; Indels 6; Gaps 2;

Qy 142 tggggtcaactactctctctctcttcttgggtgagcaatctgtctattctccagacgtt 201
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Db 163 TGGGGCCAGTACTCGCGGTACTTCTC---AGCACAAAGGATCTATTAGCTTGACATC 219
Qy 202 ccaaggggttagagttactcttcttcttcttcttcttcttcttcttcttcttcttcttctt 261
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Db 220 CCGTCGGATGCGAGGTTCACCTTTGCTTCAATCTTGTCTCGACATGGTCCGCCAACCCG 279
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QY 322 gcttcaagggtgaagctcttcttgaagacttacaactacacttgggtgctgacgac 381
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QY 382 ttgactccattcgttgaaacacaaatggttaactctggtattaaagttctacagaagatac 441
Db 400 CTCACCCCTTGGCGGAGCAGGAAATGGTCAAGTCTGGAAAGAAAGTTCTTCAAGCGCTAT 459
QY 442 aagccttggctagaaa---gattgttccattcgttttagagcttctggttctgacagagtt 498
Db 460 CAGAAGTTACGGAGAGATTCGACCCATCCCTTTGTCGAGCCTCGGGCTCTGAAAGAGTC 519
QY 499 attgctctgctgaaagttcattgaaggtttccaatctgctgaag 543
Db 520 GTCATGTCAGCGCAAGATTTTGTTCATGTGCTTCTACAAAGCCAAG 564

RESULT 4
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LOCUS mgxb0021D19r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
DEFINITION clone mgxb0021D19r, DNA sequence.
ACCESSION AQL63004
VERSION AQL63004.1 GI:3559405
KEYWORDS GSS.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 753)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasnowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 448.
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/strain="70-15"
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/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
BASE COUNT 208 a 180 c 156 g 206 t 3 others
ORIGIN

Query Match 6.3%; Score 88.6; DB 225; Length 753;
Best Local Similarity 51.3%; Pred. No. 8.1e-15;
Matches 230; Conservative 0; Mismatches 212; Indels 6; Gaps 1;

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QY 206 --aggtgttagagtacttcttcttcaagtttcttagacacacggtgttagataccacaac 263
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Db 489 GAATGATTGGGCGCTCGGCAACAGAGAACTCGGGTATTNATTTTACCAAAAGATACCA 548
QY 444 ggcttggctagaagaattgttccattcgttagagcttctggttctgacagagttattgc 503
Db 549 AAATCTGGCCAGAGGAAACCACTTTATTCGCTATGATGACAAANACCGGTTTGA 608
QY 504 ttctgctgaaagttcattgaaggtttc 531
Db 609 TAGCGCAGAACTCTGGGCTAGGGGTTTC 636

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DEFINITION clone mgxb0010F06r, DNA sequence.
ACCESSION AQL62040
VERSION AQL62040.1 GI:3558441
KEYWORDS GSS.
SOURCE Magnaporthe grisea.
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 699)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasnowski, M., Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 285.
Location/Qualifiers
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/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with

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RESULT 11
 BF637070 468 bp mRNA EST 19-DEC-2000
 LOCUS NF049F02LFI1016 Developing leaf Medicago truncatula cDNA clone
 DEFINITION BF637070
 ACCESSION BF637070.1 GI:11901228
 VERSION
 KEYWORDS
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.
 REFERENCE 1 (bases 1 to 468)
 AUTHORS Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Wellner, J.W. and May, G.D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
 JOURNAL Unpublished (2000)
 COMMENT Contact: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
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 BASE COUNT 91 a 110 c 97 g 170 t
 ORIGIN

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 QY 500 ttgcttcgtgtaaaagttcattgaaggtttcccaatctgctaagtgtggtgacccaggtg 559
 DB 136 TTAATTTTGTGAAGTTTGTGGTTCAATGTTTAAGTTCTCCGACGTTTGTTCAGTCCAA 195
 QY 560 ctacacccacacacacagctctccagttattacagttattattccagaaggtctggttaca 619
 DB 196 TTTCTCTCCCTTCCACTTCAACATGGCTTCGAAACTCTCAAAACCGTGTCTGTTCTG 255
 QY 620 acaacactttggaccacggtttgtgtactgcttccgaagaatctgaattgggtgacgacg 679
 DB 256 AAACCGCTCTCCCGTTGTTCTTCCTTCGTCGCTTTCAAGCCCTCAGCTCTTCGTTGAAGCTC 315
 QY 680 ttgaagctaacttaactgctgttttc 705
 DB 316 CGAAGCTAAACGACGCTGTGTGTTTC 341

RESULT 12
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 LOCUS AV054552 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA
 DEFINITION

ACCESSION AV054552
 VERSION AV054552.1 GI:5154299
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 341)
 AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 TITLE RIKEN Mouse ESTs
 JOURNAL Unpublished (1999)
 COMMENT Contact: Chie Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@rtc.riken.go.jp

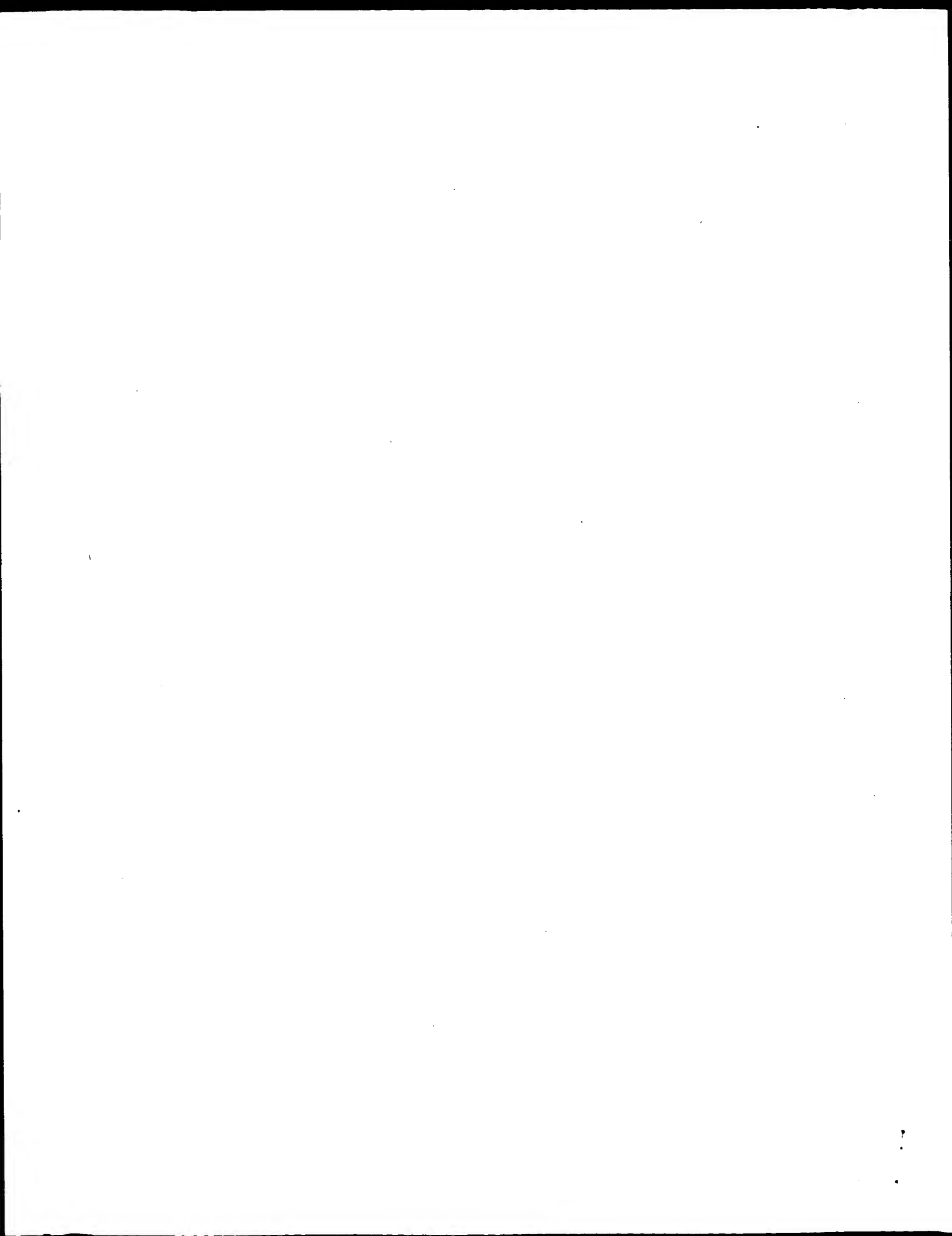
Thermolabile and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES
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1..341
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 QY 1215 tagagcttaagttgaatgatgcaatgtgaagctgaaaggaaccattggttagagttt 1274
 DB 211 CGCGCCCCAGTTGAGGAGAGAAAGTGGAGCAAGAGAAATCCGAGGAGTTGA 270
 QY 1275 gggttaacgacagagttgttccattgacggttgggtgttgacagagttgggta 1327
 DB 271 AGATGACATGGCTTCTGTTTTTTTGTGACTAAACTGTTTTTGTAAAGTGGCTA 323

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 DEFINITION DNA sequence.
 ACCESSION AQ202816
 VERSION AQ202816.1 GI:3613607
 KEYWORDS GSS.
 SOURCE human.



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Run on:      October 16, 2001, 12:02:43 ; Search time 220.1 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	%			
1	1239.8	93.7	1426	3	US-09-121-425-3	Sequence 3, Appli
2	606.4	45.8	1404	1	US-08-151-574-33	Sequence 33, Appl
3	606.4	45.8	1404	1	US-08-146-424-19	Sequence 19, Appl
4	606.4	45.8	1404	1	US-08-693-709-1	Sequence 1, Appli
5	606.4	45.8	1404	2	US-08-419-448-33	Sequence 33, Appl
6	606.4	45.8	6756	1	US-08-151-574-31	Sequence 31, Appl
7	606.4	45.8	6756	1	US-08-419-448-31	Sequence 31, Appl
8	604.6	45.7	2363	1	US-07-933-724-7	Sequence 7, Appli
9	604.6	45.7	2363	2	US-08-609-426A-7	Sequence 7, Appli
10	604.6	45.7	2379	2	US-08-374-652C-1	Sequence 1, Appli
11	595	45.0	1332	3	US-09-155-855-4	Sequence 4, Appli
12	595	45.0	1515	3	US-09-155-855-5	Sequence 5, Appli
13	355.6	26.9	2200	2	US-08-819-825-1	Sequence 1, Appli
14	355.6	26.9	2200	4	US-09-163-842-1	Sequence 1, Appli
15	131.4	9.9	1320	3	US-09-221-654-1	Sequence 1, Appli
16	131.4	9.9	1320	3	US-08-989-358A-1	Sequence 1, Appli
17	131.4	9.9	1593	3	US-08-993-359-23	Sequence 23, Appl
18	112.2	8.5	1501	3	US-08-993-359-21	Sequence 21, Appl
19	97.2	7.3	1522	3	US-08-993-359-25	Sequence 25, Appl
20	91	6.9	1642	3	US-08-993-359-27	Sequence 27, Appl
21	87.6	6.6	1536	3	US-08-993-359-29	Sequence 29, Appl
22	47.2	3.6	7218	1	US-08-232-463-14	Sequence 14, Appl
23	46.8	3.5	99	1	US-08-151-574-12	Sequence 12, Appl
24	46.8	3.5	99	2	US-08-419-448-12	Sequence 12, Appl
25	42.4	3.2	1631	2	US-08-488-263-5	Sequence 5, Appli
26	42.4	3.2	1631	2	US-09-077-060-5	Sequence 5, Appli
27	42.4	3.2	1631	3	US-08-914-583-2	Sequence 2, Appli

ALIGNMENTS

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RESULT      1
US-09-121-425-3
; Sequence 3, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus Phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: sequence
US-09-121-425-3

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Query Match	93.7%	Score 1239.8;	DB 3;	Length 1426;	
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61	tgttgagggtca	aatactct	tcattct	ctctctct	tgttgctgacgacgaatctgctatttctccagac 120
150	tgttgagggtca	aatactct	tcattct	ctctctct	tgttggaagacgaatctgctatttctccagac 209
121	gttccaaagggt	tgttagag	ttaact	tttcgttca	agttttgtctagacacggtgcttagatac 180
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Qy 361 tacaaggcttggttagaagattgttccattcgttagagcttctggttctgacagagtt 420
Db 450 tacaaggcttggttagaagattgttccattcgttagagcttctggttctgacagagtt 509
Qy 421 attgcttctgctgaaaaagttcattgaaggtttccaaatctgctaagttggctgacccaggt 480
Db 510 attgcttctgctgaaaaagttcattgaaggtttccaaatctgctaagttggctgacccaggt 569
Qy 481 gctaaaccacacacagcttctccagttattaaagttattattccagaaggtgctggttac 540
Db 570 tctcaaccacacacagcttctccagttattaaagttattattccagaaggtgctggttac 629
Qy 541 acaacacacttggaccacggttctgactgcttctcgaagaatctgaattgggtgacgac 600
Db 630 acaacacacttggaccacggttctgactgcttctcgaagaatctgaattgggtgacgac 689
Qy 601 gttgaagctaaactcactgctgtttctcgaagaatctgaattgggtgacgac 660
Db 690 gttgaagctaaactcactgctgtttctcgaagaatctgaattgggtgacgac 749
Qy 661 ttgcacaggtgtaactgaactgaagacgactgttgaacttgatggacatgtgtccattc 720
Db 750 ttgcacaggtgtaactgaactgaagacgactgttgaacttgatggacatgtgtccattc 809
Qy 721 gacactgttctgactgaactcactgaactcactcaattgtctccattctgtgacttctcact 780
Db 810 gaaactgttctgactgaactcactgaactcactcaattgtctccattctgtgacttctcact 869
Qy 781 cagcagcaatgattcaatacagactcacttgcacttcttgggtgaagtagactacggttaacggt 840
Db 870 cagcagcaatgattcaatacagactcacttgcacttcttgggtgaagtagactacggttaacggt 929
Qy 841 gctggttaacacattgggtccagctcaaggttgggttctgtaacgaattgattgctaga 900
Db 930 gctggttaacacattgggtccagctcaaggttgggttctgtaacgaattgattgctaga 989
Qy 901 ttgactcactctccagttcaagacacacacttctactaaccacacttggactctaaaccca 960
Db 990 ttgactagatctccagttcaagacacacacttctactaaccacacttggactctaaaccca 1049
Qy 961 gctactttccattgaacgctacttctgtaacgctgacttctctcgaacacacactatggtt 1020
Db 1050 gctactttccattgaacgctacttctgtaacgctgacttctctcgaacacacactatgatt 1109
Qy 1021 tctattttctcgttttgggtttgtacaacggtactaagccattgtctactactctggtt 1080
Db 1110 tctattttctcgttttgggtttgtacaacggtactaagccattgtctactactctggtt 1169
Qy 1081 gaactctattgaagaacactgacggttactgctgttcttggactgttccattcgtgctaga 1140
Db 1170 gaactctattgaagaacactgacggttactgctgttcttggactgttccattcgtgctaga 1229
Qy 1141 gttactgtgaaatgatgcaatgtgaagctgaaaggaaacattggttagagtttgggtt 1200
Db 1230 gttactgtgaaatgatgcaatgtgaagctgaaaggaaacattggttagagtttgggtt 1289
Qy 1201 aacgacagaagtttccattgacaggttgggttgggtgacaaagttgggttagatgaaagaga 1260
Db 1290 aacgacagaagtttccattgacaggttgggttgggtgacaaagttgggttagatgaaagaga 1349
Qy 1261 gacgactctgttgaaggttgggttcttctcgtatagatcgtggtgaactgggaagaatgtttc 1320
Db 1350 gacgactctgttgaaggttgggttcttctcgtatagatcgtggtgaactgggtgaatgtttc 1409
Qy 1321 gct 1323
Db 1410 gct 1412

RESULT 2
US-08-151-574-33

; Sequence 33, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Anemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; US-08-151-574-33

Query Match 45.8%; Score 606.4; DB 1; Length 1404;
Best Local Similarity 66.4%; Pred. No. 9.1e-167;
Matches 871; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

Qy 12 ttgtgacactgttgacggtgtgtaccacattgttccacagaaattctcactgtgtgggtca 71
Db 90 TTGGATACGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATCTTTGGGTCA 149
Qy 72 ataactccatttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 131
Db 150 ATACGACACCTTCTTCTCTGCGAAACGAATCGGTATCTCCCTGAGGTGCCCGCCG 209
Qy 132 ttgtagacttacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 191
Db 210 ATGACAGACTCATTCTCGTCAGGTCTCTCCCTCATGAGCGCGGTATCCGACCGACTC 269
Qy 192 taagtctaaagtagtactctgtcttcttcttcttcttcttcttcttcttcttcttcttctt 251
Db 270 CAAGGGCAAGAAATACTCCGCTCTCTATTGAGGAGATCCAGACGACGACGACCTTTGA 329

QY 252 gggtaagtaacgtcttcttgaagacttacactacacttttggtgctgacgaacttgactcc 311
Db 330 CGGAATAATAGCCTTCTTGAGACATACACTACACTTGGGTGCGAGATGACTGACTCC 389
QY 312 attcgttgaaacaaatggttaactctggtattagttctacagaagatacaagccttt 371
Db 390 CTTGCGAAGACAGGAGTAGTCAACTCGGCAATCAAGTCTACACGCGTACGAATCGT 449
QY 372 ggttagaagattgttccattggttagagcttctggttctgacagagttattgcttctgc 431
Db 450 CACAAGGAACATGTTCCATTCATCGATCCCTTGCTCCAGCGGTGATCGCTCCGG 509
QY 432 tgaagattcattgaaggtttccaatctgttaagttggtgctgacaggtgctaaacccaa 491
Db 510 CAAGAAATTCATCGAGGCTTCCAGAGCACCAAGCTGAAGGATCTTCTGCTCCAGCGGTGATCGCTCCGG 569
QY 492 ccaagcttccagtttataaagttattatccagaagtgctggttaacaaacacttt 551
Db 570 CCAATGCTGCCCAAGATCGAGTGGTGTCTATTCGAGGCCAGTCTATCCCAACACACTCT 629
QY 552 ggaacaggttggtgactgcttctgaaagaactgaattggtgacagcgttggaagctaa 611
Db 630 CGACCCAGGACCTGACACTGCTTTCGAAGACAGCGAATTCGCGGATACCGTGCAGGCCAA 689
QY 612 cttcactgctgttttgcgtccactatttagagctagattggaagctcaactgcccaggtg 671
Db 690 TTTTACCCGACGTTGCTCCCTCCATTCGTCACGTCGAGAGAGGACCTGTCGGGTG 749
QY 672 taactgactgaagacaggttggtaactggtgacatggtgctcattgacactgttgc 731
Db 750 GACTCTCAGACAGACAGAAAGTGAACCTATGACATGCTCTCTCGACACCATCTC 809
QY 732 tagaactctgacgtactcaattgtctcattctgactggttgcactcaacagcaatg 791
Db 810 CACCACACCGTCGACACCAAGCTGTCGCCCTTCTGTGACCTGTTTCCACCCATGGAATG 869
QY 792 gattcaatacagactactgcaactcttgggttaagtactacgttgcgtgctgtaaccc 851
Db 870 GATCAACTAGCACTACCTCCAGTCTTGAAAAAGTATTACGCCATGTTGACAGGTAAACC 929
QY 852 attggttcagctcaaggttgggttgggttaacgaattgattgtagactcaactc 911
Db 930 GCTGCGCCGACCCAGCGGCGTGGGTAGCTTAACGAGCTCATCGCCCGTCTGACCCACTC 989
QY 912 tccagttcaagaccactcttactaaacacacttggacttaaacacagctactttccc 971
Db 990 GCCTGTCCACAGTACACACAGTTCACACACACTTTGGACTCGAGCCCGGCTACCTTTCC 1049
QY 972 attgaacgtactttgtacgtgacttctctcagcaacacactatggtttctatttctt 1031
Db 1050 GCTCAACTCTACTCTACCGGAGCTTTTCGATGACACACGATCATCTCCATCTCTCT 1109
QY 1032 cgccttgggttggtaacaggtactaaagccattgtctactactcttctgttgtaacttga 1091
Db 1110 TGCTTTAGGTCTGTCAACGGGACCTTAAGCGGCTATCTACACAGCGGTGAGGAATATCAC 1169
QY 1092 agaaactgaacgttgaacgtcttctgactgacttccactgctgtagagttcaagttga 1151
Db 1170 CCAGACAGATGATGCTGCTGCTGACAGCGGTTCCTGCTGCTGCTGCTGCTGCTGCTG 1229
QY 1152 aatgatgcaatgtaagctgaaagaaacacttgggttagagtttgggttaacagacaggt 1211
Db 1230 GATGATGAGTGTACAGGGGACAGGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1289
QY 1212 ttttccattgacaggttgggttgggttgggttgggttgggttgggttgggttgggttgg 1271
Db 1290 TGTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1349
QY 1272 tgaaggttcttctgctgactggttgggttgggttgggttgggttgggttgggttgggt 1323
Db 1350 GAGGGGTTGAGCTTTTGTGATCTGCGGGGTGATTTGGCGGAGTGTGTTTGT 1401

RESULT 3
US-08-146-424-19
; Sequence 19, Application US/08146424
; Patent No. 5593963
; GENERAL INFORMATION:
; APPLICANT: VAN OOLJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,424
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: 44615-20011.24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1401
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 70
; US-08-146-424-19

Query Match 45.8%; Score 606.4; DB 1; Length 1404;
Best Local Similarity 66.4%; Pred. No. 9.1e-167;
Matches 871; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

QY 12 ttgtgacactgttgacggtgtgtaccgaatgttccacagaatttctcacttgggggtca 71
Db 90 TTGGGATACGTCGATCAGGGGTATCAATGCTTCTCGAGACTTCGCATCTTTGGGTCA 149
QY 72 atactctccattctcttcttggtgacgaatctgtctatttctcagagcgttccaaagg 131
Db 150 ATAGCGACCGGTTTCTCTCTGCAACGAATCGGTATCTCCCTGAGGTGCCCGCG 209
QY 132 ttgttagagttacttttcttcttgaagtttctgtagacagcgtgtgtagatacccaactcttc 191
Db 210 ATGCAGAGTCACTTCGCTCAGGTCTCTCCCTGATGAGCGCGGTATCCGACCGACT 269
QY 192 taagtctaaagactctgcttggattgaagctatttcaaaagacgctactgctttcaa 251
Db 270 CAAGGGCAAGAAATACTCCGCTCTCTATTGAGGAGATCCAGACAGACGACGACCTTTGA 329
QY 252 gggtaagtaacgtcttcttgaagacttacactacacttttgggtgacgaacttgactcc 311

Db 330 CGAAATATGCTTCCTGAAGACATACAACTACAGCTTGGTGCAGATGACCTGACTCC 389
QY 312 attcggtagaacaacaaatgggttaactctggtatttaagtctacagaagatacaagggtttt 371
Db 390 CTTCGGAGAACAGGAGCTAGTCAACTCCGGCATCAAGTTCTTACAGCGGTACGAATCGCT 449
QY 372 ggcataaagattgttcattcgttagagctctggttctgacagagttattgtctctgc 431
Db 450 CACAAGGAACATCGTTCATTCATCCGATCTCTGGCTCCAGCGCGTGATCGCTCCGG 509
QY 432 tgaagagttcattgaaggtttccactctgtaagtgtgctgaccagagtgtaacccaca 491
Db 510 CAAGAAATTCATCGAGGGCTCCAGAGCACCAAGCTGAAGGATCTCTGTCGCCAGCCGG 569
QY 492 ccaagcttccagttattaaagcttattattccagaagagtgctggtttacaaacacattt 551
Db 570 CCAATCGTCGCCCAAGATCGAGCTGGTCTATTTCCGAGCCAGCTCATCAACAAACACTCT 629
QY 552 gaccacaggtttgtactgctttcgaagaatctgaattggtgacgagcttgaagctaa 611
Db 630 CGACCCAGGACCTGCATGCTTCCGAGACAGCGAATGGCCGATACCTCGTCGAAGCCAA 689
QY 612 ctccactgctgtttcgtccacccttagagctagattggaagctcacttgccaggtgt 671
Db 690 TTTCCAGCGCAGTTCGTCCCTCCATTCGTCAACGCTCTGGAGAACGACCTGTCCGGTGT 749
QY 672 taacttgactgacgaagagctgttgaattgattgagatgtaattgctcattcgacactgttc 731
Db 750 GACTCTCAGACAGACAGAGTAGTACCTCATGATGACATGCTCTCTCGACACCATCTC 809
QY 732 tagaactctgacgtactcaattctccattctgactgttcaactcagcagcaatg 791
Db 810 CACCAGCAGCTCGACACCAACCTGTCCTCTCTGACCTGTTACCCCATGAGGATG 869
QY 792 gattcaatacagactacttgcaactctttgggttaagtactacaggtttacgtgctgtaaccc 851
Db 870 GATCAACTACGACTACTCTCAGTCTCTGAAAAGATTACGGCCATGTTGCGAGGTAAACC 929
QY 852 attggttcagctcaaggtgttgggttgaatgaagattgattgtagatgactcactc 911
Db 930 GCTCGGCCCGCCAGGGGGTGGGTACCTTACAGAGCTCACTGCGCCGCTGACCCACTC 989
QY 912 tcagttcaagaccacactctactaaccacactttgactctaaaccagctactttccc 971
Db 990 GCTGTCCACGATGACACCACTTCCAAACACACTTTGGACTCGAGCCCGGTACCTTCC 1049
QY 972 attgaacgctactttgtacgctgactctctcagcacaacactatggtttctattttctt 1031
Db 1050 GCTCAACTCTACTCTCTACGCGGACTTTTCGATGACAAACGCGCATCTCTCAATCTCTT 1109
QY 1032 cgtcttgggtttgacaacggtactaagccattgtctactactctgttgaactctatga 1091
Db 1110 TGCTTTAGGTCTGTACAAAGGACCTAAGCCGCTATCTACAGACCCGTTGGAGATATCAC 1169
QY 1092 agaaactgacggtttacgctgcttcttggactgtccattcgtcgtgtagacttaagttga 1151
Db 1170 CCAGACAGATGGATTCGTCTCTCTGAGGCTTCCGTTTGGCTTTGAGTATGATCGCGT 1229
QY 1152 aatgatacaatgtaagctgaaagaaacattggttagagtttgggttaacgaagagat 1211
Db 1230 GATGATGCAAGTGTACGCGGAGGAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1289
QY 1212 tgttccattgacggtttggttgggtgacaaagttggttgaatgaagagagacgacttcgt 1271
Db 1290 TGTCCGCTGTCATGGGTGTCGCGGTGATGCTTTGGGGAGATGTACCCGGATAGCTTTGT 1349
QY 1272 tgaaggtttgtcttctgcttagatctggttgtaactgggaagaatgttgcct 1323
Db 1350 GAGGGGGTTGAGCTTTGCTTAGATCTGGGGGTGATTTGGGGGAGTGTGTTTGCT 1401

RESULT 4

US-08-693-709-1
; Sequence 1, Application US/08693709
; Patent No. 5770413
; GENERAL INFORMATION:
; APPLICANT: VAN OOLJEN, ALBERT J.J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SLMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,709
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 800
; PRIORITY DATA:
; APPLICATION NUMBER: 08/146,424
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20011.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1401
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: 70...1401
; OTHER INFORMATION:
; NAME/KEY: Signal Sequence
; LOCATION: 1...72
; OTHER INFORMATION:
; US-08-693-709-1

Query Match 45.8%; Score 606.4; DB 1; Length 1404;
Best Local Similarity 66.4%; Pred. No. 9.1e-167;
Matches 871; Conservative 0; Mismatches 441; Indels 0; Gaps 0;
QY 12 ttgtgacactgttgacggtgtgtaccattttccagaaatttctcacttgggtggtca 71
Db 90 TTGCGATACGCTGATCAGGGTATCAATCTCTCCGAGACTTCGATCTTTGGGTCA 149
QY 72 atactctccattctcttcttggctgacgaatctgctatttctccagacgttccaaagg 131
Db 150 ATACGACCGTCTCTCTCTCGTCAACGAATCGTCAATCTCCCTCGAGTGCCCGCG 209
QY 132 ttgtagagttacttctcgaattttgttagacaggtgtgtagatacccaacttcttc 191

Db 210 ATGACAGAGTCACTTTTCGCTCAGGTCTCTCCGCTCATGGAGCGCGGTATCCGACCGACTC 269
 QY 192 taagtctaagaagtactctgtttgatgaaagctattcaaaagaacgctactgtttctca 251
 Db 270 CAAAGGCAAGAATACTCCGCTCTCATTTAGGAGATCCAGCAGAACGCGACCATCTTGA 329
 QY 252 gggtaagtacgctttcttgaagacttaacaactacacttgggtgctgacgactgactcc 311
 Db 330 CGGAAATATGCTTCTCTGAAGACATCAACTACAGCTTGGGTGAGATGACCTGACTCC 389
 QY 312 attcggtaacaacaaatggttaactctggttatttaagtctacagaagatacaaggcttt 371
 Db 390 CTTTCGGAGAACAGGAGCTAGTCAACTCCGGCATCAAGTTCTACCAAGCGGTACGAATCGCT 449
 QY 372 ggcataagaagattgttcattcgttagagcttctggttctgacagagttattgtcttgc 431
 Db 450 CACAGGACATCGTTCATTCATCCGATCTCTGGCTCCAGCGCGGTGATCGCTCCGG 509
 QY 432 tgaagattcattgaaggttttccaatctgctaagtgtgctgaccaggtgctaaccaca 491
 Db 510 CAAGAAATTCATCGAGGGCTTCCAGAGCACCAAGCTGAAGGATCCTCGTCCGACCGCG 569
 QY 492 ccaagcttctccagttataacagttattattccagaaggtggttacaacaacttt 551
 Db 570 CCAATCGTCGCCAAGATCGAGCTGCTGATTTCCGAGGCCAGCTCATCCAACAACACTCT 629
 QY 552 ggaccacggttgtgactgtcttcgaagaactgaattggtgacagcgttgaaagctaa 611
 Db 630 CGACCCAGGACCTGCTGCTCCCTCCATTCGTCACGCTCGAGAGACGACCTGTCGGGTG 689
 QY 612 cttaactgctgtttcgtccacactattagagctagattggaagctcacttgcaggtgt 671
 Db 690 TTTACCGCCACGTTGCTGCCCTCCATTCGTCACGCTCGAGAGACGACCTGTCGGGTG 749
 QY 672 taactgactgaagaagcgtgtgttaactgtatggaacatgtgtccattcgacactgtgc 731
 Db 750 GACTCTCACAGACACAGAAAGTGAACCTACCTCATGACATGTGCTTCCGACACCATCTC 809
 QY 732 tagaacttctgacgtactcaattgtctccattctgtgactgttcaactcaagcgaatg 791
 Db 810 CACAGACCGCTGCACACCAAGCTGTCCCTTCTGAAAGATTAACGCCATGTCAGGTACATG 869
 QY 792 gattcaactacgactacttgcattttgggttaagtactacggttgcggtggtgtaacc 851
 Db 870 GATCAACTACGACTACCTCCAGTCTTGAAGAGTATTACGCCATGTCAGGTATACCC 929
 QY 852 attgggtccagctcaaggtgtgtttcgttgaacgaattgattgctagattgactcact 911
 Db 930 GCTGGGCCGACCCAGGCGCTCGGCTACGCTACAGGCTCATCGCCGCTGTGACCCACTC 989
 QY 912 tccagttcaagaccacacttctactaaccacacttggacttcaaccacgactacttccc 971
 Db 990 GCCTGTCCACCATGACACCACTTCCACCACTTTGGACTCGAGCGCCGCTACCTTTCC 1049
 QY 972 attgaacgtactttgtacgtgactctctctcaacgaacactatggtttctattttctt 1031
 Db 1050 GCTCAACTCTACTCTACGGGGACTTTTCGATGACACAGGATCATCTCCATCTCTT 1109
 QY 1032 cgeittgggtttgataacaggtactaagccattgtctactactcttctgttgaactatga 1091
 Db 1110 TGCTTTAGGCTGTACACAGCGCTAAGCGGCTATCTACCAACGACCGCTGAGATATCAC 1169
 QY 1092 agaaactgacggttactgctcttctgagactgttccattcgtcgttagagcttcaagtga 1151
 Db 1170 CCACACAGATGGATTCGTGCTGCTTGGAGGTTTCCGTTTGGCTTCGCTTTGTACCTCGA 1229
 QY 1152 aatgatgcaatgtgaagctgaaaggaaacccattggttagagttttggttaacgacagagt 1211
 Db 1230 GATGATGACAGGTGTCAGCGGAGCAGGACCGCTGGTCCGCTGCTTGGTTAATGATCCGT 1289
 QY 1212 tgttccattgcaaggttgtggtgttgacaaggtgggttagatgtaagagagacactcgt 1271
 Db 1290 TGTCCCGCTGCATGGGTGTCCGGTTGATGCTTTGGGGAGATGTACCGGGGATAGCTTTGT 1349

QY 1272 tgaaggtttcttctgctagatctggtgtaactgggaagaatgttctgct 1323
 Db 1350 GAGGGGTTGAGCTTGTCTAGATCTGGGGTGTATTGGCGGAGTGTGTTGCT 1401

RESULT 5

US-08-419-448-33
 ; Sequence 33, Application US/08419448
 ; Patent No. 5863533
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert F.M. Van Gorkom
 ; APPLICANT: Willem Van Hartingsveldt
 ; APPLICANT: Petrus A. Van Paridon
 ; APPLICANT: Annemarie E. Veenstra
 ; APPLICANT: Rudolf G.M. Luttin
 ; APPLICANT: Gerardus Selten
 ; TITLE OF INVENTION: Cloning and Expression of Microbial
 ; TITLE OF INVENTION: Phytase
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster
 ; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20006-1888
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; SOFTWARE:
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/419,448
 ; FILING DATE: 10-APR-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murashige, Kate H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 24615-20026.10
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-887-1500
 ; INFORMATION FOR SEQ ID NO: 33:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1404 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Aspergillus ficuum (Aspergillus niger)
 ; STRAIN: NRRL 3135
 ; US-08-419-448-33

Query Match 45.8%; Score 606.4; DB 2; Length 1404;
 Best Local Similarity 66.4%; Pred No. 9,1e-167;
 Matches 871; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

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 QY 72 atactctccattctctcttcttggctgacgaactctctatttctccagacggtcccaagg 131
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 QY 132 ttgtagacttcttctcgttccaagtttctctagacacacggtgttagatccaactcttc 191
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QY 192 taagttaagaagtaactctgttattgaagctattacaaagaaacgctactgtttcaa 251
DB 270 CAAGGGCAAGAAATACCTCGCTTCATTTAGAGAGATCAGACAGAACCGACACCTTTGA 329
QY 252 gggtaagtaagcttcttgaagacttaacatacactttgggtgctgaagacttgactcc 311
DB 330 CGGAAATATGCTTCCTCGAAGACATACAACTACAGCTTGGGTGCAGATGACCTGACTCC 389
QY 312 attcgggtgaacaaataagtttaactctgttatttaagttctacagaagatacaaggcttt 371
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QY 372 gctagaagaattgttcattcgttagagcttctgttctgtacagagattattgtcttgc 431
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QY 432 tgaagaagttcattgaaggtttcccaatctgtaagttgggtgacccaggtgttaaccaca 491
DB 510 CAAGAAATTCATCGAGGCTTCCAGAGCACCACCAAGCTGAAGGATCTCTGTCGCCAGCCGG 569
QY 492 caaagctctccagttattacagttattattccagaaggtgctgtttacaacaacacttt 551
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QY 552 gpacacaggtttgtactgtcttcgaagaatctgaattgggtgacgacgttgagctaa 611
DB 630 CGACCCAGCACCTGCATCTGTCGAAGACAGCGAATGGCCCATACCCGTGGAAGCCAA 689
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QY 672 taactgtgactgaagaagctgttgaattgaatgaatgttgcattgcattcaacactgttc 731
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RESULT 6
US-08-151-574-31
Sequence 31, Application US/08151574
Patent No. 5436156
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,574
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 6756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Aspergillus ficuum (Aspergillus niger)
STRAIN: NRRL 3135
IMMEDIATE SOURCE:
LIBRARY: lambda AF
CLONE: pAF2-3, pAF2-6, pAF2-7
FEATURE:
NAME/KEY: exon
LOCATION: 210..253
FEATURE:
NAME/KEY: intron
LOCATION: 254..355
FEATURE:
NAME/KEY: exon
LOCATION: 356..1715
FEATURE:
NAME/KEY: CDS
LOCATION: join(210..253, 356..1715)
OTHER INFORMATION: /codon_start= 210

SEQUENCE CHARACTERISTICS:

LENGTH: 6756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Aspergillus ficuum* (*Aspergillus niger*)
STRAIN: NRRL 3135
IMMEDIATE SOURCE:
LIBRARY: Lambda AF
CLONE: pAF2-3, pAF2-6, pAF2-7
FEATURE:
NAME/KEY: exon
LOCATION: 210..253
FEATURE:
NAME/KEY: intron
LOCATION: 254..355
FEATURE:
NAME/KEY: exon
LOCATION: 356..1715
FEATURE:
NAME/KEY: CDS
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OTHER INFORMATION: /product= "Phytase"

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LOCATION: 210..380
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 381..1712
IDENTIFICATION METHOD: experimental
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OTHER INFORMATION: /phosphatase"
OTHER INFORMATION: /product= "Phytase"
OTHER INFORMATION: /evidence= EXPERIMENTAL

US-08-419-448-31

Query Match 45.8%; Score 606.4; DB 2; Length 6756;
Best local Similarity 66.4%; Pred. NO. 1.8e-166;
Matches 871; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

QY 12 ttgtgacactgttgacggtgtgttaacaaatgtttcccaagaataattctcaactgtgtgggtca 71
DB 401 ttggcagatcgggtcagatcaggggtatcaatgcttctccgagacttggcacttgggggtca 460
QY 72 atactctcattctctctgttggtgacgaactctgctattcttccagacgttccaaagg 131
DB 461 ataccgacgggttcttcttcttgacgaacgaatcggtcatctccctgaggtgcccggcg 520
QY 132 ttgtagacttcttcttcaagtgttcttagacacacggtgttagatcccaactcttc 191
DB 521 atgcagagtcactttcgctcaggtctctccggtcatggagcgggtatccgacggactc 580
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DB 581 caaggcgaagaataatctcggtcttcttctgagagatcagcagacgacacacacacac 640
QY 252 gggtaagtacgctttcttgaagactacaactacacttgggtgctgacactgactcc 311
DB 641 cggaaatgatgcttcttcttgacacatacaactacacttgggtgagatgacctgactcc 700
QY 312 attcgttgacacaaatgttttaactctgttttaagtctacagaagatacaaggcttt 371
DB 701 cttcgaggaacaggagctagtcaactcggcgtatcaagtctaccagcgggtacgaatcgct 760
QY 372 gactgaagaagtgttccattctgttagactctgttctgtctacagagattattcttcgc 431
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QY 432 tgaaaagttcattgaaggttttccaatctgcttaagtgttgctgaccagggtgctaaaccaca 491
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QY 492 ccaagcttctccagttattatacaggttattattccagaaggtgctgttatacaacaacacttt 551
DB 881 ccaatcgctgcggcccaagatcgaggtgtgtcatttccgaggccagctcatccaaacactct 940
QY 552 ggaacaaggtttgtactgctttgaaagaatctgaattgggtgacgagttgaagactaa 611
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QY 732 tagaactctgacgtactcaaatgtctcattctgtgactgttcaactcagacgaatg 791
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QY 852 attgggtccagctcgaaggtgtgtgttctgaacgaatgattgtagattgaactc 911
DB 1241 gctcggccgacccagggcgctgggtacgctaacgagctcatcgcccgctgaccacac 1300
QY 912 tccagttcaagacacacactcttactaacacacacttggacttaacccagctacttccc 971
DB 1301 gctgtccacatgacacacacacacacacacacacacacacacacacacacacacac 1360
QY 972 attgaacgtacttctgaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1031
DB 1361 gctcaactctactctctacggcgacttttgcgatgacaacggcactcatctccattctct 1420
QY 1032 cgtttgggtttgtacaaggtactaagcattgtctactacttctgttgaactctatga 1091
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QY 1092 agaaactgacggttgcgctcttggactgttccattcgtgtgactgagagcttactga 1151
DB 1481 ccagacagatggattctgctgtgttgagcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1540
QY 1152 aatgatgcaatgtgaagctgaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 1211
DB 1541 gatgatgcaggtgtcagggcgagcagggcgagcagggcgagcagggcgagcagggcgag 1600
QY 1212 gtttccattcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1271
DB 1601 tgtccccctcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1660
QY 1272 tgaaggtttgtcttccgtagatctgtgtgaactggggaagaaatgttgcgt 1323
DB 1661 caggggtgtgagcttgcctgagatctgggggtgattggggcgaggtgtgtgtgtgtgt 1712

RESULT 8

US-07-923-724-7
; Sequence 7, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Toikkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.

APPLICANT: KONDO, Hidemasa
 APPLICANT: ANAZAWA, Hideharu
 APPLICANT: KANEKO, Syunichi
 APPLICANT: NAGASHIMA, Tadashi
 APPLICANT: TANGE, Tatsuya
 TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
 FILE REFERENCE: 81356/124
 CURRENT APPLICATION NUMBER: US/09/155,855
 EARLIER FILING DATE: 1998-10-05
 EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
 EARLIER FILING DATE: 1997-04-04
 EARLIER APPLICATION NUMBER: JP 084314
 EARLIER FILING DATE: 1996-04-05
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5

LENGTH: 1515
 TYPE: DNA
 ORGANISM: Aspergillus niger
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 NAME/KEY: sig_peptide
 LOCATION: (1)..(45)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(45)
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: (157)..(183)
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (184)..(1512)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (157)..(1512)
 US-09-155-855-5

Query Match 45.0%; Score 595; DB 3; Length 1515;
 Best Local Similarity 65.8%; Pred. No. 1,9e-163;
 Matches 865; Conservative 0; Mismatches 450; Indels 0; Gaps 0;

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 QY 69 tcaactatccattctcttctgtgacgaattctgtatttccacagcttccaaa 128
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RESULT 13
 US-08-819-825-1
 ; Sequence 1, Application US/08819825
 ; Patent No. 5866118
 ; GENERAL INFORMATION:
 ; APPLICANT: Berka, Randy M.
 ; APPLICANT: Ray, Michael W.
 ; APPLICANT: Klotz, Alan V.
 ; TITLE OF INVENTION: Polypeptides Having Phytase Activity
 ; TITLE OF INVENTION: And Nucleic Acids Encoding Same
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5866118o No. 5866118th America, Inc.
 ; STREET: 405 Lexington Avenue, Suite 6400
 ; CITY: New York
 ; STATE: New York


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; FILING DATE: 07-MAY-1997
; APPLICATION NUMBER: 60/046,081
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 5101.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-221-654-1

Query Match          9.98; Score 131.4; DB 3; Length 1320;
Best Local Similarity 56.98; Pred. No. 8.2e-29;
Matches 268; Conservative 0; Mismatches 191; Indels 12; Gaps 1;

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Db 942 GCTCAGACGACGACCTGCAACATTCGCCGCTGACCGTACGTTCTACGCCGACTTCTCGCA 1001

QY 1005 egacaacactatggtttctattttctgtttctgtttgtttgtttgtttgtttgtttgttt 1055
Db 1002 TGATAACACCATGTGTGCCCATCTTTTGGCGGCTCGGGGCTCTTCAAGGCCAC 1052
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Job time: 425 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 17:47:14 ; Search time 7358.5 Seconds
(without alignments)
1699.548 Million cell updates/sec

Title: US-09-488-265-25_COPY_90_1412
Perfect score: 1323
Sequence: 1 aattctcactctgtgacac.....actgggaagaatgtttgcgt 1323

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

QY	955	aaccagctactttccattgaa	977
Db	27	AATCCGAAACAGTTTCGGTTGGA	5
RESULT 9			
CNS04ESQ			
LOCUS		DNA	GSS
DEFINITION	Tetraodon nigroviridis genome survey sequence T7 end of clone 105015 of library G from Tetraodon nigroviridis, genomic survey sequence.	21-MAY-2000	
ACCESSION	AL287459.1	GI:8025953	
VERSION			
KEYWORDS	GSS; genome survey sequence.		
SOURCE	Tetraodon nigroviridis.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acantopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.		
REFERENCE	1 (bases 1 to 1016)		
AUTHORS	Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.		
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1016)		
AUTHORS	Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.		
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 1016)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases		
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.		
FEATURES	Location/Qualifiers		
source	1..1016		
/organism="Tetraodon nigroviridis"			
/db_xref="taxon:99883"			
/clone="105015"			
/clone.lib="G"			
/note="genoscope sequence ID : COBG105AH08LP1-end : T7"			
BASE COUNT	227 a 259 c 231 g 287 t	12 others	
ORIGIN			
Query Match	3.4%; Score 45.2;	DB 221;	Length 1016;
Best Local Similarity	48.4%;	Pred. No. 0.05;	
Matches	123; Conservative	1; Mismatches 130; Indels	0; Gaps 0;
QY	497	citctccagtattaacgttatatccagaagtgctgggttacacaacacacttggacc	556
Db	722	CTGCCTGTACTGCTGTGTGTACTGCTGTGTGTACTGCTGTGTATTWACTGCTGTGTA	781
QY	557	acggttgttgactccttcgaagaactcgaattgggtgacgaogttgaagcaacttca	616
Db	782	CTGCCTGTACTGCTGTGTGTACTGCTGTGTGTACTGCTGTGTATTWACTGCTGTGTA	841
QY	617	ctgctgtttcgctccacctatttagacgtattggaagctcacctgccagggtttaact	676
Db	842	CTGCTGTGTTHACTCATGTATTACTGCTGTGTGTACTGCTGTGTATTWACTGCTGTGTA	901
QY	677	tgaactgaagaagacttttaactgatgcacatgtgtccattgcgacactgttgcagaa	736
Db	902	CTGCTGTGTTHACTGCTGTGTACGGCTGTGTGTACTGCTGTGTATTWACTGCTGTGTA	961

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RESULT 11
LOCUS      BF637070
DEFINITION BF637070 468 bp mRNA EST 19-DEC-2000
            NF049F02LF1016 Developing leaf Medicago truncatula cDNA clone
ACCESSION  BF637070
VERSION     BF637070
KEYWORDS    BF637070.1 GI:11901228
SOURCE      barrel medic.
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.
REFERENCE   1 (bases 1 to 468)
AUTHORS     Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
            Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
TITLE       Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula leaf library
JOURNAL     Unpublished (2000)
COMMENT     Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7391
            Fax: 580 221 7380
            Email: gdmay@noble.org
            Insert Length: 468 Std Error: 0.00
            Plate: 049 row: F column: 02
            Seq primer: TCACACAGGAAACAGCATGAC.
FEATURES   Location/Qualifiers
            source          1..468
                        /organism="Medicago truncatula"
                        /db_xref="taxon:3880"
                        /clone="NF049F02LF"
                        /clone_lib="Developing leaf"
                        /tissue_type="leaf"
                        /dev_stage="Pooled developmental"
                        /note="Vector: Lambda Zap; Contains a mixture of very
                        young, developing, mature and senescing leaves."
BASE COUNT 91 a 110 c 97 g 170 t
ORIGIN

Query Match 3.2%; Score 42; DB 151; Length 468;
Best Local Similarity 47.4%; Pred. No. 0.33;
Matches 126; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

Qy 362 acaaggcttggctagaagattgtccattcgttagagcttctgttctgcagaggtta 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 AGAATGTTTGAGTGATGTTTGACATTTTGTGTTACATCTAGTGACGTGACGATTTT 135
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 422 ttgcttctgctgaaagttcattgaaggtttccaattcgtctaagttggctgacccaggtg 481
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 136 TTAATTTTCTAAGTTTGTGTTCAATGTTTAAAGTTCTCGCGAGTTTAGTTTCAGTCCAA 195
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 482 ctaccacaccagcttccagttatttaacgcttattattccagaggtgctggttaca 541
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 196 TTTCTCTCCCTTCACCTTCAACAATGGCTTCCGAAACTCCTCAAAACGGTGTCTCTCTG 255
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 542 acaacacttggaccaggttctgactgtcttcgaagaatcgaattgggtgacgacg 601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 AAACCGCTTCTCCGGTGTGTTTCCTGCTGCTCTTCAAGCCTCAGCTCTCTGTTGAAGCTC 315
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 602 ttgaagctaacttcaactgctgttttc 627
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 316 CGAAGACTAAGAGCGCTGTGTGTC 341
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
LOCUS      AV054552
DEFINITION AV054552 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA
            AV054552 341 bp mRNA EST 23-JUN-1999
            AV054552 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA

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clone 1810031C08, mRNA sequence.
ACCESSION  AV054552
VERSION     AV054552.1 GI:5154299
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 341)
AUTHORS     Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
            Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara
            , A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
            Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,
            Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara
            , Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N.,
            Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
            Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
TITLE       RIKEN Mouse ESTs
JOURNAL     Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES   Location/Qualifiers
            source          1..341
                        /organism="Mus musculus"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="1810031C08"
                        /clone_lib="Mus musculus pancreas C57BL/6J adult"
                        /sex="male"
                        /tissue_type="pancreas"
                        /dev_stage="adult"
BASE COUNT 86 a 60 c 101 g 94 t
ORIGIN

Query Match 3.2%; Score 41.8; DB 109; Length 341;
Best Local Similarity 52.6%; Pred. No. 0.34;
Matches 91; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

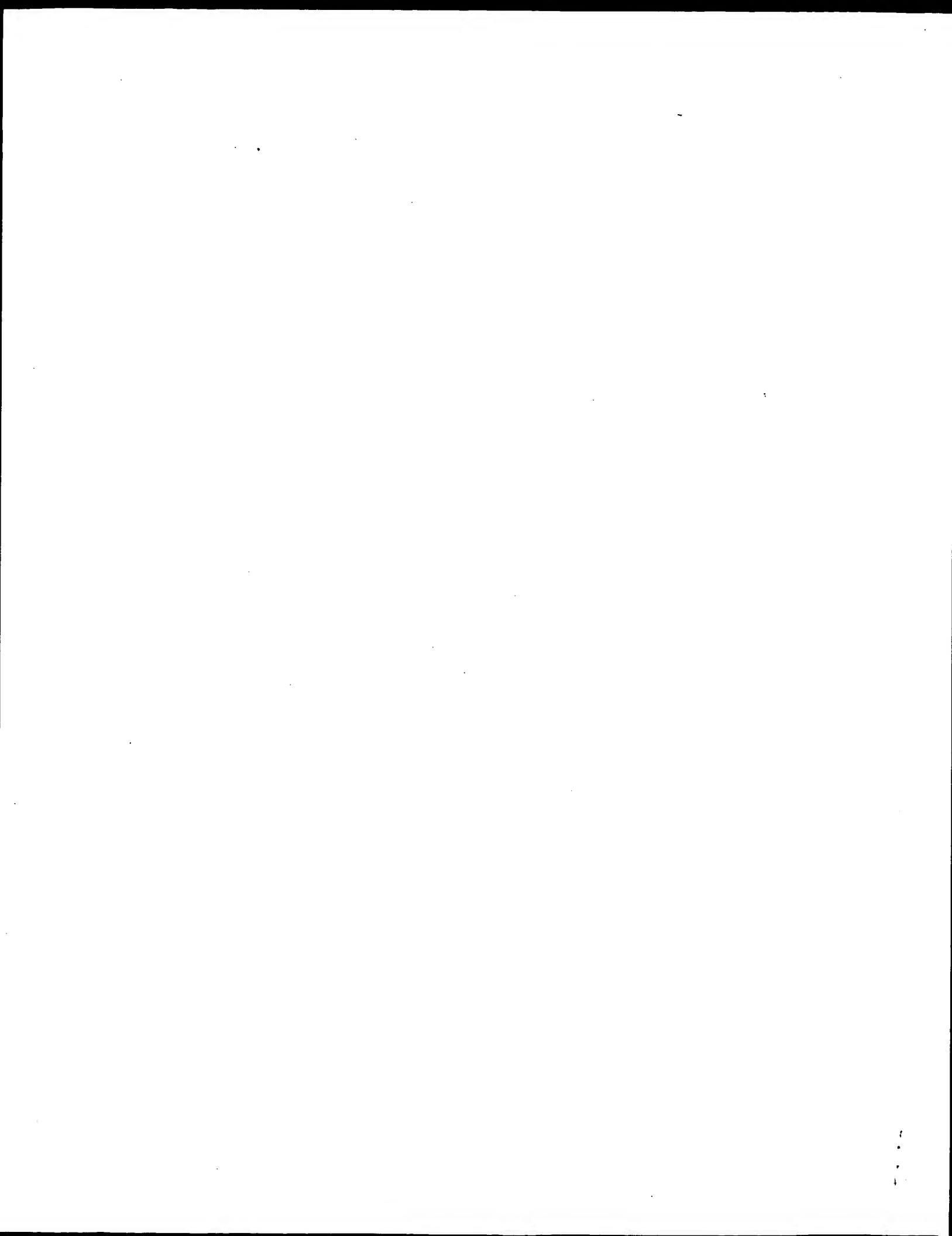
Qy 1077 tttgaatctattgaagaacgtgacgttgacgtctctcttgagactgttccattcgttcg 1136
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Db 151 TGGTGGGCGCTGTCAGAGCTGGAGTTGCGCTGCTGTTGTTGTTCCATCCACATGC 210
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Qy 1137 tagagcttcaagtgaatgatgcaatgtgaagctgaagaagcaaccattggttagagttt 1196
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 211 CGCCGCCCGCTTGAGGAGAGAAAGTGGAGCGCAAGAGGAATCCGAGGAGTTGA 270
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1197 gtttaacgacagagttgttccattgcacggttggtgtgtgtgacagttgggta 1249
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Db 271 AGATGACATGGGCTTTGTTTTTTTGGACTAAACTGTTTTTGTAAAGTTGGCTA 323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
LOCUS      AQ202816
DEFINITION AQ202816 481 bp DNA GSS
            RPC111-48J14.TK RPCI-11 Homo sapiens genomic clone RPCI-11-48J14,
            DNA sequence.
ACCESSION  AQ202816
VERSION     AQ202816.1 GI:3613607
KEYWORDS    GSS.
SOURCE      human.

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Abstract

100



PT Novel phytases with improved properties such as temperature stability,
 PT pH stability and substrate specificity, for use in pharmaceuticals and
 PT compound foods and feeds -
 XX
 PS Claim 8; Fig 5a-c; 24Opp; English.

XX The present invention describes improved phytases, preferably with
 CC increased thermostability, and methods for producing them. The methods
 CC can be used for producing phytases with improved properties e.g.
 CC temperature stability, pH stability, pH profile, temperature profile,
 CC specific activity, substrate specificity, substrate cleavage pattern,
 CC substrate binding, position specificity, the velocity and level of
 CC release of phosphate from corn, reaction rate, phytate degradation rate,
 CC and level of released phosphate. The phytases can be used to produce
 CC pharmaceutical compositions or compound food or feeds. The feed can be
 CC used to reduce levels of phytate in animal manure, by converting it
 CC into lower inositol phosphates and/or inositol and inorganic phosphate.
 CC The present sequence encodes a phytase sequence from the present
 CC invention.

XX Sequence 1426 BP; 340 A; 308 C; 310 G; 468 T; 0 other;

Query Match 100.0%; Score 1323; DB 21; Length 1426;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aattcactcttgtagacactgttgacggtgtttacacaaatgtttccacagaattctcac 60
 DB 90 aattcactcttgtagacactgttgacggtgtttacacaaatgtttccacagaattctcac 149
 QY 61 ttgtgggtgcaactcctccactctctctctgtgtgacgaatctgtatttccagac 120
 DB 150 ttgtgggtgcaactcctccactctctctgtgtgacgaatctgtatttccagac 209
 QY 121 gttccaaagggtgttagagttactttcgtttcgaatgtttgtctagacacggtgtctagatc 180
 DB 210 gttccaaagggtgttagagttactttcgtttcgaatgtttgtctagacacggtgtctagatc 269
 QY 181 ccaactctcttaagtctaaagaactctctctgtgtgacgaatctgtatttccaaagaacgct 240
 DB 270 ccaactctcttaagtctaaagaactctctgtgtgacgaatctgtatttccaaagaacgct 329
 QY 241 actgctttcaagggttaagtacgctttcttgaaactctcaactacacactttgggtgctgac 300
 DB 330 actgctttcaagggttaagtacgctttcttgaaactctcaactacacactttgggtgctgac 389
 QY 301 gacttgactcattcgttgacacacaaatggttaactctggtattatgatttctacagaaga 360
 DB 390 gacttgactcattcgttgacacacaaatggttaactctggtattatgatttctacagaaga 449
 QY 361 tacaaggcttgcttagaagaatgttccactctgttagagcttctgtgtgacagagtt 420
 DB 450 tacaaggcttgcttagaagaatgttccactctgttagagcttctgtgtgacagagtt 509
 QY 421 attgcttctgtgaaaagtctcaatgaaaggtttccaaactctgtaagtgtgctgaccacaggt 480
 DB 510 attgcttctgtgaaaagtctcaatgaaaggtttccaaactctgtaagtgtgctgaccacaggt 569
 QY 481 gtaacccacacacaaagcttctccagttattatcaactgtattattccagaaggtgtggtttac 540
 DB 570 gtaacccacacacaaagcttctccagttattatcaactgtattattccagaaggtgtggtttac 629
 QY 541 aacaacactttggaccacggtttgtgactgtttcgaagaatctgaatgtggtgacgac 600
 DB 630 aacaacactttggaccacggtttgtgactgtttcgaagaatctgaatgtggtgacgac 689
 QY 601 gttgaagcttaactcactgctgttttcgctccacactattagagctagattggaagctcac 660
 DB 690 gttgaagcttaactcactgctgttttcgctccacactattagagctagattggaagctcac 749
 QY 661 ttgcccaggtgttaacttgactgacgaagaacggttgtttaactgtgacatgtgtccattc 720
 DB 1412 ttgcccaggtgttaacttgactgacgaagaacggttgtttaactgtgacatgtgtccattc 809
 QY 721 gacactgttgcttagaactctgacgctactcaattgtctccattctgactgtgactgtgtcact 780
 DB 810 gacactgttgcttagaactctgacgctactcaattgtctccattctgactgtgactgtgtcact 869
 QY 781 cagcagaatgattcaatacagactacttgcaatctttgggttaagtactacggttacggt 840
 DB 870 cagcagaatgattcaatacagactacttgcaatctttgggttaagtactacggttacggt 929
 QY 841 gctgtaacccacttggtgtccagctcaagggtgtgtgttctgttaacgaattgattgctaga 900
 DB 930 gctgtaacccacttggtgtccagctcaagggtgtgtgttctgttaacgaattgattgctaga 989
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 DB 990 ttagactcactctccagttcaagaacacacactcttacttaacacacactttggactctaaccca 1049
 QY 961 gtaactttccacttgaaacgctactttgtacgctgactctctctcagcaacacactatggtt 1020
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 QY 1021 tctattttctcgtttgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1080
 DB 1110 tctattttctcgtttgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1169
 QY 1081 gaactctattgaagaactgacggtttacgctgtctctgtgactgttccattcgtcgtcgtaga 1140
 DB 1170 gaactctattgaagaactgacggtttacgctgtctctgtgactgttccattcgtcgtcgtaga 1229
 QY 1141 gcttactgttgaaatgatgcaatgtgaagctgaaaggaaagcaaccattgtgttagagttttggtt 1200
 DB 1230 gcttactgttgaaatgatgcaatgtgaagctgaaaggaaagcaaccattgtgttagagttttggtt 1289
 QY 1201 aacgaacagagttgttccattgacaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
 DB 1290 aacgaacagagttgttccattgacaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1349
 QY 1261 gacgactctcgttgaaaggtttgtcttctcgtagatctgtgtgtgtgtgtgtgtgtgtgtgt 1320
 DB 1350 gacgactctcgttgaaaggtttgtcttctcgtagatctgtgtgtgtgtgtgtgtgtgtgtgt 1409
 QY 1321 gct 1323
 DB 1410 gct 1412

RESULT 2

AAZ59642

ID AAZ59642 standard; DNA; 1426 BP.

XX AAZ59642;

XX AC AAZ59642;

XX DT 19-APR-2000 (first entry)

XX XX

DE DNA encoding phytase-10, a consensus phytase.

XX XX

XX Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;

XX thermostable; animal feed; monogastric animal; phytate phosphorus;

XX phosphate availability; consensus; phytase-10; ds.

XX XX

OS Aspergillus terreus 9A1.

OS Aspergillus terreus cbs16.46.

OS Aspergillus niger var. awamori.

OS Aspergillus niger str. NRRL3135.

OS Aspergillus fumigatus ATCC13073.

OS Aspergillus fumigatus ATCC32722.

OS Aspergillus fumigatus ATCC58128.

OS Aspergillus fumigatus ATCC26906.

OS Aspergillus fumigatus ATCC32239.

OS Emericella nidulans.

OS Talaromyces thermophilus ATCC20186.

OS Myceliophthora thermophila.

OS Paxillus involutus NN005693.
OS Trametes pubescens NN9343.
OS Agrocyste pediades NN009289.
OS Peniophora lycii NN006113.
OS Thermomyces lanuginosa.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 12..1415
FT /*tag= a
FT /product= "Phytase-10"
FT 12..89
FT sig_peptide
FT /*tag= b
FT /note= "Signal peptide from Aspergillus terreus cbs16.46"
FT mat_peptide
FT 90..1412
FT /*tag= c
FT /product= "Mature phytase-10"
XX
XX EP969089-A1.
PN
XX
XX 05-JAN-2000.
PD
XX
XX 23-JUN-1999; 99EP-0111949.
XX
XX 29-JUN-1998; 98EP-0111960.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Brugger R, Lehmann M, Wyss M;
XX WPI; 2000-099429/09.
XX
XX New stabilized enzyme formulation, useful for feed compositions for
XX monogastric animals -
XX
XX Example 4; Fig 17; 101pp; English.
XX
XX The invention relates to a novel stabilised dry or liquid enzyme
XX formulation, comprising phytase (myo-inositol hexakisphosphate
XX phosphohydrolase) and one or more stabilising agents including
XX xylitol or ribitol; polyethylene glycols with a molecular weight of 600
XX to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
XX glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
XX The stabilised phytase formulation is used in a method for preparing a
XX feed composition for monogastric animals (e.g., pigs, poultry) and
XX provides a monogastric animal with its dietary requirements of
XX phosphorus. Although a large amount of phosphate is present in animal
XX feed in the form of phytate phosphorus, monogastric animals are unable
XX to utilise this form of phosphate, resulting in the addition of extra
XX phosphate to the feed of such animals. Phytase enhances the nutritional
XX value of plant material without the need for adding additional phosphate
XX to the feed. The level of phosphate pollution in the environment is
XX reduced by adding phytase to animal feed, as the animal can make use of
XX the inorganic phosphate liberated from phytate phosphorus using the
XX enzyme. The phytase formulation of the invention has an improved
XX thermostability and can therefore remain stable during long-term storage
XX and can withstand feed processing methods such as extrusion, expansion
XX and pelleting. The present sequence represents DNA encoding a consensus
XX sequence, designated Phytase-10, which was derived from the mature
XX phytase sequences from a variety of fungi (AAV69544-Y69546,
XX AAV69548-Y69556, AAV69564) and the Basidiomycetes phytase consensus
XX AAV69563 and additionally contains the Aspergillus terreus cbs16.46
XX signal peptide at the N-terminus.
XX
XX Sequence 1426 BP; 340 A; 308 C; 310 G; 468 T; 0 other;

Query Match 100.0%; Score 1323; DB 21; Length 1426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 aatctcactcttgacactgttgacggtggttaccacatgtttcccgaaattttctcac 60
|||||

Db 90 aattctcactctgtgacactgttgacggtggtttaccacatgtttcccgaaattttctcac 149
Qy 61 ttgtggggtcaataactctccattctctcttggctgacgaatctgtattctccagac 120
|||||
Db 150 ttgtggggtcaataactctccattctctcttggctgacgaatctgtattctcccgac 209
Qy 121 gtcccaagggtgttagagttactttcgttcaagtgtttgtctagacacggtgtgctagatc 180
|||||
Db 210 gtcccaagggtgttagagttactttcgttcaagtgtttgtctagacacggtgtgctagatc 269
Qy 181 coactcttcttaagtcttaagaagtactctgtttgattgaagtatttcaaaaagacgct 240
|||||
Db 270 coactcttcttaagtcttaagaagtactctgtttgattgaagtatttcaaaaagacgct 329
Qy 241 actgtttcaagggttaagtacgctttttgaagacttacaactacactttgggtgctgac 300
|||||
Db 330 actgtttcaagggttaagtacgctttttgaagacttacaactacactttgggtgctgac 389
Qy 301 gacttgactccattcggtgaacacacaaatggttaactctggtatttaagttctcagaaga 360
|||||
Db 390 gacttgactccattcggtgaacacacaaatggttaactctggtatttaagttctcagaaga 449
Qy 361 tacaaggctttggctagaagaattgttccattcgttagagcttctggtttgacagagtt 420
|||||
Db 450 tacaaggctttggctagaagaattgttccattcgttagagcttctggtttgacagagtt 509
Qy 421 attgcttctgctgaaaagtctcattgaagggtttccaaatctgcttaagtgtgctgacccaggt 480
|||||
Db 510 attgcttctgctgaaaagtctcattgaagggtttccaaatctgcttaagtgtgctgacccaggt 569
Qy 481 gctaaccacacacacagcttctccagttatttaacggtattattccagaagggtgctggttac 540
|||||
Db 570 gtaaccacacacacagcttctccagttatttaacggtattattccagaagggtgctggttac 629
Qy 541 aacaacactttggaccacggtttgtgtactgotttcgaagaatctgaattgggtgacgac 600
|||||
Db 630 aacaacactttggaccacggtttgtgtactgotttcgaagaatctgaattgggtgacgac 689
Qy 601 gttagagtaacttcaactgctgttttctgctccacatttagagctagattggaagctcac 660
|||||
Db 690 gttagagtaacttcaactgctgttttctgctccacatttagagctagattggaagctcac 749
Qy 661 ttgcaggtgttaacttgaactgaacgaacagctgtttaacttgatgacatgtgtccattc 720
|||||
Db 750 ttgcaggtgttaacttgaactgaacgaacagctgtttaacttgatgacatgtgtccattc 809
Qy 721 gacactgttctagaactcttgacgctactcaatttgtctccattctgtgactttgctact 780
|||||
Db 810 gacactgttctagaactcttgacgctactcaatttgtctccattctgtgactttgctact 869
Qy 781 caagcagaatggattcaatacagactacttgaacttgaatttgggttaagtacggttacggt 840
|||||
Db 870 caagcagaatggattcaatacagactacttgaacttgaatttgggttaagtacggttacggt 929
Qy 841 gctgttaaccactatgggtccagctcaagggtgtgtgttcgttaacgaattgattgctaga 900
|||||
Db 930 gctgttaaccactatgggtccagctcaagggtgtgtgttcgttaacgaattgattgctaga 989
Qy 901 ttgactcactctccagtttaagacacacacttctactaacacactttggaacttaaccca 960
|||||
Db 990 ttgactcactctccagtttaagacacacacttctactaacacactttggaacttaaccca 1049
Qy 961 gtaactttccattgaacgctactttgtacgctgactctctctcagacacacactatggtt 1020
|||||
Db 1050 gtaactttccattgaacgctactttgtacgctgactctctctcagacacacactatggtt 1109
Qy 1021 tctattttctcgctttgtggtttgtacacggttacttaagccattgtctactacttctgtt 1080
|||||
Db 1110 tctattttctcgctttgtggtttgtacacggttacttaagccattgtctactacttctgtt 1169
Qy 1081 gaactctattgaagaactgacggtttacgctgtcttcttgactgtttccattcgtgctaga 1140
|||||
Db 1170 gaactctattgaagaactgacggtttacgctgtcttcttgactgtttccattcgtgctaga 1229
|||||

QY 1141 gcttaccgttgaaatgatgcaatgtgaagctgaaaggaaccattggttagagtttgggtt 1200
 |||||
 Db 1230 gcttaccgttgaaatgatgcaatgtgaagctgaaaggaaccattggttagagtttgggtt 1289
 |||||
 QY 1201 aacgacagagttgtccattgcacggttgggttgacaaagttgggttagagttgaagaga 1260
 |||||
 Db 1290 aacgacagagttgtccattgcacggttgggttgacaaagttgggttagagttgaagaga 1349
 |||||
 QY 1261 gacgacttcgttgaaagttgttcttcgtcgtatagctggttgaaagttgggttagagtttgc 1320
 |||||
 Db 1350 gacgacttcgttgaaagttgttcttcgtcgtatagctggttgaaagttgggttagagtttgc 1409
 |||||
 QY 1321 gct 1323
 |||||
 Db 1410 gct 1412

RESULT 3
 AAZ31521
 ID AAZ31521 standard; DNA; 1404 BP.
 XX
 AC AAZ31521;
 XX
 DT 06-JAN-2000 (first entry)
 XX
 DE Consensus phytase-10-thermo(3)-Q50R-K91A coding sequence.
 XX
 KW Phytase; animal feed preparation; thermostable phytase; transgenic plant;
 KW consensus sequence; ds.
 XX
 OS Synthetic.
 XX
 PN WO948380-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 22-MAR-1999; 99WO-DK00154.
 XX
 PR 23-MAR-1998; 98DK-0000407.
 PR 19-JUN-1998; 98DK-0000806.
 PR 18-SEP-1998; 98DK-0001176.
 PR 22-JAN-1999; 99DK-0000091.
 PR 22-JAN-1999; 99DK-0000093.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Petersen S;
 XX
 DR WPI: 1999-591030/50.
 DR P-PSDB; AAY43170.
 XX
 PT Preparing animal feed using a thermostable phytase -
 PS Example 3; Fig 10; 71pp; English.
 XX
 CC This sequence encodes the consensus phytase-10-thermo(3)-Q50R-K91A.
 CC The invention relates to a process for preparing animal feed by
 CC agglomerating feed ingredients with a thermostable phytase, which is
 CC added before or during agglomeration. The thermostable phytase is useful
 CC for expression in transgenic plants. These plants are useful in the
 CC preparation of animal feed itself. The thermostable phytase allows animal
 CC feed to be produced more efficiently, in addition to improved
 CC phytase-expressing transgenic plants. These plants provide a feed
 CC ingredient and a feed additive (phytase) simultaneously.
 XX
 SQ Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;

Query Match 98.8%; Score 1307; DB 20; Length 1404;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1313; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 aattctcaactcttgacactgttgacggttggttaccaatgtttccacagaatttctcac 60
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 Db 79 aactctcaactcttgacactgttgacggttggttaccaatgtttccacagaatttctcac 138
 |||||
 QY 61 ttgtggggttcaactctccattcttcttcttgggtgacgaattctgtatttctccagac 120
 |||||
 Db 139 ttgtggggttcaactctccattcttcttcttgggtgacgaattctgtatttctccagac 198
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 QY 121 gttccaaaggggttagagttactcttcgttccaaagtttcttagacacggtgctagatcac 180
 |||||
 Db 199 gttccaaaggggttagagttactcttcgttccaaagtttcttagacacggtgctagatcac 258
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 QY 181 ccaacttctcttaagtctaaagaagttactctgcttctgattgaagctatttccaaagaagcgt 240
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 Db 259 ccaacttctctgctctaaagggttactctgcttctgattgaagctatttccaaagaagcgt 318
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 QY 241 actgctttcaagggtlaagtagcgtcttcttgaagacttacaactacacttttgggtgctgac 300
 |||||
 Db 319 actgctttcaagggtlaagtagcgtcttcttgaagacttacaactacacttttgggtgctgac 378
 |||||
 QY 301 gacttgactccattcgttgacacacaaagtgttaactctctgtatttaagtctctacagaaga 360
 |||||
 Db 379 gacttgactccattcgttgacacacaaagtgttaactctctgtatttaagtctctacagaaga 438
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 QY 361 tacaaggcttggctagaaagattgttccattcgttagagcttctggtctgacagagtt 420
 |||||
 Db 439 tacaaggcttggctagaaagattgttccattcgttagagcttctggtctgacagagtt 498
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 QY 421 atgcttctctgaaagttcattgaagtttccaatctgctaagttggtgacacacaggt 480
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 Db 499 atgcttctctgaaagttcattgaagtttccaatctgctaagttggtgacacacaggt 558
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 QY 481 gctaaacccacacaaagcttctccagttatttaacgtttatttaccagaaggtgctggttac 540
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 Db 559 gctaaacccacacaaagcttctccagttatttaacgtttatttaccagaaggtgctggttac 618
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 QY 541 aacaacactttgacacacaggttctgactgcttccgaagaatctgaattgggtgacgac 600
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 Db 619 aacaacactttgacacacaggttctgactgcttccgaagaatctgaattgggtgacgac 678
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 QY 601 gttgaagctaaactcactgctgttttcgctccacatttagagctagattggaagctcac 660
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 Db 679 gttgaagctaaactcactgctgttttcgctccacatttagagctagattggaagctcac 738
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 QY 661 ttgccaggtgttaactgactgacgaagcgttctgatttaactgattgacatgtgtccattc 720
 |||||
 Db 739 ttgccaggtgttaactgactgacgaagcgttctgatttaactgattgacatgtgtccattc 798
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 QY 721 gacactgttgctagaacttctgacgctactcactgctccattctgtgacttcttcaact 780
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 Db 799 gacactgttgctagaacttctgacgctactcactgctccattctgtgacttcttcaact 858
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 QY 781 cagcagaatgattccaatacactacttgcacttgcacttgcacttgcacttgcacttgcact 840
 |||||
 Db 859 cagcagaatgattccaatacactacttgcacttgcacttgcacttgcacttgcacttgcact 918
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 QY 841 gctggtaacccattgggtccagctcaaggtgttgggttctgatttaacgaattgtgattctaga 900
 |||||
 Db 919 gctggtaacccattgggtccagctcaaggtgttgggttctgatttaacgaattgtgattctaga 978
 |||||
 QY 901 ttgactcactctccagttccaagacacacactcttactaacacacactttggactctaaccaca 960
 |||||
 Db 979 ttgactcactctccagttccaagacacacactcttactaacacacactttggactctaaccaca 1038
 |||||
 QY 961 gctacttcccaattgaacgctacttgcgtgacttctctcagacacacacttgcacttgcact 1020
 |||||
 Db 1039 gctacttcccaattgaacgctacttgcgtgacttctctcagacacacacttgcacttgcact 1098
 |||||
 QY 1021 tctattttcttcgcttgggtttgtacacaggtacttaagcattgtctactacttctgt 1080
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 Db 1099 tctattttcttcgcttgggtttgtacacaggtacttaagcattgtctactacttctgt 1158
 |||||
 QY 1081 gaattattgaagaactgacggttacgctgcttcttggactgttccattcgtgctgtaga 1140

Db 1039 gctactttccattgaacgtaactttgtacgctgaacttctctcacgacacactatggtt 1098
 QY 1021 tctattttcttcgtttgggtttgtaacacggtactaagccattgtctactacttctgtt 1080
 Db 1099 tctattttcttcgtttgggtttgtaacacggtactaagccattgtctactacttctgtt 1158
 QY 1081 gaactctatgaagaactgaacggttacgctgcttcttggactgttccattcgtctagata 1140
 Db 1159 gaactctatgaagaactgaacggttacgctgcttcttggactgttccattcgtctagata 1218
 QY 1141 gcttactgtgaatgatgcaatgtgaagctgaagaaagaaacattggttagagtttgggtt 1200
 Db 1219 gcttactgtgaatgatgcaatgtgaagctgaagaaagaaacattggttagagtttgggtt 1278
 QY 1201 aacgacagaggtgttccattgcacggtgttgggttgacaaagtgggttagatgtaagaga 1260
 Db 1279 aacgacagaggtgttccattgcacggtgttgggttgacaaagtgggttagatgtaagaga 1338
 QY 1261 gacgactctgtgaagaagttgttcttcgtctagatctggtgtaactgggaaagaatgtttc 1320
 Db 1339 gacgactctgtgaagaagttgttcttcgtctagatctggtgtaactgggaaagaatgtttc 1398
 QY 1321 gct 1323
 Db 1399 gct 1401

RESULT 5

AAZ59716
ID AAZ59716 standard; DNA; 1404 BP.

AC AAZ59716;

XX 19-APR-2000 (first entry)

DE DNA encoding a mutant phytase-10, phytase-10-thermo[3]-Q50T-K91A.

KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
 KW thermostable; animal feed; monogastric animal; phytate phosphorus;
 KW phosphate availability; consensus; mutant; ds.

XX Aspergillus terreus 9A1.
 OS Aspergillus terreus CBS16.46.
 OS Aspergillus niger var. awamori.
 OS Aspergillus niger str. NRRL3135.
 OS Aspergillus fumigatus ATCC13073.
 OS Aspergillus fumigatus ATCC32722.
 OS Aspergillus fumigatus ATCC58128.
 OS Aspergillus fumigatus ATCC26906.
 OS Aspergillus fumigatus ATCC32239.
 OS Emericella nidulans.
 OS Talaromyces thermophilus ATCC20186.
 OS Myceliophthora thermophila.
 OS Paxillus involutus NN005693.
 OS Trametes pubescens NN9343.
 OS Agrocybe pediades NN009289.
 OS Peniophora lycii NN006113.
 OS Thermomyces lanuginosa.
 OS Synthetic.

Key Location/Qualifiers

CDS 1..1404
 FT //tag= a
 FT /product= "Phytase-10-thermo[3]-Q50T-K91A"

EP969089-A1.

XX 05-JAN-2000.

PF 23-JUN-1999; 99EP-0111949.

XX 29-JUN-1998; 98EP-0111960.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA Brugger R, Lehmann M, Wyss M;
 PI WPI; 2000-099429/09.

New stabilised enzyme formulation, useful for feed compositions for monogastric animals -

Example 5; Fig 19; 101pp; English.

The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilising agents including xylitol or ribitol; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal feed in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents DNA encoding a mutant phytase-10 consensus sequence, phytase-10-thermo[3]-Q50T-K91A, which has a temperature optimum and melting point 4 degrees Celsius higher than that of phytase-10 (AAI69566). Its specific activity with phytate as a substrate is also strongly increased.

Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;

Query Match 98.8%; Score 1307; DB 21; Length 1404;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1313; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 aattctcaactcttctgacacactgttgacggtgttgtaacaaatgtttccacagaaattctcac 60
 Db 79 aactctcaactcttctgacacactgttgacggtgttgtaacaaatgtttccacagaaattctcac 138
 QY 61 ttgtggggtcaataactctctcattctctcttggctgaacgaatctgctatttctccagac 120
 Db 139 ttgtggggtacataactctcattctctcttggctgaacgaatctgctatttctccagac 198
 QY 121 gttccaaagggttgtagagttactcttcgttcaagtttctctagacacggtgctagatac 180
 Db 199 gttccaaagggttgtagagttactcttcgttcaagtttctctagacacggtgctagatac 258
 QY 181 ccaactctcttaagctctaagaagtactctgctttgattgaagctattcaaaagaacact 240
 Db 259 ccaactctctgctctaaaggcgtactctgctttgattgaagctattcaaaagaacact 318
 QY 241 actgctttcaagggttaagtacgctcttcttgaagacttacaactacactttgggtgctgac 300
 Db 319 actgctttcaagggttaagtacgctcttcttgaagacttacaactacactttgggtgctgac 378
 QY 301 gacttgactccattcgggtgaacaaacaaatggttaactctggtatttaagtctacagaaga 360
 Db 379 gacttgactccattcgggtgaacaaacaaatggttaactctggtatttaagtctacagaaga 438
 QY 361 tacaaggctttgctagaagaagtgttccattcgttagagcttctggtctctgacagagtt 420
 Db 439 tacaaggctttgctagaagaagtgttccattcgttagagcttctggtctctgacagagtt 498

QY	421	atgctctctgctgaagaagttcaattgaagggtttccaaatctgtgaagtgtggtgacccaggt	480
DB	499	attgctctctgctgaagaagttcaattgaagggtttccaaatctgtgaagtgtggtgacccaggt	558
QY	481	gctaaccacacacaagctctccagttacttaacggttatattccagaaggtgctggtttac	540
DB	559	gctaaccacacacaagctctccagttacttaacggttatattccagaaggtgctggtttac	618
QY	541	aacaacactttggaccacaggtttgtgtactgctttccagaagaatctgaattgggtgacgac	600
DB	619	aacaacactttggaccacaggtttgtgtactgctttccagaagaatctgaattgggtgacgac	678
QY	601	gttgaagctaacttcaactgctgttttcgctccacatattagagtagatgtggaagctcac	660
DB	679	gttgaagctaacttcaactgctgttttcgctccacatattagagtagatgtggaagctcac	738
QY	661	tgcgcagggttaacttgactgaagaaagcgtgtgttaactgtatgagacatgtgtccattc	720
DB	739	tgcgcagggtttaaacttggactgaagaaagcgtgtgttaactgtatgagacatgtgtccattc	798
QY	721	gacactgttgcctagaaacttctgacgctactcaaatgtgtccattctctgtgacttgttcaact	780
DB	799	gacactgttgcctagaaacttctgacgctactcaaatgtgtccattctctgtgacttgttcaact	858
QY	781	cacgacgaatggattcaataacgactacttgaacatctttgggtgaagtagtaacggttaacggt	840
DB	859	cacgacgaatggattcaataacgactacttgaacatctttgggtgaagtagtaacggttaacggt	918
QY	841	gctggttaaccacttgggtccagctcaaggtgttggtttcggttaacgaatctgattgctaga	900
DB	919	gctggttaaccacttgggtccagctcaaggtgttggtttcggttaacgaatctgattgctaga	978
QY	901	ttgactcaactctccagttccaagaccacactctataaccacactttggactcttaacccca	960
DB	979	ttgactcaactctccagttccaagaccacactctataaccacactttggactcttaacccca	1038
QY	961	gctaactttccattgaacgctactttgtacgctgactctctctccagacaacactatgggtt	1020
DB	1039	gctaactttccattgaacgctactttgtacgctgactctctctccagacaacactatgggtt	1098
QY	1021	tctattttctcgctttgggtttgtacaacggtactaaagccattgtctactactctggtt	1080
DB	1099	tctattttctcgctttgggtttgtacaacggtactaaagccattgtctactactctggtt	1158
QY	1081	gaatctattgaagaaactgacggttacgctgctcttggactgttccattcgctgctaga	1140
DB	1159	gaatctattgaagaaactgacggttactctgcttctggactgttccattcgctgctaga	1218
QY	1141	gcttaagttgaatgatgcaattggaagctgaaagggaaccatctggttagagttttgggtt	1200
DB	1219	gcttaagttgaatgatgcaattggaagctgaaagggaaccatctggttagagttttgggtt	1278
QY	1201	aacgacagagttgttccattgacaggttgtggtgttgacaagttgggttagatgtaagaga	1260
DB	1279	aacgacagagttgttccattgacaggttgtggtgttgacaagttgggttagatgtaagaga	1338
QY	1261	gacgactctgtgaagagtttgtcttcgctagatctggtgttaactgggaagaatgttttc	1320
DB	1339	gacgactctgtgaagagtttgtcttcgctagatctggtgttaactgggaagaatgttttc	1398
QY	1321	gct 1323	
DB	1399	gct 1401	

RESULT	6
AAA73292	
ID	AAA73292 standard; DNA; 1404 BP.
XX	
AC	AAA73292;
XX	
DT	05-DEC-2000 (first entry)
XX	

DE Consensus phytase 10 thermo 5 Q50T polynucleotide SEQ ID NO:94.

XX Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;

XX temperature stability; pH profile; temperature profile; reaction rate;

KW specific activity; substrate specificity; substrate cleavage pattern;

KW substrate binding; position specificity; phytate degradation rate;

KW food; feed; phytate; manure; ds.

XX Synthetic.

OS

XX WO200043503-A1.

PN

XX 27-JUL-2000.

XX

XX 21-JAN-2000; 2000WO-DK00025.

PF

XX

XX 22-JAN-1999; 99DK-0000092.

PR

PR 21-SEP-1999; 99DK-0001340.

XX

XX (NOVO) NOVO NORDISK AS.

PA

XX Lehmann M;

PI

XX WPI; 2000-491161/43.

DR

DR P-PSDB; AAB20533.

XX

XX Novel phytases with improved properties such as temperature stability,

PT pH stability and substrate specificity, for use in pharmaceuticals and

PT compound foods and feeds -

XX

XX Disclosure; Fig 24a-c; 240pp; English.

PS

XX

CC The present invention describes improved phytases, preferably with

CC increased thermostability, and methods for producing them. The methods

CC can be used for producing phytases with improved properties e.g.

CC temperature stability, pH stability, pH profile, temperature profile,

CC specific activity, substrate specificity, substrate cleavage pattern,

CC substrate binding, position specificity, the velocity and level of

CC release of phosphate from corn, reaction rate, phytate degradation rate,

CC and end level of released phosphate. The phytases can be used to produce

CC pharmaceutical compositions or compound food or feeds. The feed can be

CC used to reduce levels of phytate in animal manure, by converting it

CC into lower inositol phosphates and/or inositol and inorganic phosphate.

CC The present sequence encodes a phytase sequence from the present

CC invention.

XX

XX Sequence 1404 BP; 331 A; 311 C; 303 G; 459 T; 0 other;

SQ

Query Match	98.1%;	Score 1297.4;	DB 21;	Length 1404;
Best Local Similarity	98.8%;	pred. No. 0;		
Matches 1307;	Conservative 0;	Mismatches 16;	Indels 0;	Gaps 0;
Qy	1	aattctcactcttgtgacactgttgacggtgtggtttaccacaattttccccagagaattttctc	ac	60
Db	79	aattctcactcttgtgacactgttgacggtgtggtttaccacaattttccccagagaattttctc	ac	138
Qy	61	ttgtggggtcaataactctccattctctctttgtgtgcagcaatctgtattctccagac	120	
Db	139	ttgtggggtacatactctccattctctctttgtgtgcagcaatctgtattctccagac	198	
Qy	121	gttccaaagggtgttagaggttactttcgttccaaagttttgtctagacacggtgcttagatac	180	
Db	199	gttccaaagggtgttagaggttactttcgttccaaagttttgtctagacacggtgcttagatac	258	
Qy	181	ccaactcttctaagttctaaagttactctctgtttgattgaagctattccaagaacgc	240	
Db	259	ccaactcttctaagttctaaagttactctctgtttgattgaagctattccaagaacgc	318	
Qy	241	actgctttccaagggttaagtlacgctttcttgaaagacttacaactacatttgggtgc	300	
Db	319	actgctttccaagggttaagtlacgctttcttgaaagacttacaactacatttgggtgc	378	

301	QY	gacttgactccaattcgggtgaaacacaaatggttaactctgggtattagttctacagaaga	360
379	Db	gacttgactcccaattcgggtgaaacacaaatggttaactctgggtattagttctacagaaga	438
361	QY	tacaagggcttggcttagaagaattgttccattcgtttagagctctcgttctcgacagagtt	420
439	Db	tacaagggcttggcttagaagaattgttccattcgtttagagctctcgttctcgacagagtt	498
421	QY	attgctctcgtcgtgaaaagtctcaattgaaaggtttccaatctgctaagttggctgaccocaggt	480
499	Db	attgctctcgtcgtgaaaagtctcaattgaaaggtttccaatctgctaagttggctgaccocaggt	558
481	QY	gctaaccacacacgaagctctccagttataaacgttattataccagaaggtcgtggttac	540
559	Db	gctaaccacacacgaagctctccagttataaacgttataccagaaggtcgtggttac	618
541	QY	aacaacactttggaccacgggtttgtgactcgtttcgaagaatctgaattgggtgacgac	600
619	Db	aacaacactttggaccacgggtttgtgactcgtttcgaagaatctccctagggtgacgac	678
601	QY	gittgaagctaaacttaactcgtctgttttctccactattagagctagattggaaagctcac	660
679	Db	gittgaagctaaacttaactcgtctgttttctccactattagagctagattggaaagctcac	738
661	QY	ttagcaggtgtttaacttgactgacgaagaagcttgtttaacttgaaggacatgtgtccattc	720
739	Db	ttagcaggtgtttaacttgactgacgaagaagcttgtttaacttgaaggacatgtgtccattc	798
721	QY	gaacttgtctgtagaaactctgaagctactcaattgtctccattctcgtacttgttcaact	780
799	Db	gaacttgtctgtagaaactctgaagctactcaattgtctccattctcgtacttgttcaact	858
781	QY	cacgacgaatgattcaatagactactcgaactcgaactcgttggttgggttaagtaactcaaggttacggt	840
859	Db	cacgacgaatgattcaatagactactcgaactcgaactcgttggttgggttaagtaactcaaggttacggt	918
841	QY	gctggttaaccattgggttccagctcaaggtgtgtggttcgtttaacgaatttgattgctaga	900
919	Db	gctggttaaccattgggttccagctcaaggtgtgtggttcgtttaacgaatttgattgctaga	978
901	QY	ttagactcaactctccagttcaagaccacacactctactaaccacactttggactctaaacca	960
979	Db	ttagactcaactctccagttcaagaccacacactctactaaccacactttggactctaaacca	1038
961	QY	gctactttcccaattgaacgctactttgaecgtgaactctctcagacacacactatggtt	1020
1039	Db	gctactttcccaattgaacgctactttgaecgtgaactctctcagacacacactatggtt	1098
1021	QY	tctattttcttcgctttgggtttgtacaacggttactaaagccatttgtctactactctgtt	1080
1099	Db	tctattttcttcgctttgggtttgtacaacggttactaaagccatttgtctactactctgtt	1158
1081	QY	gaactattgaagaacactgacggttacgctgctctcttggaactgttccattcgcgtctaga	1140
1159	Db	gaactattgaagaacactgacggttacgctgctctcttggaactgttccattcgcgtctaga	1218
1141	QY	gcttacggttgaatgatgcaatgtgaagctgaaaggaacacattgggttagagttttggtt	1200
1219	Db	gcttacggttgaatgatgcaatgtgaagctgaaaggaacacattgggttagagttttggtt	1278
1201	QY	aacgcagagagtttgttccattgcaaggttgtggtgttgacaagattgggttagatgaagaga	1260
1279	Db	aacgcagagagtttgttccattgcaaggttgtggtgttgacaagttgggttagatgaagaga	1338
1261	QY	gacgcattcgtttgaaggttgttctttcgcgtagatctggttggaactcgggaagaatgtttc	1320
1339	Db	gacgcattcgtttgaaggttgttctttcgcgtagatctggttggaactcgggaagaatgtttc	1398
1321	QY	gct 1323	
1399	Db	gct 1401	

RESULT 7

AA73293

ID AAA73293 standard; DNA; 1404 BP.

XX AC

XX AAA73293;

DT 05-DEC-2000 (first entry)

XX DE

XX Consensus phytase 10 thermo 5 Q50T K91A polynucleotide SEQ ID NO:96.

XX KW

XX Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;

XX KW

XX temperature stability; pH profile; temperature profile; reaction rate;

XX KW

XX specific activity; substrate specificity; substrate cleavage pattern;

XX KW

XX substrate binding; position specificity; phytate degradation rate;

XX KW

XX food; feed; phytate; manure; ds.

XX OS

XX Synthetic.

OS WO200043503-A1.

PN XX

XX 27-JUL-2000.

PD XX

XX 21-JAN-2000; 2000WO-DK00025.

XX PF

XX 22-JAN-1999; 99DK-0000092.

XX PR

XX 21-SEP-1999; 99DK-0001340.

XX PA

XX (NOVO) NOVO NORDISK AS.

XX PI

XX Lehmann M;

XX PT

XX WPI: 2000-491161/43.

DR DR

DR P-PSDB; AAB20534.

XX DR

XX Novel phytases with improved properties such as temperature stability,

PT PT

PT pH stability and substrate specificity, for use in pharmaceuticals and

PT PT

PT compound foods and feeds -

XX PS

XX Disclosure; Fig 25a-c; 240pp; English.

XX CC

XX The present invention describes improved phytases, preferably with

CC CC

CC increased thermostability, and methods for producing them. The methods

CC CC

CC can be used for producing phytases with improved properties e.g.

CC CC

CC temperature stability, pH stability, pH profile, temperature profile,

CC CC

CC specific activity, substrate specificity, substrate cleavage pattern,

CC CC

CC substrate binding, position specificity, the velocity and level of

CC CC

CC release of phosphate from corn, reaction rate, phytate degradation rate

CC CC

CC and end level of released phosphate. The phytases can be used to produce

CC CC

CC pharmaceutical compositions of compound food or feeds. The feed can be

CC CC

CC used to reduce levels of phytate in animal manure, by converting it

CC CC

CC into lower inositol phosphates and/or inositol and inorganic phosphate

CC CC

CC The present sequence encodes a phytase sequence from the present

CC CC

CC invention.

XX SQ

XX Sequence 1404 BP: 329 A; 312 C; 304 G; 459 T; 0 other;

1
2
3
4
5
6

QY	181	csaacttcttctaagtctctaagaagtactctgctgttgattgaagctattctaaagaacgct	240
Db	259	csaactctctgcgtctaaggcttactctgcttctgattgaagctattctaaagaacgct	318
	241	actgctttcaagggtaaagtacgctttcttgaaagcttcaactacacttttgggtgctgac	300
Db	319	actgctttcaagggttaagtacgcttctcttgaagacttacaattacactttgggtgctgac	378
QY	301	gacttgactccattcgggtgaacacaaatgggttaactctggtattaaagtctctacagaaga	360
Db	379	gacttgactccattcgggtgaacacaaatgggttaactctggtattaaagtctctacagaaga	438
QY	361	tacaaaggctttgggtagaaagattgtccattcgttagagctctbgtgtcttgacagagtt	420
Db	439	tacaaaggctttgggtagaaagattgtccattcgttagagctctbgtgtcttgacagagtt	498
QY	421	attgctctctgcgaaagttcattgaaggtttccaatctgctaagtttgggtgacctcaggt	480
Db	499	attgctctctgcgaaagttcattgaaggtttccaatctgctaagtttgggtgacctcaggt	558
QY	481	gctaaaccacaccaaagcttctccagttattaaagcttatttccagaaggtgctgggttac	540
Db	559	gctaaaccacaccaaagcttctccagttattaaagcttatttccagaaggtgctgggttac	618
QY	541	aaacacactttggaccacaggtttgtgaactgcttccgaagaatctggaattggttgacgac	600
Db	619	aaacacactttggaccacaggtttgtgaactgcttccgaagaatctggaattggttgacgac	678
QY	601	gttgaagctaaacttcaactgctgttttgcctccacattattagctagattggaagctcac	660
Db	679	gttgaagctaaacttcaactgctgttttgcctccacaaattagagctagattggaagctcac	738
QY	661	ttgccagggtttaacttgactgaacgaagcgtgtgttaacttgattggaactgtgtccattc	720
Db	739	ttgccagggtttaacttgactgaacgaagcgtgtgttaacttgaaggacactgtgtccattc	798
QY	721	gacactgttgtctagaacttctgacgctactcaaatgtgtccattctgtgacttgttcaact	780
Db	799	gacactgttgtctagaacttctgacgctactcaaatgtgtccattctgtgacttgttcaact	858
QY	781	cacgacgaattggattcaattacgactacttgaactcttttgggttaagtactacggttaacggt	840
Db	859	cacgacgaattggattcaattacgactacttgaactcttttgggttaagtactacggttaacggt	918
QY	841	gctgggtaaaccatttgggtccagctcaaggtgttgggttcgttcaacgaattgattgctaga	900
Db	919	gctgggtaaaccatttgggtccagctcaaggtgttgggttcgttcaacgaattgattgctaga	978
QY	901	ttgactcaactctccaggttcaagaccacacttctactaaccacacttttggactctaaoccca	960
Db	979	ttgactcaactctccaggttcaagaccacacttctactaaccacacttttggactctaaoccca	1038
QY	961	gctactttcccattgaacgctactttgtgaactgactctctctcaacgacacactatggtt	1020
Db	1039	gctactttcccattgaacgctactttgtgaactgactctctctcaacgacacactatggtt	1098
QY	1021	tctattttctgcgtttgggtttgacaacggttactaagccattgtctactactctggt	1080
Db	1099	tctattttctgcgtttgggtttgacaacggttactaagccattgtctactactctggt	1158
QY	1081	gaatctattgaagaaactgacggttaccgctgcttcttggactgttccattcgtgctaga	1140
Db	1159	gaatctattgaagaaactgacggttaccgctgcttcttggactgttccattcgtgctaga	1218
QY	1141	gcttaagttgaaatgatgcaattgaagctgaaaggaaacacttgggttagagttttggtt	1200
Db	1219	gcttaagttgaaatgatgcaattgaagctgaaaggaaacacttgggttagagttttggtt	1278
QY	1201	aacgacagagttgttccattgacaggttgtggtgttgacaagtttgggttagatgtaagaga	1260
Db	1279	aacgacagagttgttccattgacaggttgtggtgttgacaagtttgggttagatgtaagaga	1338
QY	1261	gaagactctgtgaaggtttgtcttctgcgtagactctggttggttaactgggaagaatgtttc	1320

Db	1339	gacgacttcgtgaaggtttcttccgcgtatcgtggtagtggaactgggaagaattgttc	
Qy	1321	gct 1323	
Db	1399	gct 1401	
 RESULT 8			
ID	AAZ27423	standard; cDNA; 1426 BP.	
XX	AAZ27423		
DT	07-DEC-1999	(first entry)	
DE	Ascomycete consensus phytase coding sequence.		
XX			
KW	Phytase; variant; enzyme; phosphorus liberation; phytase substrate;		
KW	phytate level reduction; animal manure; food preparation;		
KW	soy processing; inositol manufacture; ss.		
OS	Synthetic.		
XX			
PN	WO9949022-A1.		
PD	30-SEP-1999.		
XX			
PF	22-MAR-1999;	99WO-DK00153.	
XX			
PR	23-MAR-1998;	98DK-0000407.	
PR	19-JUN-1998;	98DK-0000806.	
PR	18-SEP-1998;	98DK-0001176.	
PR	22-JAN-1999;	99DK-0000091.	
XX			
PA	(NOVO) NOVO-NORDISK AS.		
XX			
PI	Svendsen A;		
XX			
DR	WPI; 1999-580444/49.		
DR	P-PSDB; AAY39906.		
XX			
PT	New variant phytase enzymes, used for liberating phosphorus from a		
PT	phytase substrate, for reducing phytate levels in animal manure and in		
PT	feed and food preparations -		
XX			
PS	Disclosure; Fig 9f-g; 141pp; English.		
XX			
CC	This sequence encodes the consensus Ascomycete phytase sequence.		
CC	The invention relates to variant phytase enzymes with specific amino a		
CC	substitutions for improved properties. The phytase variants can be us		
CC	for liberating phosphorus from a phytase substrate. They can be used f		
CC	reducing phytate levels in animal manure. They can be used in feed or		
CC	food preparations. The phytase DNA can also be used to produce transge		
CC	plants which can be used in feeds or foods. The phytase variants can a		
CC	be used in soy processing and in the manufacture of inositol or		
CC	derivatives. The phytase variants can have altered activities such as		
CC	stability, temperature stability, pH profile, temperature profile.		
CC	specific activity (in particular in relation to pH and temperature).		
CC	substrate specificity, substrate cleavage pattern, substrate binding,		
CC	position specificity, the velocity and level of release of phosphate		
CC	from corn, reaction rate, phytase degradation rate and end level of		
CC	released phosphate reached.		
XX			
SQ	Sequence 1426 BP; 338 A; 311 C; 308 G; 469 T; 0 other;		
Query Match 93.7%; Score 1239.8; DB 20; Length 1426;			
Best Local Similarity 96.1%; Pred. No. 0;			
Matches 1271; Conservative 0; Mismatches 52; Indels 0; Gaps			
Qy	1	aattctcactcttgtgacactgttgacgttggttaccaatttcccagaatttctcac	60

Matches	1271;	Conservative	0;	Mismatches	52;	Indels	0;	Gaps	0;
Qy	1	aattctcaactctgtgacactgttgacggtgtgttaccaaatgtttccacagaaattctcac							60
Db	90	aattctcaactctgtgacactgttgacggtgtgttaccaaatgtttccacagaaattctcac							149
Qy	61	ttgtgggtgcatactctccattctctcttctgtgtgacgaatactgtctatttctccagac							120
Db	150	ttgtgggtgtcaatactctccatactctctcttgggaagacgaatctgtctatttctccagac							209
Qy	121	gttccaaaagggttagagttactttctgttccaaatttctgtctagacacggtgtgatacac							180
Db	210	gttccagacagcttagagttactttctgaatttctgtctagacacggtgtgatacac							269
Qy	181	ccaaactcttcaagtctaaagaagctactctgtttgtattgaagctattcaaaagaacgct							240
Db	270	ccaaactcttcaagtctaaaggctactctgtttgtattgaagctattcaaaagaacgct							329
Qy	241	actgtttccaagggtaagtaagctttcttgaagacttacaactacactttgggtgtgtcac							300
Db	330	actgtttccaagggtaagtaagctttcttgaagacttacaactacactttgggtgtgtcac							389
Qy	301	gacttgactccattcgggtgaacacaaatgtttaactctggatttaagtcttcacagaaga							360
Db	390	gacttgactccattcgggtgaacacaaatgtttaactctggatttaagtcttcacagaaga							449
Qy	361	tacaagctttggctagaaaagattgtccattctgttagagcttctgttctgcacagatt							420
Db	450	tacaagctttggctagaaaagattgtccattctgttagagcttctgttctgcacagatt							509
Qy	421	attgtctctgtcgaaaaagtctcatgaaaggtttccaaatctgtcaagttggctgaccaggt							480
Db	510	attgtctctgtcgaaaaagtctcatgaaaggtttccaaatctgtcaagttggctgaccaggt							569
Qy	481	gtctaacccacacaaagcttctccagttattaaagcttatttccagaagagtgctgtgttac							540
Db	570	tctcaaccacacaaagcttctccagttattaaagcttatttccagaagagtcgctgtttac							629
Qy	541	aacaaacactttggacacagctttgtgtactcttccagaagaactctgaattgggtgcagac							600
Db	630	aacaaacactttggacacagctttgtgtactcttccagaagactctgaattgggtgcagac							689
Qy	601	gttgaaagctaaacttcaactctgtctttctgcaccactattagagctagattgggaagctcac							660
Db	690	gttgaaagctaaacttcaactctgtctttctgcaccactattagagctagattgggaagctcac							749
Qy	561	ttgccaggtgttaacttgactgacgaagaagctgtgttaacttgatggacatgtgtccattc							720
Db	750	ttgccaggtgttactttgactgacgaagaacgctgtgttacttgatggacatgtgtccattc							809
Qy	721	gacactgtgtgtagaactctgacgctactcaattgtctccattctgtgacttgttcaact							780
Db	810	gaaactgtgtgtagaactctgacgctactcaattgtctccattctgtgacttgttcaact							869
Qy	781	cacgacgaatggatttcaatcacgactacttgcgaacttttgggaagtagtactacggtttacggt							840
Db	870	cacgacgaatggagacaaacacgactacttgcgaacttcttgggaagtagtactacggtttacggt							929
Qy	841	gctgggtaacccattggggtccagctcaaggtgtgggtttcgtttaacgaattgattgtctaga							900
Db	930	gctgggtaacccattggggtccagctcaaggtgtgggtttcgtttaacgaattgattgtctaga							989
Qy	901	ttgactcaactctccagttcaagacacacacttctactaaccacactttggactctaaacca							960
Db	990	ttgacttagatctccagttcaagacacacacttctactaaccacactttggactctaaacca							1049
Qy	961	gctactttccatttgaaacgtacttttgcgctgacttctctcacgacaaacactatgttt							1020
Db	1050	gctactttccatttgaaacgtacttttgcgctgacttctctcacgacaaacactatgtatt							1109
Qy	1021	tctattttctgtctttggggtttgtacaacggtactaagccattgtctactacttctgtt							1080
Db	1110	tctattttctgtctttggggtttgtacaacggtactgtctactacttctgtctactacttctgtt							1169

Qy	1081	gaatctattgaagaactgacgggttacgcgtctctcttggaactgttccaattcgctgctaga	1144
Db	1170	gaatctattgaagaactgacggttactctctcttggaactgttccaattcgctgctaga	1229
Qy	1141	gcttacggttgaagtatgcaatgtaagctgaagctgaagaaggaaccattgggttagagtttggtt	1200
Db	1230	gcttacggttgaagtatgcaatgtaagctgaagaaggaaccattgggttagagtttggtt	1289
Qy	1201	aacgcagacagttgttccattgcacggttggtgttgacaagttgggttagatgtaagaga	1260
Db	1290	aacgcagacagttgttccattgcacggttggtgttgacaagttgggttagatgtaagaga	1349
Qy	1261	gacgaacttcgttaagagttgtcttttcgcatactggtgtaactgggaagaatgtttc	1320
Db	1350	gacgaacttcgttaagagttgtcttttcgcatactggtgtaactgggaagaatgtttc	1409
Qy	1321	gct 1323	
Db	1410	gct 1412	
RESULT 10			
AAAT73231			
ID	AAAT73231 standard; DNA; 1426 BP.		
XX			
AC	AAAT73231:		
XX			
DT	05-DEC-2000 (first entry)		
XX			
DE	Consensus phytase polynucleotide sequence SEQ ID NO:15.		
XX			
KW	Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;;		
KW	temperature stability; pH profile; temperature profile; reaction rate;		
KW	specific activity; substrate specificity; substrate cleavage pattern;		
KW	substrate binding; position specificity; phytate degradation rate;		
KW	food; feed; phytate; manure; ds.		
XX			
OS	Synthetic.		
XX			
PN	W0200043503-A1.		
XX			
PD	27-JUL-2000.		
XX			
PF	21-JAN-2000; 2000WO-DK00025.		
XX			
PR	22-JAN-1999; 99DK-0000092.		
PR	21-SEP-1999; 99DK-0001340.		
XX			
PA	(NOVO) NOVO NORDISK AS.		
XX			
PI	Lehmann M;		
XX			
DR	WPI; 2000-491161/43.		
DR	P-PSDB; AAB20515.		
XX			
PT	Novel phytases with improved properties such as temperature stability,		
PT	pH stability and substrate specificity, for use in pharmaceuticals and		
PT	compound foods and feeds -		
XX			
PS	Example 9; Fig 2a-c; 240pp; English.		
XX			
CC	The present invention describes improved phytases, preferably with		
CC	increased thermostability, and methods for producing them. The methods		
CC	can be used for producing phytases with improved properties e.g.		
CC	temperature stability, pH stability, pH profile, temperature profile,		
CC	specific activity, substrate specificity, substrate cleavage pattern,		
CC	substrate binding, position specificity, the velocity and level of		
CC	release of phosphate from corn, reaction rate, phytate degradation rate		
CC	and end level of released phosphate. The phytases can be used to produce		
CC	pharmaceutical compositions or compound food or feeds. The feed can be		
CC	used to reduce levels of phytate in animal manure, by converting it		
CC	into lower inositol phosphates and/or inositol and inorganic phosphates		

CC The present sequence encodes a phytase sequence from the present
 XX invention.
 SQ Sequence 1426 BP; 338 A; 311 C; 308 G; 469 T; 0 other;

Query Match 93.7%; Score 1239.8; DB 21; Length 1426;
 Best Local Similarity 96.1%; Pred. No. 0;
 Matches 1271; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY	1	aattctcactcttgacacactgttgacggtgtgtaccacgaattttccacgaattttccac	60
DB	90	aattctcactcttgacacactgttgacggtgtgtaccacgaattttccacgaattttccac	149
QY	61	ttgtgggtgcaatactctccactctctctctgtggtgacgaactgtgctatttccagac	120
DB	150	ttgtgggtgcaatactctccactctctctgtggtgacgaactgtgctatttccagac	209
QY	121	gttccaaagggtgtgagagttacttctgttcgaagttttgtctagacacggtgctagatc	180
DB	210	gttccagacgactgtagagttacttctgttcgaagttttgtctagacacggtgctagatc	269
QY	181	ccaactctcttaagtctaaagaactctctgttctgttgaagctattccaaagaacgct	240
DB	270	ccaactctcttaagtctaaagaactctctgttctgttgaagctattccaaagaacgct	329
QY	241	actgcttccaagggttaagtacgcttctctgaagcttcaactacactttgggtgctgac	300
DB	330	actgcttccaagggttaagtacgcttctctgaagcttcaactacactttgggtgctgac	389
QY	301	gacttgactccattcgttgacacacaaatgttaactctgtgtattacagagga	360
DB	390	gacttgactccattcgttgacacacaaatgttaactctgtgtattacagagga	449
QY	361	tacaaggcttggctagaaagtgttctcattctgttgaagcttctgttctgacagagtt	420
DB	450	tacaaggcttggctagaaagtgttctcattctgttgaagcttctgttctgacagagtt	509
QY	421	attgcttctgctgaaaggcttccatgaaggttccactctgtaagttggtgacctcaggt	480
DB	510	attgcttctgctgaaaggcttccatgaaggttccactctgtaagttggtgacctcaggt	569
QY	481	gctaaccacacacacagcttctccagttattacagcttattattccagaaggtgctggtac	540
DB	570	tctcaaccacacacacagcttctccagttattacagcttattattccagaaggtgctggtac	629
QY	541	aacaacacttggaccacggttctgtactgcttctcgaagaactgaattggtgacac	600
DB	630	aacaacacttggaccacggttctgtactgcttctcgaagaactgaattggtgacac	689
QY	601	gttgaagcttaacttcaactgctgttctcgtctccactattagagctagattggaagctcac	660
DB	690	gttgaagcttaacttcaactgctgttctcgtctccactattagagctagattggaagctcac	749
QY	661	ttgcagggttgaacttgactgacgaagaagctgtgttaactgtatggacatgtgtccattc	720
DB	750	ttgcagggttgaacttgactgacgaagaagctgtgttaactgtatggacatgtgtccattc	809
QY	721	gacactgttctgtagaactctgacgctactcaattgtctccattctgtgactgttcaact	780
DB	810	gacactgttctgtagaactctgacgctactcaattgtctccattctgtgactgttcaact	869
QY	781	cacgacgaatgattcaatcagactctgcaactcttctgtggttaagtactacggttacggt	840
DB	870	cacgacgaatgattcaatcagactctgcaactcttctgtggttaagtactacggttacggt	929
QY	841	gctggttaaccattgggttcacagctcaagggtgtgtgttctgttaacgaattgtgttaga	900
DB	930	gctggttaaccattgggttcacagctcaagggtgtgtgttctgttaacgaattgtgttaga	989
QY	901	ttgactcactctcagttcaagacacacactcttactaaacacacactttgagacttaacca	960
DB	990	ttgactcactctcagttcaagacacacactcttactaaacacacactttgagacttaacca	1049

RESULT 11

AAZ59637

ID AAZ59637 standard; DNA; 1426 BP.

XX AAZ59637;

XX 19-APR-2000 (first entry)

XX DNA encoding phytase-1, a consensus phytase.

XX Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;

XX thermostable; animal feed; monogastric animal; phytate phosphorus;

XX phosphate availability; consensus; phytase-1; ds.

XX Aspergillus terreus 9A1.

XX Aspergillus terreus CBS16.46.

XX Aspergillus niger var. awamori.

XX Aspergillus niger T213.

XX Aspergillus niger str. NRRL3135.

XX Aspergillus fumigatus ATCC13073.

XX Aspergillus fumigatus ATCC32722.

XX Aspergillus fumigatus ATCC58128.

XX Aspergillus fumigatus ATCC26906.

XX Aspergillus fumigatus ATCC32239.

XX Emericella nidulans.

XX Talaromyces thermophilus ATCC20186.

XX Myceliophthora thermophila.

XX Synthetic.

XX Key

FH Location/Qualifiers

FT 12..1415

FT /tag= a

FT /product= "Phytase-1"

FT sig_peptide

FT 12..89

FT /tag= b

FT /note= "Signal peptide from Aspergillus terreus cbs16.46"

FT mat_peptide

FT 90..1412

FT /tag= c

FT /product= "Mature phytase-1"

XX EP969089-A1.

XX 05-JAN-2000.

PD

AAA73233
ID AAA73233 standard; DNA; 1404 BP.

AC AAA73233;

DT 05-DEC-2000 (first entry)

Consensus phytase 1 thermo 8 q50t, k91a polynucleotide SEO ID NO:28

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
temperature stability; pH profile; temperature profile; reaction rate;
specific activity; substrate specificity; substrate cleavage pattern;
substrate binding; position specificity; phytate degradation rate;
food; feed; phytate; manure; ds.

OS Synthetic.

AA
PN
WO200043503-A1.

XX
PD
27-JUL-2000.

21-JAN-2000: 2000WO-DK00025

XX
PR 22-JAN-1999. 99DK-00000092

PR 21-SEP-1999; 99DK-0001340.
XX

PA (NOVO) NOVO NORDISK AS.

PI Lehmann M;

DR WPI; 2000-491161/43.

UR P-PSDB; AAB20526.
yy

PT Novel phytases with improved properties such as temperature stability,
PT pH stability and substrate specificity, for use in pharmaceuticals and
PT compound foods and feeds -

PS Claim 10; Fig 7a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present invention.

Sequence 1404 BP; 329 A; 319 C; 304 G; 452 T; 0 other;

```
Query Match          93.5%; Score 1236.6; DB 21; Length 1404;
Best Local Similarity 95.9%; Pred. NO. 0;
Matches 1269; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
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Db 79 aattctcactctttgtgacacactgtttgacggttggttaccgaatgtttccccagaaaattttctcac 138

QY 61 ttgtggggtcaatactctccattctctctcttttggctgacgaatctgctatttctccagac 120

Db
139 ttatgqqgtacctaactctccatactctctttggcagacgaaatctgctatttctccagac 198

Qy 121 qttccaaaggqgttqtatagagtactttcgttcaagtttttgtctagacacaggtgctagatac 180

Db 199 qttccagacqactqtatagaqtttacttttcqttcqaagttttqcttagacacaggtgctagatac 258

Qy 181 ccaacttcttctaagtctaagaaqtactcttgcctttgattgaaqctattcaaaaagaaacgct 240

DB 1339 gacgacttgtaaggtttgtcttcgctagatctggtgtaactggtggtgaatgtttc 1398
 QY 1321 gct 1323
 DB 1399 gct 1401
 RESULT 14
 AA259715
 ID AA259715 standard; DNA; 1404 BP.
 XX
 AC AA259715;
 XX
 DT 19-APR-2000 (first entry)
 XX
 DE DNA encoding a mutant phytase-1, phytase-1-thermo[8]-Q50T-K91A.
 XX
 KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
 KW thermostable; animal feed; monogastric animal; phytate phosphorus;
 KW phosphate availability; consensus; mutant; ds.
 XX
 OS Aspergillus terreus 9A1.
 OS Aspergillus terreus cbs16.46.
 OS Aspergillus niger var. awamori.
 OS Aspergillus niger str. NRRL3135.
 OS Aspergillus fumigatus ATCC13073.
 OS Aspergillus fumigatus ATCC32722.
 OS Aspergillus fumigatus ATCC58128.
 OS Aspergillus fumigatus ATCC26906.
 OS Aspergillus fumigatus ATCC32239.
 OS Emericella nidulans.
 OS Talaromyces thermophilus AFCC20186.
 OS Myceliophthora thermophila.
 OS Synthetic.
 XX
 FH Key
 FT Location/Qualifiers
 FT 1..1404
 FT /*tag= a
 FT /product= "Phytase-1-thermo[8]-Q50T-K91A"
 XX
 EP969089-A1.
 XX
 PD 05-JAN-2000.
 XX
 PF 23-JUN-1999; 98EP-0111949.
 XX
 PR 29-JUN-1998; 98EP-0111960.
 XX
 PA (HOPF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Brugger R, Lehmann M, Wyss M;
 XX
 DR WPI; 2000-099429/09.
 DR P-PSDB; AAY69568.
 XX
 PT New stabilised enzyme formulation, useful for feed compositions for
 PT monogastric animals -
 XX
 PS Example 5; Fig 19; 101pp; English.
 XX
 CC The invention relates to a novel stabilised dry or liquid enzyme
 CC formulation, comprising phytase (myo-inositol hexakisphosphate
 CC phosphohydrolase) and one or more stabilising agents including
 CC xylitol or ribitol; polyethylene glycols with a molecular weight of 600
 CC to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
 CC glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
 CC The stabilised phytase formulation is used in a method for preparing a
 CC feed composition for monogastric animals (e.g., pigs, poultry) and
 CC provides a monogastric animal with its dietary requirements of
 CC phosphorus. Although a large amount of phosphate is present in animal
 CC feed in the form of phytate phosphorus, monogastric animals are unable
 CC to utilise this form of phosphate, resulting in the addition of extra
 CC phosphate to the feed of such animals. Phytase enhances the nutritional

CC value of plant material without the need for adding additional phosphate
 CC to the feed. The level of phosphate pollution in the environment is
 CC reduced by adding phytase to animal feed, as the animal can make use of
 CC the inorganic phosphate liberated from phytate phosphorus using the
 CC enzyme. The phytase formulation of the invention has an improved
 CC thermostability and can therefore remain stable during long-term storage
 CC and can withstand feed processing methods such as extrusion, expansion
 CC and pelleting. The present sequence represents DNA encoding a mutant
 CC phytase-1 consensus sequence, phytase-1-thermo[8]-Q50T-K91A, which has a
 CC temperature optimum and melting point 7 degrees Celsius higher than that
 CC of phytase-1 (AAY69558).
 XX
 SQ Sequence 1404 BP; 329 A; 319 C; 304 G; 452 T; 0 other;

Query Match 93.5%; Score 1236.6; DB 21; Length 1404;
 Best Local Similarity 95.9%; Pred. No. 0;
 Matches 1269; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
 QY 1 aattctcactctgtgacactgttgacggtgtgtacacatgtttccacagaaattctcac 60
 DB 79 aattctcactctgtgacactgttgacggtgtgtacacatgtttccacagaaattctcac 138
 QY 61 ttgtgggggtcaatactctccattctctctttgttgacgagaaatctgtattttccagac 120
 DB 139 ttgtgggggtacactactctccattctctctttgttgacgagaaatctgtattttccagac 198
 QY 121 gtcccaaaaggttgtagagttactcttcgttcaagttttcttagacacggtgctagatcac 180
 DB 199 gtcccaagacgtgtagagttactcttcgttcaagttttcttagacacggtgctagatcac 258
 QY 181 ccaactcttcttaagtctaaagaagtactctgtttgattgaagctattcaaaagaacgct 240
 DB 259 ccaactcttctgcttaaggtactctgtttgattgaagctattcaaaagaacgct 318
 QY 241 actgcttctaaaggttaagtacgctttcttgagacactcaacactacactttggtgctgac 300
 DB 319 actgcttctaaaggttaagtacgctttcttgagacactcaacactacactttggtgctgac 378
 QY 301 gacttgactccattcggtgaacacaaatggttaactctggtatttaagttcacagaaga 360
 DB 379 gacttgactccattcggtgaacacaaatggttaactctggtatttaagttcacagaaga 438
 QY 361 tacaagctttgctgtagaagattgttccattcgttagagcttctggtctgacagagtt 420
 DB 439 tacaagctttgctgtagaagattgttccattcgttagagcttctggtctgacagagtt 498
 QY 421 attgcttctgctgaaaagttcattgaagtttccaatctgctaagtgtgctgaccaggt 480
 DB 499 attgcttctgctgaaaagttcattgaagtttccaatctgctaagtgtgctgaccaggt 558
 QY 481 gctaacccacacacacagcttctccagttattacgtttatttattccagaaggtgctgac 540
 DB 559 tctcaaccacacacacagcttctccagttattacgtttatttattccagaaggtgctgac 618
 QY 541 acaacacactttgaccacacggtttgtgactgctttccagaagaatctgaattggtgacgac 600
 DB 619 acaacacactttgaccacacggtttgtgactgctttccagaagaatctgaattggtgacgac 678
 QY 601 gttgaagctaaactcactgctgtttctccacactattagagctagattggaagctcac 560
 DB 679 gttgaagctaaactcactgctgtttctccacactattagagctagattggaagctcac 738
 QY 661 ttcccaggttttaactgactgacgagcgtttgttaactgtatgacatgtgtccattc 720
 DB 739 ttcccaggttttaactgactgacgagcgtttgttaactgtatgacatgtgtccattc 798
 QY 721 gacactgttctgtagaactctctgacgctactcaattgtctccattctgtgactgttcaact 780
 DB 799 gacactgtcgtagaactctctgacgctactgaattgtctccattctgtgttcaact 858
 QY 781 cagcagcgaattggaattcaactgactacttgcaatcttttgggtaagtactacaggttcaact 840

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 12:11:11 ; Search time 573.71 seconds

(without alignments)
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	1385	98.9	1404	21	AAZ59716
6	1375.4	98.2	1404	21	AAZ73292
7	1372.2	97.9	1404	21	AAZ73293
8	1317.8	94.1	1426	20	AAZ27423
9	1317.8	94.1	1426	20	AAZ3022
10	1317.8	94.1	1426	21	AAZ73231
11	1317.8	94.1	1426	21	AAZ59637
					Consensus phytase
					DNA encoding phytase
					Consensus phytase
					DNA encoding a mut
					Consensus phytase
					DNA encoding a mut
					Consensus phytase
					Ascomycete consens
					Fungal phytase gen
					Consensus phytase
					DNA encoding phytase

12	1314.6	93.8	1404	20	AAZ31520	Consensus phytase-
13	1314.6	93.8	1404	21	AAZ73233	Consensus phytase
14	1314.6	93.8	1404	21	AAZ59715	DNA encoding a mut
15	1313	93.7	1404	21	AAZ73290	Consensus phytase
16	1309.8	93.5	1404	21	AAZ73291	Consensus phytase
17	1265	90.3	1426	20	AAZ31523	Consensus phytase
18	1265	90.3	1426	21	AAZ73236	Consensus phytase
19	1265	90.3	1426	21	AAZ59738	DNA encoding phytase
20	652.8	46.6	1404	20	AAZ31522	A. fumigatus phytase
21	652.8	46.6	1404	21	AAZ73235	Aspergillus fumiga
22	652.8	46.6	1404	21	AAZ59717	DNA encoding a mut
23	621.8	44.4	1404	18	AAZ65136	Aspergillus ficum
24	620.2	44.3	1404	12	AAZ11175	Chromosomal phytas
25	620.2	44.3	1404	20	AAZ27421	A. ficum phytase
26	617	44.0	1404	12	AAZ13878	Phytase gene. Asp
27	616.2	44.0	2363	15	AAQ58126	Phytase gene. Asp
28	616.2	44.0	2379	15	AAQ56944	A. niger phytase g
29	616.2	44.0	6756	12	AAQ11174	Sequence, from ove
30	616.2	44.0	6756	18	AAZ65137	Aspergillus ficum
31	614.2	43.8	1571	19	AAZ03144	Aspergillus fumiga
32	614.2	43.8	1571	20	AAZ27422	A. fumigatus phytase
33	589.6	42.1	1515	18	AAZ96709	Aspergillus niger
34	580	41.4	1931	19	AAZ03142	Aspergillus nidula
35	580	41.4	1931	20	AAZ27413	A. nidulans phytas
36	572.4	40.9	1912	17	AAZ03743	Phytase chimeric q
37	549	39.2	1845	19	AAZ03143	Talaromyces thermo
38	547.4	39.1	1845	20	AAZ27416	T. thermophilus ph
39	533.4	38.1	1567	19	AAZ03145	Aspergillus terreu
40	533.4	38.1	2327	17	AAZ03736	Phytase gene. Asp
41	533.4	38.1	2327	20	AAZ27414	A. terreus phytase
42	510	36.4	1464	22	AAZ77030	P. hordei phytase c
43	510	36.4	1584	22	AAZ77029	Part of P.hordei p
44	510	36.4	1922	22	AAZ77028	P.hordei phytase D
45	410.4	29.3	4898	22	AAZ77031	P.hordei phytase c

ALIGNMENTS

RESULT 1
AAA73232
ID AAA73232 standard; DNA; 1426 BP.

AC AAA73232;

XX 05-DEC-2000 (first entry)

XX Consensus phytase 10 polynucleotide sequence SEQ ID NO:25.

XX Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
XX temperature stability; pH profile; temperature profile; reaction rate;
XX specific activity; substrate specificity; substrate cleavage pattern;
XX substrate binding; position specificity; phytate degradation rate;
XX food; feed; phytate; manure; ds.

OS Synthetic.

XX WO200043503-A1.

XX 27-JUL-2000.

XX 21-JAN-2000; 2000WO-DK00025.

XX 22-JAN-1999; 99DK-0000092.

XX 21-SEP-1999; 99DK-0001340.

PA (NOVO) NOVO NORDISK AS.

PI Lehmann M;

XX WPI; 2000-491161/43.

XX P-PSDB; AAB20524.

PT Novel phytases with improved properties such as temperature stability,
PT pH stability and substrate specificity, for use in pharmaceuticals and
PT compound foods and feeds -

Claim 8; Fig 5a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present invention.

Sequence 1426 BP; 340 A; 308 C; 310 G; 468 T; 0 other; XX

Query Match 100.0%; Score 1401; DB 21; Length 1426;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	atgggggtgtctgctgtactgtccattgccacctgtctgggttccacatccggtacc	60
DB			
DB	12	atgggggtgtctgctgtactgtccattgccacctgtctgggttccacatccggtacc	71
QY	61	gccttgggtcctcgttgagtaatttctactctctgtgacacgttgacaggttgacaaagt	120
DB			
DB	72	gccttgggtcctcgttgagtaatttctactctctgtgacacgttgacaggttgacaaagt	131
QY	121	ttccagaaatttctcaacttgggttccaaactctccattctctcttggctgacgaa	180
DB			
DB	132	ttccagaaatttctcaacttgggttccaaactctccattctctcttggctgacgaa	191
QY	181	ttctgctatttctccagacgttccaaagggtgtgagagttactttogtccaagttttgtct	240
DB			
DB	192	ttctgctatttctccagacgttccaaagggtgtgagagttactttogtccaagttttgtct	251
QY	241	agacacgtgtcagatcacccaaactcttctaaagttctaaagtaactctctttgattgaa	300
DB			
DB	252	agacacgtgtcagatcacccaaactcttctaaagttctaaagtaactctctttgattgaa	311
QY	301	gctattccaaagaacgctactgctttccaaagggttaagtcagcttcttgaagacttacaac	360
DB			
DB	312	gctattccaaagaacgctactgctttccaaagggttaagtcagcttcttgaagacttacaac	371
QY	361	tacactttgggtgctgacgacttgactccattcgtgtgaacacaaatggttctaactctgt	420
DB			
DB	372	tacactttgggtgctgacgacttgactccattcgtgtgaacacaaatggttctaactctgt	431
QY	421	attaagttctacagaagatcacaggctttggctgagaagaattgtccattcgttagagct	480
DB			
DB	432	attaagttctacagaagatcacaggctttggctgagaagaattgtccattcgttagagct	491
QY	481	tctggttctcacagagttattgcttctgctgaaagtctcattgaaagtttccaactctgt	540
DB			
DB	492	tctggttctcacagagttattgcttctgctgaaagtctcattgaaagtttccaactctgt	551
QY	541	aagtttggtgacccagggtgtaaccacacccaaggcttctccagttatttaacgttattt	600
DB			
DB	552	aagtttggtgacccagggtgtaaccacacccaaggcttctccagttatttaacgttattt	611
QY	601	ccagaaggtgctggttacacaacacatttggaccacggtttgtgtactgttccgaagaa	660
DB			
DB	612	ccagaaggtgctggttacacaacacatttggaccacggtttgtgtactgttccgaagaa	671
QY	661	tctgaattgggtgacgacggttgagctaacttcaactgctgttttccgtccactattaga	720

Db	672	tcgaaattgggtgacagcgttgagagctaaacttcactgctgtgttttcgctccacctattaga	731
Qy	721	gctagattggaagctcacctgcaggtgttaacttgactgacgacgacggtgtttaaacttg	780
Db	732	gctagattggaagctcacctgcaggtgttaacttgactgacgacgacggtgtttaaacttg	791
Qy	781	atggacatggtgtccattcgacacgtgtgtctagaaccttctgacgttactcaattgtctcca	840
Db	792	atggacatggtgtccattcgacacgtgtgtctagaaccttctgacgttactcaattgtctcca	851
Qy	841	ttctgtgactgttccactcacgaagaatgattcaatacagctactctgcaactcttgggt	900
Db	852	ttctgtgactgttccactcacgaagaatgattcaatacagctactctgcaactcttgggt	911
Qy	901	aagtactacggtttacggtgctggtgaaccatcgggtccagctcaaggtgtgtggtttcggt	960
Db	912	aagtactacggtttacggtgctggtgaaccatcgggtccagctcaaggtgtgtggtttcggt	971
Qy	961	aacgaaattgattgctagattgaotcactctccagttccagttcaagaccacacttctactaaccac	1020
Db	972	aacgaaattgattgctagattgaotcactctccagttccagttcaagaccacacttctactaaccac	1031
Qy	1021	actttggactctaacccagctactttcccatggaagcgtactttgtacgctgactctctct	1080
Db	1032	actttggactctaacccagctactttcccatggaagcgtactttgtacgctgactctctct	1091
Qy	1081	cacgacaacactatggtttctattttcttcgcttttgggtttgtacaacggtactaagcca	1140
Db	1092	cacgacaacactatggtttctattttcttcgcttttgggtttgtacaacggtactaagcca	1151
Qy	1141	ttgtctactactctgtgtgaattatattgaagaaactgcaggttaogctgtcttcttgact	1200
Db	1152	ttgtctactactctgtgtgaattatattgaagaaactgcaggttaogctgtcttcttgact	1211
Qy	1201	gttccattcgcgtctagagcttacgttgaattgatgcaaatgtgaagctgaaaggaacca	1260
Db	1212	gttccattcgcgtctagagcttacgttgaattgatgcaaatgtgaagctgaaaggaacca	1271
Qy	1261	ttggttagagtttttggttaacgacagagttgtcccatcgcacggttgtgtgttgacaag	1320
Db	1272	ttggttagagtttttggttaacgacagagttgtcccatcgcacggttgtgtgttgacaag	1331
Qy	1321	ttgggttagatgtgaagagagacgactcgttggaagtttgtcttttcgctagatctgggtgt	1380
Db	1332	ttgggttagatgtgaagagagacgactcgttggaagtttgtcttttcgctagatctgggtgt	1391
Qy	1381	aactgggaagaatgtttcgct 1401	
Db	1392	aactgggaagaatgtttcgct 1412	
RESULT	2		
ID	AAZ59642		
XX	AAZ59642 standard; DNA; 1426 BP.		
AC	AAZ59642;		
XX			
DT	19-APR-2000 (first entry)		
XX			
DE	DNA encoding phytase-10, a consensus phytase.		

RESULT	2	
AAZ59642		
ID	AAZ59642	standard; DNA; 1426 BP.
XX		
XX	AAZ59642;	
XX		
DT	19-APR-2000	(first entry)
XX		
DE	DNA encoding	phytase-10, a conserved
XX		
KW	Phytase:	myo-inositol hexakisphosphate
KW	thermostable;	animal feed; monoglyceride
KW	phosphate	availability; consensus
XX		
OS	<i>Aspergillus terreus</i>	9A1.
OS	<i>Aspergillus terreus</i>	cbst16.46.
OS	<i>Aspergillus niger</i>	var. awamori.
OS	<i>Aspergillus niger</i>	str. NRRL3135.
OS	<i>Aspergillus fumigatus</i>	ATCC13073.
OS	<i>Aspergillus fumigatus</i>	ATCC32722.
OS	<i>Aspergillus fumigatus</i>	ATCC58128.
OS	<i>Aspergillus fumigatus</i>	ATCC26906.

QY 1081 cagcaacacactaggtttctattttcttcgtcttgggtttgtacacggtactaaagcca 1140
 DB 1092 cagcaacacactaggtttctattttcttcgtcttgggtttgtacacggtactaaagcca 1151
 QY 1141 ttgtctactacttctgttgaaatctattgaagaactgacggttactcgtcttcttgact 1200
 DB 1152 ttgtctactacttctgttgaaatctattgaagaactgacggttactcgtcttcttgact 1211
 QY 1201 gttccattcgtctagagcttactgttgaaatgatgcaatgtgaagctgaaaggaacca 1260
 DB 1212 gttccattcgtctagagcttactgttgaaatgatgcaatgtgaagctgaaaggaacca 1271
 QY 1261 ttggttagagtttgggttaacgacagaggttctccattgacaggttgggttgacaag 1320
 DB 1272 ttggttagagtttgggttaacgacagaggttctccattgacaggttgggttgacaag 1331
 QY 1321 ttggttagagtttaagagagacgacttctgttgaaaggttcttcttcgtctagatctggt 1380
 DB 1332 ttggttagagtttaagagagacgacttctgttgaaaggttcttcttcgtctagatctggt 1391
 QY 1381 aactgggaagaatgtttcgt 1401
 DB 1392 aactgggaagaatgtttcgt 1412

RESULT 3
 ID AAZ31521 standard; DNA; 1404 BP.
 XX AC AAZ31521;
 XX DT 06-JAN-2000 (first entry)
 XX DE Consensus phytase-10-thermo(3)-Q50T-K91A coding sequence.
 XX KW Phytase; animal feed preparation; thermostable phytase; transgenic plant;
 XX KW consensus sequence; ds.
 XX OS Synthetic.
 XX PN W09948380-A1.
 XX XX 30-SEP-1999.
 XX XX 22-MAR-1999; 99WO-DK00154.
 XX XX 23-MAR-1998; 98DK-0000407.
 XX XX 19-JUN-1998; 98DK-0000806.
 XX XX 18-SEP-1998; 98DK-0001176.
 XX XX 22-JAN-1999; 99DK-0000091.
 XX XX 22-JAN-1999; 99DK-0000093.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX XX Petersen S;
 XX DR WPI; 1999-591030/50.
 XX DR P-PSDB; AAY43170.
 XX XX Preparing animal feed using a thermostable phytase -
 XX XX Example 3; Fig 10; 71pp; English.
 XX CC This sequence encodes the consensus phytase-10-thermo(3)-Q50T-K91A.
 XX CC The invention relates to a process for preparing animal feed by
 XX CC agglomerating feed ingredients with a thermostable phytase, which is
 XX CC added before or during agglomeration. The thermostable phytase is useful
 XX CC for expression in transgenic plants. These plants are useful in the
 XX CC preparation of animal feed itself. The thermostable phytase allows animal
 XX CC feed to be produced more efficiently, in addition to improved
 XX CC phytase-expressing transgenic plants. These plants provide a feed
 XX CC ingredient and a feed additive (phytase) simultaneously.

XX
 SQ Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;
 Query Match 98.9%; Score 1385; DB 20; Length 1404;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1391; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 atggcggtgtcgtcgtactactgtccattgccaccttggcttccacatccggtaacc 60
 DB 1 atggcggtgtcgtcgtactactgtccattgccaccttggcttccacatccggtaacc 60
 QY 61 gctctgggtcctcgttgtaattctcaactctctgtgacactgttgacggtggttacaatgt 120
 DB 61 gctctgggtcctcgttgtaattctcaactctctgtgacactgttgacggtggttacaatgt 120
 QY 121 tccacagaaattctcaattgtggggtcaactactctcaactctctctcttcttggctgacgaa 180
 DB 121 tccacagaaattctcaattgtggggtcaactactctcaactctctctcttcttggctgacgaa 180
 QY 181 tctgctatttctccagacgttccaaagggtgtgaggttacttcttgcgttcaagttttgtct 240
 DB 181 tctgctatttctccagacgttccaaagggtgtgaggttacttcttgcgttcaagttttgtct 240
 QY 241 agacacggtgctagatacccaacttcttcttaagtcttaagaagtactctgtttgattgaa 300
 DB 241 agacacggtgctagatacccaacttcttcttaagtcttaagaagtactctgtttgattgaa 300
 QY 301 gctattcaaaagaacgtactgttcttcaagggttaagtacgcttcttctgaaactacaac 360
 DB 301 gctattcaaaagaacgtactgttcttcaagggttaagtacgcttcttctgaaactacaac 360
 QY 361 tacactttgggtgctgacgacttgactcctcgttgacacaaatggttaactctcgtt 420
 DB 361 tacactttgggtgctgacgacttgactcctcgttgacacaaatggttaactctcgtt 420
 QY 421 attagttctacagaagatacaaggtttgctagaagaattgttccattctttagagct 480
 DB 421 attagttctacagaagatacaaggtttgctagaagaattgttccattctttagagct 480
 QY 481 tctggtctgacagagttattgttctcgtgaaagttcattgaagtttcccaatctgct 540
 DB 481 tctggtctgacagagttattgttctcgtgaaagttcattgaagtttcccaatctgct 540
 QY 541 aagtttgggtgacccaggtgctaaacccacacaaagcttctccagttattaaacttatt 600
 DB 541 aagtttgggtgacccaggtgctaaacccacacaaagcttctccagttattaaacttatt 600
 QY 601 ccagaaggtgctggttacaacacacttggacacacttggacacacttggactgtttcgagaagaa 660
 DB 601 ccagaaggtgctggttacaacacacttggacacacttggacacacttggactgtttcgagaagaa 660
 QY 661 tctgaattgggtgacgacgttgaagctaaactcactcactgttcttgcgtccaccattaga 720
 DB 661 tctgaattgggtgacgacgttgaagctaaactcactcactgttcttgcgtccaccattaga 720
 QY 721 gctagattggaagctcacttgcaggtgttaacttgactgacgaagacgttgttaacttg 780
 DB 721 gctagattggaagctcacttgcaggtgttaacttgactgacgaagacgttgttaacttg 780
 QY 781 atggacatggtccattcgcacactgttctgagaacttctgacgctactcaattgtctcca 840
 DB 781 atggacatggtccattcgcacactgttctgagaacttctgacgctactcaattgtctcca 840
 QY 841 tctctgacttctcactcagacgaatggattcaatcagactacttcaactcttgggt 900
 DB 841 tctctgacttctcactcagacgaatggattcaatcagactacttcaactcttgggt 900
 QY 901 aagttactcaggtttagcgtgtggttaacccattgggttccagctcgaaggtgttgggttctgt 960
 DB 901 aagttactcaggtttagcgtgtggttaacccattgggttccagctcgaaggtgttgggttctgt 960
 QY 961 aacgaattgattgtagattgactcactcctcaggttccaggttcaagaccacttctactaaccac 1020

QY 1 atggcggttcctgctgactgtccattgccacccttctggttccacatccggtacc 60
Db 1 atggcggttcctgctgactgtccattgccacccttctggttccacatccggtacc 60
QY 61 gccctgggtcctcgtgtaattctcaactcttctgtagacactgttgacggtgttaccatgt 120
Db 61 gccctgggtcctcgtgtaattctcaactcttctgtagacactgttgacggtgttaccatgt 120
QY 121 tcccaagaattctcaactgtgggtgcaatactctccattcttcttggctgacgaa 180
Db 121 tcccaagaattctcaactgtgggtgcaatactctccattcttcttggctgacgaa 180
QY 181 tctgctatttccagacgttccaaaagggtttagagttactcttccgttccaaagtttctct 240
Db 181 tctgctatttccagacgttccaaaagggtttagagttactcttccgttccaaagtttctct 240
QY 241 agacacggtgctagatacccaactcttcttaagttcttaagtagtactctgtttgattgaa 300
Db 241 agacacggtgctagatacccaactcttcttaagttcttaagtagtactctgtttgattgaa 300
QY 301 gctattcaaaagacgctactgtcttcaagggttaagtacgcttcttgaagacttacaac 360
Db 301 gctattcaaaagacgctactgtcttcaagggttaagtacgcttcttgaagacttacaac 360
QY 361 tacactttgggtgctgacgactgtactccattcgttggaacacaaatgggttaactctggt 420
Db 361 tacactttgggtgctgacgactgtactccattcgttggaacacaaatgggttaactctggt 420
QY 421 attaaagtctcagaagaatacaaggcttgggtgtagaagattgttccattcgttagagct 480
Db 421 attaaagtctcagaagaatacaaggcttgggtgtagaagattgttccattcgttagagct 480
QY 481 tctggtctcagacagttattgtcttctgctgaagaagttcattgaagtttcccaactcgt 540
Db 481 tctggtctcagacagttattgtcttctgctgaagaagttcattgaagtttcccaactcgt 540
QY 541 aagttggctgacccaggtgcttaacccacacacacagcttctcagttatttaacgttattatt 600
Db 541 aagttggctgacccaggtgcttaacccacacacacagcttctcagttatttaacgttattatt 600
QY 601 ccagaaggtgctgtgtacacacacacttgggtgtagaagcttctgtagctgtttgagaaga 660
Db 601 ccagaaggtgctgtgtacacacacacttgggtgtagaagcttctgtagctgtttgagaaga 660
QY 661 tctgaattgggtgacgacgcttgaagcttaactcactcgtgtttcgtccacactattaga 720
Db 661 tctgaattgggtgacgacgcttgaagcttaactcactcgtgtttcgtccacactattaga 720
QY 721 gctagattggaagctcacttgcacggtgttaacttgactgacgaagacgttgttaacttg 780
Db 721 gctagattggaagctcacttgcacggtgttaacttgactgacgaagacgttgttaacttg 780
QY 781 atggacattgttccattcagacactgttctgtagaactctcagcgtactcacttctccca 840
Db 781 atggacattgttccattcagacactgttctgtagaactctcagcgtactcacttctccca 840
QY 841 tctgtgactgttctcactcagcgaatggattcaatacactacttgcgaactcttgggt 900
Db 841 tctgtgactgttctcactcagcgaatggattcaatacactacttgcgaactcttgggt 900
QY 901 aagtactcgggttaccggtgctggttaacccattgggtcagctcaggtgttgggttctggt 960
Db 901 aagtactcgggttaccggtgctggttaacccattgggtcagctcaggtgttgggttctggt 960
QY 961 aacgaattgattgtagattgactcactcactcactcactcactcactcactcactcactc 1020
Db 961 aacgaattgattgtagattgactcactcactcactcactcactcactcactcactcactc 1020
QY 1021 acttggactctaaacacgacttctccattgacgctacttctgtagcgtgacttctct 1080
Db 1021 acttggactctaaacacgacttctccattgacgctacttctgtagcgtgacttctct 1080
QY 1081 caccgacacacatggtttctattttcttcttcttcttcttcttcttcttcttcttctt 1140

Db 1081 caccgacacacatggtttctattttcttcttcttcttcttcttcttcttcttcttctt 1140
QY 1141 ttgtctactactcttcttgaattctatttgaagaactgacggttactcgtcttcttggact 1200
Db 1141 ttgtctactactcttcttgaattctatttgaagaactgacggttactcgtcttcttggact 1200
QY 1201 gttccattcgtcgttagagcttactgttgaatgtagcaatgtgtagcgtgaaaggaacca 1260
Db 1201 gttccattcgtcgttagagcttactgttgaatgtagcaatgtgtagcgtgaaaggaacca 1260
QY 1261 ttggttagagtttgggttaacgacagagttgttccattgacaggttgggttggtagacaag 1320
Db 1261 ttggttagagtttgggttaacgacagagttgttccattgacaggttgggttggtagacaag 1320
QY 1321 ttgggttagatgtaagagacgacttcttgaagtttcttcttcttcttcttcttcttctt 1380
Db 1321 ttgggttagatgtaagagacgacttcttgaagtttcttcttcttcttcttcttcttctt 1380
QY 1381 aactgggaagaatgttctcgt 1401
Db 1381 aactgggaagaatgttctcgt 1401
RESULT 7
AAA73293
ID AAA73293 standard; DNA; 1404 BP.
XX
AC AAA73293;
XX
DT 05-DEC-2000 (first entry)
XX
Consensus phytase 10 thermo 5 Q50T K91A polynucleotide SEQ ID NO:96.
DE
XX
KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW temperature stability; pH profile; temperature profile; reaction rate;
KW specific activity; substrate specificity; substrate cleavage pattern;
KW substrate binding; position specificity; phytate degradation rate;
KW food; feed; phytate; manure; ds.
XX
OS Synthetic.
XX
PN WO200043503-A1.
XX
PD 27-JUL-2000.
XX
PF 21-JAN-2000; 2000WO-DK00025.
XX
PR 22-JAN-1999; 99DK-0000092.
XX
PR 21-SEP-1999; 99DK-0001340.
XX
PA (NOVO) NOVO NORDISK AS.
XX
PI Lehmann M;
XX
DR WPI; 2000-491161/43.
XX
DR P-PSDB; AAB20534.
PT Novel phytases with improved properties such as temperature stability,
PT pH stability and substrate specificity, for use in pharmaceuticals and
PT compound foods and feeds -
XX
PS Disclosure; Fig 25a-c; 240pp; English.
XX
CC The present invention describes improved phytases, preferably with
CC increased thermostability, and methods for producing them. The methods
CC can be used for producing phytases with improved properties e.g.
CC temperature stability, pH stability, pH profile, temperature profile,
CC specific activity, substrate specificity, substrate cleavage pattern,
CC substrate binding, position specificity, the velocity and level of
CC release of phosphate from corn, reaction rate, phytate degradation rate,
CC and end level of released phosphate. The phytases can be used to produce
CC pharmaceutical compositions or compound food or feeds. The feed can be

XX Disclosure; Fig 9f-g; 141pp; English.
 PS This sequence encodes the consensus Ascomycete phytase sequence.
 CC The invention relates to variant phytase enzymes with specific amino acid
 CC substitutions for improved properties. The phytase variants can be used
 CC for liberating phosphorus from a phytase substrate. They can be used for
 CC reducing phytate levels in animal manure. They can be used in feed or
 CC food preparations. The phytase DNA can also be used to produce transgenic
 CC plants which can be used in feeds or foods. The phytase variants can also
 CC be used in soy processing and in the manufacture of inositol or
 CC derivatives. The phytase variants can have altered activities such as pH
 CC stability, temperature stability, pH profile, temperature profile,
 CC specific activity (in particular in relation to pH and temperature),
 CC substrate specificity, substrate cleavage pattern, substrate binding,
 CC position specificity, the velocity and level of release of phosphate
 CC from corn, reaction rate, phytase degradation rate and end level of
 CC released phosphate reached.
 XX SQ Sequence 1426 BP; 338 A; 311 C; 308 G; 469 T; 0 other;

Query Match 94.1%; Score 1317.8; DB 20; Length 1426;
 Best Local Similarity 96.3%; Pred. No. 0;
 Matches 1349; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
 Qy 1 atggcgctgttcgtgctactgtccatgcccacgttgcggtccacatccggtacc 60
 Db 12 atggcgctgttcgtgctactgtccatgcccacgttgcggtccacatccggtacc 71
 Qy 61 gccttggtgctcgtggttaattcactctgttgacactgttgacggtgttaccatgt 120
 Db 72 gccttggtgctcgtggttaattcactctgttgacactgttgacggtgttaccatgt 131
 Qy 121 ttccagaaatttctactgtgggtgcaatactctccactcttcttcttgggtgacgaa 180
 Db 132 ttccagaaatttctactgtgggtgcaatactctccactcttcttcttgggtgacgaa 191
 Qy 181 tctgctatttccagacttccaaagggtgtgagttacttcttgcggttgcgtctgtct 240
 Db 192 tctgctatttccagacttccaaagggtgtgagttacttcttgcggttgcgtctgtct 251
 Qy 241 agacacggtgctagatacccaacttcttcttaagtcttaagaagtactctgttggattgaa 300
 Db 252 agacacggtgctagatacccaacttcttcttaagtcttaagaagtactctgttggattgaa 311
 Qy 301 gctattcaaaagaacgctactgttccaaagggttaagtaagcttcttgcggttgcgtctgt 360
 Db 312 gctattcaaaagaacgctactgttccaaagggttaagtaagcttcttgcggttgcgtctgt 371
 Qy 361 tacacttgggtgctgacgacttgcactccatcgtgtaacacaaatgggttaactctggt 420
 Db 372 tacacttgggtgctgacgacttgcactccatcgtgtaacacaaatgggttaactctggt 431
 Qy 421 attaaagttctacagaagatacaaggcttgggtgtagaagattgttccattcgttagagct 480
 Db 432 attaaagttctacagaagatacaaggcttgggtgtagaagattgttccattcgttagagct 491
 Qy 481 tctggttctgacagattgtcttctgctgaaagggttcaagggttccaaatctgct 540
 Db 492 tctggttctgacagattgtcttctgctgaaagggttcaagggttccaaatctgct 551
 Qy 541 aagttggctgacccaggtgcttaacccacacacacacacacacacacacacacacacacac 600
 Db 552 aagttggctgacccaggtgcttaacccacacacacacacacacacacacacacacacacac 611
 Qy 601 ccagaaggtgctggtttacacacacacacacacacacacacacacacacacacacacacacac 660
 Db 612 ccagaaggtgctggtttacacacacacacacacacacacacacacacacacacacacacacac 671
 Qy 661 tctgaattgggtgacgacttgaagcttaacttcaacttcaacttcaacttcaacttcaacttca 720
 Db 672 tctgaattgggtgacgacttgaagcttaacttcaacttcaacttcaacttcaacttcaacttca 731

Qy 721 gctagattggaagctcacttgcaggtgtttaacttgactgacgaagacgttgttaacttg 780
 Db 732 gctagattggaagctcacttgcaggtgtttaacttgactgacgaagacgttgttaacttg 791
 Qy 781 atggacatgtgtccattgacacactgttctgtagaacttctgacgtactcaacttctgctcca 840
 Db 792 atggacatgtgtccattgacacactgttctgtagaacttctgacgtactcaacttctgctcca 851
 Qy 841 ttctgtgacttctcactcagacgaatggatggaatggaatggaatggaatggaatggaatgga 900
 Db 852 ttctgtgacttctcactcagacgaatggatggaatggaatggaatggaatggaatggaatgga 911
 Qy 901 aagtactacggttgcaggtgctgctgtaacccattgggtccacgtcctcaagggttgggttctg 960
 Db 912 aagtactacggttgcaggtgctgctgtaacccattgggtccacgtcctcaagggttgggttctg 971
 Qy 961 aacgaattgattgctagattgactcactctccagttccagttccagttccagttccagttccag 1020
 Db 972 aacgaattgattgctagattgactcactctccagttccagttccagttccagttccagttccag 1031
 Qy 1021 acttgggacttaacccagctacttccacttccacttccacttccacttccacttccacttccact 1080
 Db 1032 acttgggacttaacccagctacttccacttccacttccacttccacttccacttccacttccact 1091
 Qy 1081 cagcacaacactatgtttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1140
 Db 1092 cagcacaacactatgtttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1151
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 Db 1152 ttgtctactactctctgttgatctcttcttcttcttcttcttcttcttcttcttcttcttcttct 1211
 Qy 1201 gttccattcgtctgtagacttaccgttgaatgtgaaatgtgaaatgtgaaatgtgaaatgtgaa 1260
 Db 1212 gttccattcgtctgtagacttaccgttgaatgtgaaatgtgaaatgtgaaatgtgaaatgtgaa 1271
 Qy 1261 ttgggttagagtttgggttaacacacagagttgttccattgacaggttgggttgggttggacaag 1320
 Db 1272 ttgggttagagtttgggttaacacacagagttgttccattgacaggttgggttgggttggacaag 1331
 Qy 1321 ttgggttagagtttgggttaacacacagagttgttccattgacaggttgggttgggttggacaag 1380
 Db 1332 ttgggttagagtttgggttaacacacagagttgttccattgacaggttgggttgggttggacaag 1391
 Qy 1381 aactgggaagaatgttctgct 1401
 Db 1392 aactgggaagaatgttctgct 1412

RESULT 9
 AAX23022
 ID AAX23022 standard; DNA; 1426 BP.
 XX AAX23022;
 AC AAX23022;
 XX 11-JUN-1999 (first entry)
 DT Fungal phytase gene consensus DNA.
 DE Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food;
 KW feed additive; variant; mutein; feed; pharmaceutical; ds.
 XX Fungi.
 OS
 XX Key Location/Qualifiers
 FH CDS 12..1415
 FT /*tag= a
 FT /product= "phytase"
 XX EP897985-A2.
 XX 24-FEB-1999.
 PD

[illegible]

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Qy	1261	ttggttagagttttggttaacgacagagttgtccattgcacggtttgtggtgttgacaag	1320
Db	1261	ttggttagagttttggttaacgacagagttgtccattgcacggtttgtggtgttgacaag	1320
Qy	1321	ttgggtagatgtaagagagacgacttcgttggaagtttgttcttcgctagatctggtggt	1380
Db	1321	ttgggtagatgtaagagagacgacttcgttggaagtttgttcttcgctagatctggtggt	1380
Qy	1381	aactgggaagaatgtttcgcct	1401
Db	1381	aactgggctgaatgtttcgcct	1401
RESULT 15			
AAAY3290			
ID	AAA/3290 standard; DNA; 1404 BP.		
XX			
AC	AAA73290;		
XX			
DT	05-DEC-2000 (first entry)		
XX			
DE	Consensus phytase 3 thermo 11 Q50T polynucleotide SEQ ID NO:90.		

RESULT 15

AAA73290

ID AAA73290 standard; DNA: 1404 BP.

AC AAA73290:

05-DEC-2000 (first entry)

XX
DE Consensus phytase 3 thermo 11 050T polynucleotide seq ID NO:90.

XX
KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW temperature stability; pH profile; temperature profile; reaction rate;
KW specific activity; substrate specificity; substrate cleavage pattern;
KW substrate binding; position specificity; phytate degradation rate;
KW food; feed; phytate; manure; ds.

OS Synthetic

XX PN WO200043503-A1.

XX
PD
27-JUL-2000

21-JAN-2000: 2000WO-DK00025-XX PF

XX
PR 22-JAN-1999: 99DK-00000092.

PR	21-SEP-1999;	99DK-0001340.
PR	22 JAN 1999;	99DK 0000092.

PA (NOVO) NOVO NORDISK AS.

PI Lehmann M:

AA
DR
WPI: 2000-491161/43.

DR P-PSDB; AAB20531.

Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -

PS Disclosure; Fig 22a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate.

CC The present sequence encodes a phytase sequence from the present
XX invention.

SQ Sequence 1404 BP; 330 A; 320 C; 302 G; 452 T; 0 other;

Query Match 93.7%; Score 1313; DB 21; Length 1404;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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QY 61 gccctgggtcctcggtgtaattctcaactctgtgacactgttgacggtgtaccatgt 120
DB 61 gccctgggtcctcggtgtaattctcaactctgtgacactgttgacggtgtaccatgt 120

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DB 121 ttccagaaatttctcaactgtgggttcaatactctccattctctctcttcttggctgacgaa 180

QY 181 tctgctatttctcagacggttccaaaggtttagagttaacttcttcgaagttttgtct 240
DB 181 tctgctatttctcagacggttccaaaggtttagagttaacttcttcgaagttttgtct 240

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DB 241 agacacggtgctagatataccaaactctctaaagtctaagtagtactctgctttgattgaa 300

QY 301 gctattcaaaaagacgctactgctttcaagggttaagtagtactcttcttgaagacttaaac 360
DB 301 gctattcaaaaagacgctactgctttcaagggttaagtagtactcttcttgaagacttaaac 360

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DB 361 tacactttgggtgctgacgactgaactccattccgtgtaacaaataaggttaactctggt 420

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QY 541 aagttgctgacccaggtgctaaaccaacacccaagcttctccagttataacgttattatt 600
DB 541 aagttgctgacccaggtgctaaaccaacacccaagcttctccagttataacgttattatt 600

QY 601 ccagaaggtgctggtttacaacaacactttggaccacggtttgtgactgctttcgaagaa 660
DB 601 ccagaaggtgctggtttacaacaacactttggaccacggtttgtgactgctttcgaagaa 660

QY 661 tctgaattgggtgacgacgcttgaagctaaacttcaactgctgttttgcgtccacattattaga 720
DB 661 tctaccctaggtgacgacgcttgaagctaaacttcaactgctgttttgcgtccacattattaga 720

QY 721 gctagattggaagctcaacttgcagaggtgttaacttgaactgacgaagacgttgttaacttg 780
DB 721 gctagattggaagctcaacttgcagaggtgttaacttgaactgacgaagacgttgttaacttg 780

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Job time: 916 sec

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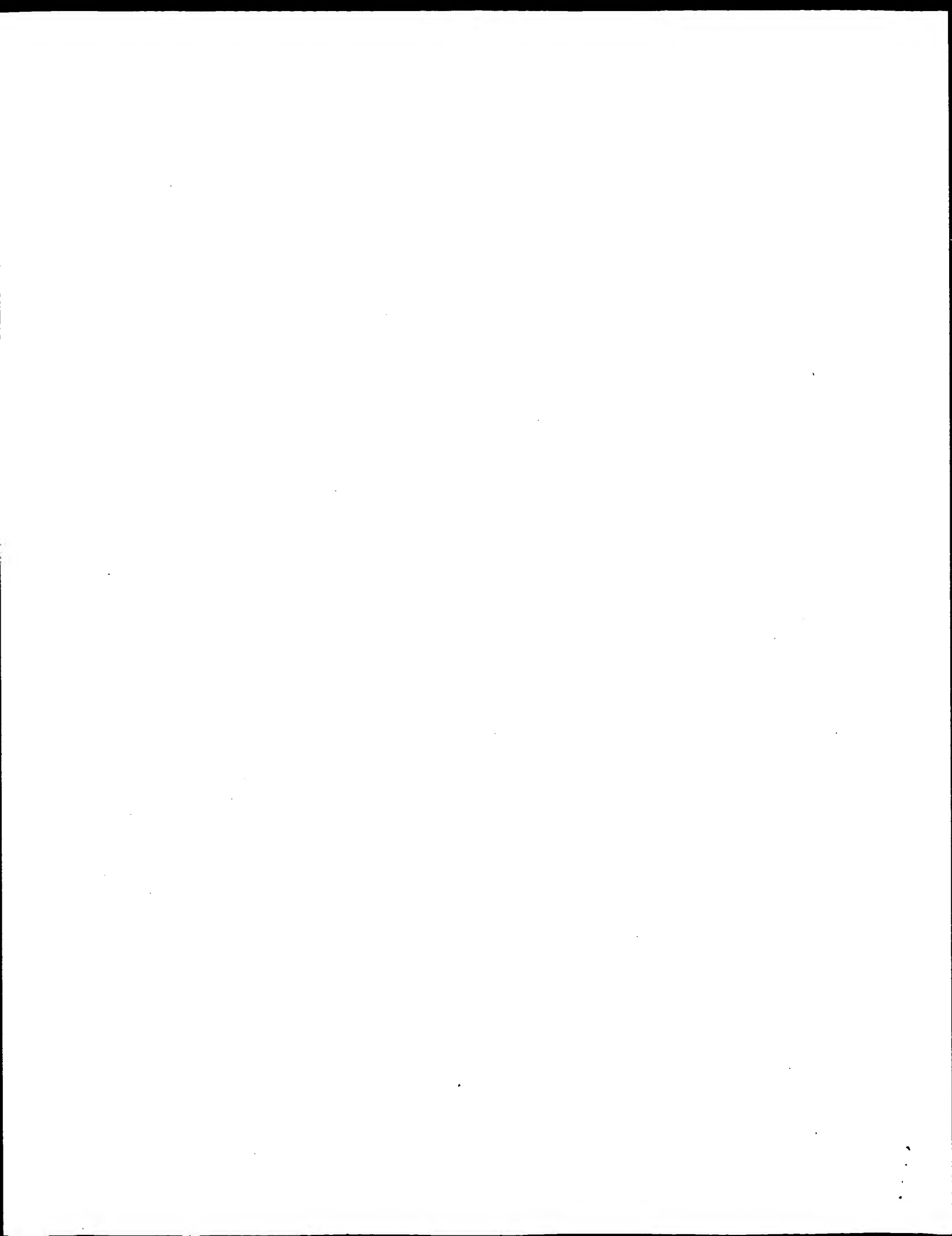
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QY 1381 aactggggaagaatgtttcgtct 1401
DB 1381 aactggggtgaatgtttcgtct 1401
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 15:45:00 ; Search time 12806.7 Seconds
(without alignments)
1692.110 Million cell updates/sec

Title: US-09-488-265-25_COPY_12_1412
Perfect score: 1401
Sequence: 1 atgggcgtgttcgtcgtct.....actgggaagaatgttcgct 1401

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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95: gb_rod:*
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98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1317.8	94.1	1426	9	AX021809
2	787.8	56.2	1350	56	AF295325
3	620.2	44.3	1404	9	AF295325 Synthetic
4	620.2	44.3	1404	10	AF295325 Synthetic
5	620.2	44.3	1404	10	AF295325 Synthetic
6	616.2	44.0	2000	13	AF295325 Synthetic
7	616.2	44.0	2363	9	AF295325 Synthetic
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RESULT 2
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 VERSION AF295325.1 GI:10732782
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 synthetic construct.
 artificial sequence.
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 Yang, L., Chen, Z., Bei, J., Liao, L. and Wang, X.
 Synthetic sequence of phytase gene for expression in *Pichia*
pastoris
 Unpublished
 2 (bases 1 to 1350)
 Chen, Z.
 Direct Submission
 Submitted (11-AUG-2000) Animal Science Institute, Guangdong Academy
 of Agricultural Sciences, Guangzhou, Guangdong 510640, China
 3 (bases 1 to 1350)
 Yang, L., Bei, J., Liao, L. and Wang, X.
 Direct Submission
 Submitted (11-AUG-2000) Biopharmaceutical Center, Zhongshan
 University, Guangzhou, Guangdong 510275, China
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BASE COUNT
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KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1404)
 AUTHORS Van Ooijen, A.J.J., Rietveld, K., Hoekema, A., Pen, J., Sijmons, P.C., and Verwoerd, T.C.
 TITLE Expression of phytochrome in plants
 JOURNAL Patent: US 5593963-A 19 14-JAN-1997;
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 source 1..1404
 BASE COUNT 293 a 436 c 344 g 331 t
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Query Match 44.38; Score 620.2; DB 10; Length 1404;
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 QY 121 tcccagaaatttcactgtgggtgcaataactctcattctctcttctggtgacgaa 180
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RESULT 6
 ANPHYAG A.niger phyA gene.
 LOCUS 216414
 DEFINITION 216414.1 GI:2392
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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Aspergillus niger.
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 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 REFERENCE 1 (bases 1 to 2000)
 AUTHORS van Hartingsveldt, W., Van Zeijl, C.M.J., Harteveld, M.G., Gouka, R.J., Suykerbuyk, M.E.G., Luiten, R.G.M., Van Paridon, P.A., Sellen, G.C.M., Veenstra, A.E., Van Gorcom, R.F.M. and Van Den Hondel, C.A.M.J.
 TITLE Cloning, molecular characterization and overexpression of the
 phyA gene (phyA) of Aspergillus niger
 JOURNAL Gene (1992) In press
 REFERENCE 2 (bases 1 to 2000)
 AUTHORS van Hartingsveldt, W.
 TITLE Direct Submission
 JOURNAL Submitted (05-OCT-1992) Van Hartingsveldt W., TNO Medical
 Biological Laboratory, Lange Kleiweg 139, Rijswijk, The Netherlands
 FEATURES
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BASE COUNT 463 a 603 c 456 g 478 t
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Query Match      44.08; Score 616.2; DB 13; Length 2000;
Best Local Similarity 65.28; Pred. No. 2.4e-152;
Matches 906; Conservative 0; Mismatches 483; Indels 0; Gaps 0;

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DB 384 TCGAATAATCAATCCAGTTGGGATACGGTCGATCAGGGGTATCAATGCTTCCGAGACT 443
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DB 444 TCGCATCTTTGGGGTCAATACGACCGCTTCTCTCTGGAACGAAGTATCGGTATCTCC 503
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QY 193 ccagacgttccaaaggggttagagttacttcttcaagtttctctagacacggtgct 252
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RESULT 7

AR018076

LOCUS

AR018076

Sequence

7 from patent

US 5780292.

AR018076

AR018076.1

GI:3973679

2363 bp

DNA

PAT

05-DEC-1998

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 2363)

AUTHORS

Nevalainen, H.K.M., Paloheimo, M.T., Miettinen-Oinonen, A.S.K.,

Torkkeli, T.K., Cantrell, M., Piddington, C.S., Rambousek, J.A.,

Turunen, M.K., and Fagerstrom, R.B.

TITLE

Production of phytate degrading enzymes in trichoderma

JOURNAL

Patent: US 5780292-A 7 14-JUL-1998;

FEATURES

Location/Qualifiers

1..2363

/organism="unknown"

BASE COUNT 559 a 732 c 510 g 562 t

ORIGIN

Query Match 44.0%; Score 616.2; DB 9; Length 2363;

Best Local Similarity 65.2%; Pred. No. 2.4e-152;

Matches 906; Conservative 0; Mismatches 483; Indels 0; Gaps 0;

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8

AR051916

LOCUS

AR051916

DEFINITION

Sequence 7 from patent US 5830733.

ACCESSION

AR051916

VERSION

AR051916.1

KEYWORDS

GI:5975280

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 2363)

AUTHORS

Nevalainen, H.K.M., Paloheimo, M.T., Miettinen-Oinonen, A.S.K.,

Torkkeli, T.K., Cantrell, M., Piddington, C.S., Rambousek, J.A.,

Turunen, M.K., Fagerstrom, R.B. and Houston, C.S.

Nucleic acid molecules encoding phytase and ph2.5 acid phosphatase

Patent: US 5830733-A 7 03-NOV-1998;

Location/Qualifiers

1..2363

/organism="unknown"

BASE COUNT 559 a 732 c 510 g 562 t

ORIGIN

Query Match 44.0%; Score 616.2; DB 9; Length 2363;

Best Local Similarity 65.2%; Pred. No. 2.4e-152;

Matches 906; Conservative 0; Mismatches 483; Indels 0; Gaps 0;

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 DEFINITION L02421.1 GI:166518
 phytase.

ACCESSION L02421.1
 VERSION L02421.1
 KEYWORDS Aspergillus niger (strain ALK0243, sub-species awamori) DNA.

ORGANISM Aspergillus niger

REFERENCE 1 (sites)
 AUTHORS Piddington,C.S., Houston,C.S., Paloheimo,M., Cantrell,M.,
 Miettinen-Oinonen,A., Nevalainen,H. and Rambosek,J.

TITLE The cloning and sequencing of the genes encoding phytase (phy) and
 pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.

JOURNAL awamori
 MEDLINE Gene 133 (1), 55-62 (1993)
 REFERENCE 94040796
 2 (bases 1 to 2379)

AUTHORS Carter,J.R., Franden,M.A., Aebersold,R.H. and McHenry,C.S.
 TITLE Molecular cloning, sequencing and overexpression of the gene
 encoding the psi subunit of E. coli DNA polymerase III holoenzyme

JOURNAL Unpublished (1992)
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 BASE COUNT 561 a 735 c 518 g 565 t

ORIGIN

Query Match 44.0%; Score 616.2; DB 13; Length 2379;
 Best Local Similarity 65.2%; Pred No. 2.4e-152;
 Matches 906; Conservative 0; Mismatches 483; Indels 0; Gaps 0;

Qy 13 gtcgtgctacttgccattgcoacttggcttgcgttccacatccgggtaccgcttgggtct 72
 Db 534 GTGGGACTACTGATCGCTGACAACTGTCGAGAGTCACCTCGGACTCGGAGTCCCGCC 593

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QY 373 gctgacgactgactccattcggtgaacaaataagtttaactctggtatttaagttctac 432

Db 894 GCAGTACCTGACTTCTTCGAGAGCAGGAGCTAGTCAACTCCGGCATCAAGTTCTAC 953

QY 433 agaagatacaaggcttggctagaagaattgttccattcgttagagcttctgcttctgac 492

Db 954 CAGGATACCAATCGCTCACAGGACATCATTTCCGTTTATCCGATCCCTGCTGCCACG 1013

QY 493 agagttattgcttctgctgaaggttcaatgaaggttccaatctgctgaagttggctgac 552

Db 1014 CGGTGATCGCTCCCGCGAGAAATTCATTGAGGGCTTCCAGAGCACAAGCTGAAGGAT 1073

QY 553 ccaggtgctaacccacacacagcttccagttatttaagttatttaccagaagtgct 612

Db 1074 CTCGTGCCCGCGGCCAATCGTCCCAAGATCGAGCTGTGTCATTTCCGAGGCCAGC 1133

QY 613 ggttacacaacacttggaccaggttggctgactgcttctgaagaatctgaattgggt 672

Db 1134 TCATCCAAACAACTCTCGACCCAGGACCTGCATCTTCTTGAACAGACGAATTTGGCC 1193

QY 673 gacgaogttgaacttaacttactgctgttcttctgctccactattagagctagattggaa 732

Db 1194 GATACCGCTGAAGCAATTTACCGCCACGTTCCGCCCTCCATTCGTAACGCTCGGAG 1253

QY 733 gctcactgacaggttaactgactgacgaagaagctgttgaactgtgacatgtgt 792

Db 1254 AAGCACTGTCTGGGTGACTCTCACAGACACAGAAGTGAACCTTACCTCATGTGACATGTGC 1313

QY 793 ccattgacactgtgtgtagaacttctgacgtactcaattgtctcattctgactgactg 852

Db 1314 TCCTTCGACACCATCTCCACCACCGTCGACACCAAGCTGTCCCTCTCTGTGACCTG 1373

QY 853 tcaactacagaagaatgattcaactacgactactgcaatcttgggtgaagtactacgt 912

Db 1374 TTCACCATGACGAATGGATCCACTACGACTACCTCCAGTCCCTGAAAAAATACTACGGC 1433

QY 913 tacggtgctgtaaacccattgggtccagctcaaggtgttgggttctgaacgaattgatt 972

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QY 973 gctagattgactcactctccagttcaagacacacacttctactaacacacacttggactct 1032

Db 1494 GCCGTCTCACCCACTCGCTGTCCAGATGATACACACGCTCAACACACACTTGGACTCG 1553

QY 1033 aacccagctacttcccattgaacgctactttagtgaacttctctcagcaacact 1092

Db 1554 AACCCAGCTACCTTCCCGCTCAACTCTACTCTACGCGGACTTTTCCACGACATAAGCGC 1613

QY 1093 atgggttctatttctgcttgggttggtagaagcgttacttaagccattgtctactact 1152

Db 1614 ATCATCTCTATCTCTTGTCTTGGGTCTGTACAAAGGACACTAAAGCCGCTGTCTACCGAG 1673

QY 1153 tctgttgaattctattgaagaactgacggttacgctgcttctgactgttccattcgtct 1212

Db 1674 ACCGTGAGAAATATACCCAGACAGATGGTCTCTCTCTGTGGACGCTCCGTTTGTCT 1733

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Db 1734 TCGCGTCTGTACGTCGAGATGATGCAAGTCCAGGGCGGACGAGGCGGCTGTCTCCGTGTC 1793

QY 1273 ttggttaacagacagaggttggccattgacagcgttggtagtggtagatgt 1332

Db 1794 TTGGTTAATGATCGCGTTTCCTCCGCTGCATGGGTTCCTCAATTCGCTTTGGGAGATGT 1853

QY 1333 aagaagacgacttctgtagaaggttcttctcagatctggtgtaactgggaagaa 1392

Db 1854 ACCCGGATAGCTTGTGAGGGGTGAGCTTTGTAGATCTGGGGGTGATTGGCGGAG 1913

QY 1393 tgttctgct 1401

Db 1914 TGTCTGCT 1922

RESULT 11

ASNPHYTASE 2665 bp DNA PLN 27-APR-1993

LOCUS Aspergillus niger myo-inositol hexaphosphate phosphohydrolyase gene, complete cds.

DEFINITION M94550

ACCESSION M94550.1 GI:166520

VERSION myo-inositol hexaphosphate phosphohydrolyase; phytase.

KEYWORDS Aspergillus niger (library: EMBL 3; NRRL 3135) DNA.

SOURCE Aspergillus niger

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

REFERENCE 1 (bases 1 to 2665)

AUTHORS Mullaney,E.J., Gibson,D.M and Ullah,A.H.

TITLE Positive identification of a lambda gt11 clone containing a region of fungal phytase gene by immunoprobe and sequence verification

JOURNAL Appl. Microbiol. Biotechnol. 35, 611-614 (1991)

MEDLINE 92000601

REFERENCE 2 (bases 1 to 2665)

AUTHORS Mullaney,E.J.

TITLE Sequence of the Aspergillus niger (ficus) phytase gene

JOURNAL Unpublished (1992)

FEATURES

Location/Qualifiers

source 1..2665

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/db_xref="taxon:5061"

/tissue_lib="EMBL 3; NRRL 3135"

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intron 727..828

exon 829..2188

mat_peptide 842..2176

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/EC_number="3.1.3.8"

/function="catalyzes the hydrolysis of phytic acid"

/product="myo-inositol hexaphosphate phosphohydrolyase"

BASE COUNT 633 a 808 c 574 g 650 t

ORIGIN

Query Match 44.0%; Score 616.2; DB 13; Length 2665;

Best Local Similarity 65.2%; Pred. No. 2.5e-152;

Matches 906; Conservative 0; Mismatches 483; Indels 0; Gaps 0;

QY 13 gtcgtgactgtccattgacaccttctgctgttccacatcccggtaccgcttggtcct 72

Db	797	GTGGGACTACTGATCGCTGACTATCTGTGCGAGCTCACTCCGACATGGCAGTCCCGGCC	856
Qy	73	cgfsgtaattctcaactcttgtaacactgttaacggtggttaaccaatgtttccagaaatt	132
Db	857	TCGAGAAATCAATTCAGTTGCGATACGGTCGATCAGGGGTATCAATGCTTCTCCGAGACT	916
Qy	133	tctcacttgtgggtgcaatcactctccattctctctctttggctgacgaatctgctattct	192
Db	917	TCGCATCTTTGGGTCAATACCGACCGTCTCTCTCTGGCAACGGAATCGGTCACTCC	976
Qy	193	ccagacggttccaaaggtgtagattactttcgttcaagtttttgtctagacacggtgct	252
Db	977	CCTGAGGTGCCCGGATGCAGATCACTTTGGCTCAGGTCCCTCCCGTCATGGAGCG	1036
Qy	253	agatacccaacttcttaagttcaagaagtactctggttgattgaagctattccaaag	312
Db	1037	CGGTATCCGACCGACTCCAAAGGCAAGAAATACTCCGCTCTCATTTAGGAGATCCACGAG	1096
Qy	313	aacgctactgctttcaagsgttaagtcagctttcttgaaagacttacaactacaactttgggt	372
Db	1097	AACGCCACCACCTTTGCAGGAAATATGCCCTCTCTGAAGACATACACTACAGCTTGGGT	1156
Qy	373	gctgacgaattgactccattctgggtgaacacaaatgggttaactctggttataagtctac	432
Db	1157	GCAGATGACTGACTCCCTTCGGAGAACGAGGAGCTAGTCAACTCCGGCATCAAGTTCTAC	1216
Qy	433	agaagatacaaggcttggctagaagaattgttccattcgtagagcttctggtttgac	492
Db	1217	CAGCGGTACGAATCGCTCAACAGGAACATCGTTTCATTTCATCCGACTCTTGGCTCCAGC	1276
Qy	493	agagttatgtctctgctgaagaagttcatgtgaagtttcccaatctgctaaagttgctgac	552
Db	1277	CGCGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGCACCAGCTGAAGGAT	1336
Qy	553	ccaggtgctaacccacacacaaagcttctccagttataacgttattattccagaaggtgct	612
Db	1337	CCTCGTGCACGCCCGCCAAATCGTCCGCCAAGATCGACGTGGTCAITTCGAGGCCAGC	1396
Qy	613	ggttaacacacacacttggacacaggtttgtactgcttccagaagaatctgaattgggt	672
Db	1397	TCATTCACAAACACACTTCGACCGAGGCACCTGCATCTGTTTCGAAGACAGCGAAATGGCC	1456
Qy	673	gacgacgttgaagctaaactcactgctgttttcgctccactattagagctagattggaa	732
Db	1457	GATACCGTCGAGGCCAATTTTACCCGCCAGGTTCGTCCCTCCATTCGTCAACGCTCGAG	1516
Qy	733	gctcacttccagggtgttaacttgactgacgaagacgltgttaactgatggacatggt	792
Db	1517	AACGAGCTGTCCGGTGTGACTCTCAGACACAGAAAGTACCTACCTATGSGACATGTC	1576
Qy	793	caattgacacactgtgtgagaactctgaagctactcaattgtctccattctgtgacttg	852
Db	1577	TCCTTTTCGACACCATCTCCACACGACCGTCGACACCAAGCTGTCCCCCTTCTGTGACCTG	1636
Qy	853	ttcaactcacgacgaatggattcaatacagactacttgcaactctttgggttaagctactacgtt	912
Db	1637	TTCACCCATGACGAATGGATCAACTACGACTACCTTCCAGTCTTCTTGAAAAAGATTACGGC	1696
Qy	913	tacggtgctgggttaaccatttgggtccagctcaaggtgttggtttcgttaacgaattgatt	972
Db	1697	CATGGTGCAGGTAACCCGCTCGGCCCGACCCAGGGCGTGGCTACGCTAACGAGCTCATC	1756
Qy	973	gctagattgactcaactctccagttcaagacacacacttctactaacacacactttggactct	1032
Db	1757	GCCCGTCTGAOCCACTCGCGCTCTGCACGATGACACAGCTTCCAACCCACACTTTGGACTCG	1816
Qy	1033	aacccagctactttccatttgaacgctactttgtacgctgacttctctcacgacacact	1092
Db	1817	AGCCCGGCTACCTTTCCGCTCAACTCTACTCTTACGCGGACTTTTTCGATGACACCGC	1876
Qy	1093	atgggttctattttcttggctttgggtttgtacaacggtactaagccaattgtctactact	1152

Db	1877	ATCATCTCCATTCTCTTTGCTTGTGTTACAGTCTGTGTACAACGGCAGCTAAGACCGCTATCTACACAG	1936
Qy	1153	tctgtgaactctattgaagaaactgacggttacgctgcttcttggaactgtccattcgct	1212
Db	1937	ACCGTGGAGAAATATACCCAGACAGATGGAATCTCGTCTGCTTGGACCGTTCGGTTGCT	1996
Qy	1213	gctagagcttacgttgaataatgatgcaatgtgaagctgaaaaaggaaccatttggttagagct	1272
Db	1997	TCGGTGTGTACGTCGAGATGATGCAGTGTCAAGCGGAGCAGGACCGCTGGTCCGTGTC	2056
Qy	1273	tgggttaacgacagagttgttcattcgacggttggtggttggttgacaagtgggttagatgt	1332
Db	2057	TTGGTTAATGATCGCGTGTCCCGCTGCATGGGTGTCCGSGTTGATGCTTTGGGGAGATGT	2116
Qy	1333	aagagacacgactcttgaaggtttgtcttcgctagatctggtggttaactgggaagaa	1392
Db	2117	ACCGGGATAGCTTTGTGAGGGGTTTGACCTTTGCTAGATCTGGGGGTGATTGGCGGAG	2176
Qy	1393	tgttctgct 1401	
Db	2177	TGTTTGTCT 2185	
RESULT	12		
LOCUS	A19451		
DEFINITION	phytase gene locus of plasmids pAF 2-3, pAF 2-6, pAF 2-7.		
ACCESSION	A19451		
VERSION	A19451.1	GI:583193	
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct.		
ORGANISM	artificial sequence.		
REFERENCE	1 (bases 1 to 6756)		
AUTHORS	van Gorcom,R.F.M., van Hartingsveldt,W., van Paridon,P.A., Veenstra,A.E., Luiten,R.G.M. and Seltien,G.C.M.		
TITLE	Cloning and expression of microbial phytase		
JOURNAL	Patent: EP 0420358-A 40 03-APR-1991;		
	GTT-BROCADES N.V.		
FEATURES	Location/Qualifiers		
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exon	210..254		
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	SGSRVIAKGGKFIIEGFSQTKLPDRAQPGQSPKIDWTSEASSNNTLDPGTIS		
	ESESLADTVEANFTATFVPSIKORLENDLSGVTITDTEVYLMDCSFDITST		
	KLSPCDGLFTHDEWNIYDLSKKYYGHGAGNPLGPTQGVGVANELIARLTHS		
	DYSSNHTLDSSPATFLYVLENDLIYADFSDNGIISILFALGYNLTKYKLSLTTVEN		
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BASE COUNT	1615 a 1712 c 1712 g 1714 t		3 others

ORIGIN

Query Match 44.0%; Score 616.2; DB 9; Length 6756;
Best Local Similarity 65.2%; Pred. No. 2.6e-152;
Matches 906; Conservative 0; Mismatches 483; Indels 0;

Qy	13	gtcgtgctactgtccattgccaaccttctcgtgttccacatcccggtaccgctctgggtcct	72
Db	324	GTGGGACTACTACGCTGACTATCTTGTGAGAGTCACTCCGAGCTGGCAGTCCCGCGC	383
Qy	73	ctgtgtaattctcactctgtgacactgtgacggtggttaccaaatttcccagaaatt	132
Db	384	TCGAGAAATCAATCCAGTTGCGATACGGTCAATCAGGGGTATCAATGCTTCTCCGAGACT	443
Qy	133	tctcaacttgggggtccaaactctccattcttctcttcttgggtgacgaatctgtatttct	192
Db	444	TCGCATCTTTGGGGTCAATACGACCGTCTCTCTCTGCGCAACGAATCGGTCACTCC	503
Qy	193	ccagacgttccaaaagggtgtagagttaacttctgccaagtgttccaaatttctcagacacggtgc	252
Db	504	CCYGAGTGGCCGGATGCGAGATCACTTTCGTCTAGGTCCCTCCCGTCAATGAGCG	563
Qy	253	agatacccaactctctaagtctaaagaactctgctgtgttgattgaagctatttccaaaag	312
Db	564	CGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCGCTCTCAATGAGGAGATCCACGAC	623
Qy	313	aacgtactgcttccaagggttaagtacgcttcttcttgaagacttcaactacacactttgggt	372
Db	624	AACCGACCACTTTTCAGCGAAATATGCTTCTCTGAAGACATACAACACTACAGCTGGGT	683
Qy	373	gctgacgaactgactccattcgggtgaacacacaaatggttaactctggtattaaagtctac	432
Db	684	GCAGATGACCTGACTCCCTTCGGAGAACAGGAGCTAGTCACTCGGCGATCAAGTCTTAC	743
Qy	433	agaagatacagaagcttgggtgagaagattgttcattctgttagagcttctggttctgcac	492
Db	744	CAGCGGTACGAATCGGTCAACAGGAACATCGTTTCCATTCATCCGATCCTTGGCTCCAGC	803
Qy	493	agagttaattctctgtcaaaagttcattgaagtttccaatctgctaagttggtgcac	552
Db	804	CGCGTGATCGCTTCCGGCAGAAATTCATCGAGGGCTTCCAGAGCACCAAGCTCAAGGAT	863
Qy	553	ccaggtgtcaaccacacacgaactctccagttattaaactgtattattccagaagagtgct	612
Db	864	CCTGTCGCCAGCGCGCCAAATCGTCGCCAAGATCGACGTGGTCAATTCCTGAGGCGCAGC	923
Qy	613	ggttacacaaacatttggaccacggttgtgtactgctgttcgaagaactcgaattgggt	672
Db	924	TCATCCAAACAACTCTCGACCGACGACCTGCATCTGTTTGGAGACAGCGGAATGGCC	983
Qy	673	gacgaagtgaagtaacttcaactgctgttttcgctccacactattagagctlagattggaa	732
Db	984	GATACCGTCGAGGCCAATTTACCGGCCAGTTCGTCTCCCTCCATTCGTCAACGCTGGAG	1043
Qy	733	gctcaattgccaggtgttaacttgcactgcacgaagcgttgtttaacttgatggacatggt	792
Db	1044	AACGACCTGTCCGGTGTGACTCTCAGACACACAGAAGTGACCTACTCATGAGCATGTGC	1103
Qy	793	ccattcgaactgttctagaactctcgaagctactcgaattgtctccactctgtgacttg	852
Db	1104	TCTTTCGACACCATCTCCACACACCGTCGACACCAAGCTGTCCCCCTTCTGTGACCTG	1163
Qy	853	ttoactcacgacgaatgattcaatacgaactacttgcacttcttgggttaagtaactacggt	912
Db	1164	TTCACCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTGAAAAAGATTATAGGC	1223
Qy	913	tacggtgctgtaaccattgggtccagctcaaggtgttggttctgttaacgaattgatt	972
Db	1224	CATGTTGCAGTAACTCCGCTTCGGCCGACCCAGGGCGTCGGGTACGCTAAGCAGCTCATC	1283
Qy	973	gctagattgactcactctccagtttcaagacacacacttctactaaacacactttgactct	1032

Db	1284	GCCGCTGTGACCACACTCGCTCTCCACGATGACACCAAGTTCACACCACTTTGGACTCG	1343
Qy	1033	aaccagctactttccattgaacgctactttgtacgctgacttctctcacgacaacact	1092
Db	1344	AGCCCGGCTACCTTTCCGTCACACTCTACTCTACGGGACTTTTCGCATGACACGGC	1403
Qy	1093	atggttctattttcttgcctttgggtttgtacaacggtactaaagccattgtctactact	1152
Db	1404	ATCATCTCCATCTCTTTGCTTAGGTCTGTACACGGCACTAACCCGCTATCTACCACG	1463
Qy	1153	tctgttgaaacttatgtgaagaaactgacggttacgctgtctcttggactgttccattcgct	1212
Db	1464	ACCGTGGAGAAATATACCCAGACAGATGGATTCTCGTCTGCTTGGACGTTCCGTTTGCT	1523
Qy	1213	gctagagcttacgtttgaaatgatgcaatgtgaagctgaaaaggaaccattggttagagtt	1272
Db	1524	TCGGTTTGTGACGTCGAGATGATGCAGTGTACGGCGGACAGGAGCCGTGGTCCGTGTC	1583
Qy	1273	ttggttaacgacagagttgttccattgcacggttgtggttggtgacaagttgggttagatgt	1332
Db	1584	TTGGTTAATGATCGCGTTGTCCCGCTGCATGGGTGTCGCGTTTGATGCTTTGGGGAGATGT	1643
Qy	1333	aagagagacgactcttgtaaggtttgtctttcttcgttagactctggttggttaactgggaaaga	1392
Db	1644	ACCCGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTTAGATCTGGGGGTGATTGGCGCGG	1703
Qy	1393	tggttcgct	1401
Db	1704	tggttttgct	1712

RESULT 13

I13429	LOCUS	I13429	6756 bp	DNA		PAT	26-JUL-1995
DEFINITION	Sequence 31 from patent US 5436156.						
ACCESSION	I13429						
VERSION	I13429.1						
KEYWORDS	GI:910770						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	Unclassified.						
AUTHORS	1 (bases 1 to 6756)						
TITLE	Van Gorm, R.F.M., Van Hartingsveldt, W., Van Paridon, P.A.,						
	Veenstra, A.E., Luiten, R.G.M. and Selten, G.C.M.						
	Cloning and expression of phytase from aspergillus						
FEATURES	Patent: US 5436156-A 31 25-JUL-1995;						
	Location/Qualifiers						
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BASE COUNT	1615	a	1714	c	1712	g	1715 t
ORIGIN							

Query Match	44.0%	Score	616.2	DB	10	Length	6756
Best Local Similarity	65.2%	Pred. NO.	2.6e-152				
Matches	906	Conservative	0	Mismatches	483	Indels	0
						Gaps	0

Qy	13	gtcgtgctactgtccattgccacattgttgccacattccacatccgcgtacccgcttgggtgct	72
Db	324	GTGGGACTACTGATCGCTGACTATCTGTGCAGAGTCACCTCCGACCTGGCAGTCCCGGCC	384
Qy	73	cgtggttaattctactcttctgtgacacitgttgacaggtgtgtaccaatgttttcccagaatt	132
Db	384	TCGAGAAATCAATCCAGTTGGCATACGGTCGATCAGGGGTATCAATGCTTCTCGAGACT	444
Qy	133	tctcaacttgtgggttcaatactctccattctctcttggctgcagaaatctgctatttct	192
Db	444	TCGCATCTTTGGGGTCAATACGCACCGTTCTCTCTCTGGCAACGAATCGGTCACTCC	504
Qy	193	ccagacgttccaaagggtgttagatgttactttgttccaaagtttgtctagacacggtgtct	252
Db	504	CTGAGGTGCCGCGGATGCAGAGTCACTTTGCTCAGTGCCTCTCCGCTCATGAGACG	564

QY	253	agataccaacttcttaagctctaaagtaactctgtcttggattgaagctattctaaag	311
DB	564	CGGTATCCGACCGACTCCAAAGGGCAAGAAATACTCCGCTCTCATTTGAGGAGATCCAGAG	623
QY	313	aacgtactgtcttcaagggttaagtacgtttttgaagactacaactacactttgggt	372
DB	624	AACGGGACCACTTTGACGGAAATATGCGCTTCTGAAGACATATCAACTATACAGCTTGGGT	683
QY	373	gctgacgacttgactccattcggtagaacaacaatggttaactctgttattaaagttctac	432
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QY	433	agaagatacaagggttggctagaaagattgttccattogttagaactctctgtttctgac	492
DB	744	CAGCGGTACGAATCGCTACAAAGGAACATGTTCCATTATCCGATCCCTTGCTCCAGC	803
QY	493	agagattatgtctgtgaaagttcaattgaagggtttccaaactctgtctaagtgtgctgac	552
DB	804	CCGTGTATCGGCTCCGGCAGAAATTCATCAGGGGTTCCAGAGCACCAGCTGAAGAT	863
QY	553	ccaggtgtcaaccacacccaaggtcttccaagttattaaagttattattccagaagtgct	612
DB	864	CCTCGTCCGACGCCGCCAATCGTCCGCCAAAGATCGAGTGGTGTATTTCGAGGCCACG	923
QY	613	ggttaacaacaacttggaccacggttgtgtactgctttcgaagaactctgaattgggt	672
DB	924	TCATCCAACAACACTCGACCCAGGCACCTGCACCTGTCTTCCGAGACAGCGAATTGGCC	983
QY	673	gacgactgaagctaacttcaactgctgttttgcgtccactattagagtagattgaa	732
DB	984	GATACCGTCGAAGCCAATTTACCGGCCAGGTTGTCGCCCTCCATTTCGTAACGCTGGAG	1043
QY	733	gtcacttgcaggtgttaacttgactgacgaagacgtttgtaactgtatgagcaattgt	792
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QY	793	ccattgacactgtgtagaactcttgacgtactcaattgtctccactctgtgacttg	852
DB	1104	TCTTTCGACACCATCTCCACGACCGTCGACACCAAGCTGCCCTTCTGTGACCTG	1163
QY	853	ttcactcacgaacttgattcaatcacgactacttgcattgtttgggttaagtactacggt	912
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RESULT 14
AX000634
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DEFINITION Sequence 5 from Patent EP0897010.
ACCESSION AX000634
VERSION AX000634.1 GI:7241015
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Van,L.A. and Wyss,M.
TITLE Modified phytases
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